

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
10 January 2002 (10.01.2002)

PCT

(10) International Publication Number
WO 02/02055 A2

- (51) International Patent Classification⁷: **A61K** [IN/US]; 250 Buckminster Drive, Apt. 105, Norwood, MA 02062 (US). ZHU, Shuhao [CN/US]; 301 Lincoln Street, Waltham, MA 02451 (US). LONG, Fan [CN/US]; 51-10 Garden Circle, Waltham, MA 02452 (US). DAVIDOV, Eugene [US/US]; 3 Linwood Road, Natick, MA 01760 (US). THOMPSON, Craig, M. [US/US]; 15 College Avenue, Arlington, MA 02474 (US).
- (21) International Application Number: PCT/US01/20592
- (22) International Filing Date: 28 June 2001 (28.06.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/215,164 29 June 2000 (29.06.2000) US
60/224,457 10 August 2000 (10.08.2000) US
- (71) Applicant (for all designated States except US): **ANADYS PHARMACEUTICALS, INC.** [US/US]; 610 Lincoln Street, Waltham, MA 02451 (US).
- (72) Inventors; and
- (73) Inventors/Applicants (for US only): **MOORE, Jeffrey** [US/US]; 20 Chappel Street, Apt. A307, Brookline, MA (US). **BUURMAN, Ed, T.** [NL/US]; 122 Warren Street, Arlington, MA 02474 (US). **DESILVA, Thamare** [US/LK]; 37 St. Mary's Street, Apt. 4, Brookline, MA 02215 (US). **HARRIS, Sandra** [US/US]; 356 Ridge Road, Apt. 18, Dayton, NJ 08810 (US). **KOMARNITSKY, Svetlana** [RU/US]; 317 Tappan Street, Apt. 4, Brookline, MA 02445 (US). **MENDILLO, Marc [I]**; 11 Bentley Street, Brighton, MA 02445 (US). **MOORE, Daniel** [US/US]; 191 Boston Avenue, Medford, MA 02155 (US). **MCCOY, Melissa** [US/US]; 17 Marion Road, Arlington, MA 02474 (US). **SANDERSON, Karen** [US/US]; 13 Auburn Street, Charlestown, MA 02129 (US). **HAQ, Tariq**
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SI, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/02055 A2

(54) Title: ANTIFUNGAL COMPOUNDS AND METHODS OF USE

(57) Abstract: The invention provides screening methods for detecting and identifying compounds that bind to fungal specific target proteins and nucleic acids, as well as compounds which, upon binding or otherwise interacting with the target protein, can inhibit fungal growth, a method of preventing or inhibiting fungal growth in culture, a method of preventing or inhibiting fungal growth in a mammal and a method of studying pathogenic mycetes using such nucleic acid and/or protein sequences. Particularly preferred is the inhibition of the fungus *Candida albicans*.

5

10

ANTIFUNGAL COMPOUNDS AND METHODS OF USE**PRIORITY**

This application claims priority under 35 U.S.C. § 119 from Provisional Patent Application Serial Number 60/215,164, filed June 29, 2000, and Provisional Patent Application Serial Number 60/224,457, filed August 10, 2000, which are hereby incorporated by reference in their entireties.

15

FIELD OF THE INVENTION

The invention encompasses the use of fungal cidal targets in the screening for, isolation and development of antifungal chemicals and drugs to be used in the treatment of fungal infections, such as infections with *Candida albicans*. The invention encompasses methods of determining fungal cidal targets. Such fungal cidal targets are encompassed by nucleic acid and protein sequences encoded by such nucleic acid sequences which are isolated from *S. cerviseae*, shown to be present in other fungi such as *Candida albicans*, and are shown to be both essential and fungal specific in both *Sacchromyces cerviseae* and *Candida albicans*. The essential fungal specific nucleic acid and protein sequences may also be used in studying pathogenic mycetes or fungi.

20

25

BACKGROUND OF THE INVENTION

Fungi are a distinct class of microorganisms, of which most are free-living. They are eukaryotic organisms containing a nuclear membrane, mitochondria and endoplasmic reticulum. In addition, they are non-motile, do not contain chlorophyll and develop from spores (*i.e.* yeasts, molds, mushrooms and rusts). The cell structure usually includes a rigid cell wall of mannan, glucan and chitin and a cytoplasmic membrane with a large percentage of ergosterol. The size and morphology of fungi vary from monomorphic yeasts like *Cryptococcus* and *Saccharomyces* species and dimorphic fungi like *Candida albicans* to filamentous fungi like *Aspergillus* species.

In contrast to bacteria, which are generally considered mammalian pathogens, fungi tend to be plant pathogens. However, in addition to the well recognized group of dermatophytes (*e.g.* cause of "athlete's foot"), an increasingly large group of fungi turn out to be able to act as opportunistic human pathogens producing disease only in compromised individuals. As the result of an aging population as well as an increase in the number of immunocompromised patients, *e.g.*, patients with acquired immunodeficiency syndrome (AIDS), patients undergoing cancer chemotherapy, or immunosuppressive therapy (*e.g.* treatment with corticosteroids) and patients undergoing organ transplantation, the incidence of fungal infections is increasing rapidly.

Fungi parasitize many different tissues. Most infections begin by colonization of the skin, a mucosal membrane or the respiratory epithelium. Superficial fungi and subcutaneous pathogens cause indolent lesions of the skin. Passage through the initial surface barrier is accomplished through a mechanical break in the epithelium. Although most fungi are readily killed by neutrophils, some species are resistant to phagocytic killing and can infect otherwise healthy individuals. The most virulent fungi cause systemic infections, a progressive disease leading to deep seated visceral infections in otherwise healthy individuals (see *e.g.* *Sherrie Medical Microbiology, Third Edition*, Kenneth J. Ryan, ed., Appleton & Lange, Norwalk, CT, 1994).

The major fungal pathogens in North America are *Histoplasma capsulatum*, *Coccidioides immitis*, *Blastomyces dermatitidis*, *Cryptococcus neoformans*, *Candida* species, such as but not limited to *Candida albicans* and *Aspergillus* species (*Medically Important Fungi, Second Edition*, Davise H. Larone, Ed., American Society for Microbiology, Washington, D.C.). The yeast *C. albicans* (*C. albicans*) is one of the

most pervasive fungal pathogens in humans. It is the cause of an increasing financial and logistic burden on the medical care system and its providers due to its ability to opportunistically infect a diverse spectrum of immunocompromised hosts, which are a quickly growing population of patients in today's society. Although *C. albicans* is a member of the normal flora of the mucous membranes in the respiratory, gastrointestinal, and female genital tracts, it may gain dominance in such locations (*e.g.* upon treatment with antibacterial antibiotics, in patients with diabetes or in patients using corticosteroids) and be associated with pathologic conditions. In addition, almost all HIV-positive individuals suffer from a *Candida* infection prior to the onset of developing full-blown AIDS.

Sometimes *C. albicans* produces progressive systemic disease, particularly if cell-mediated immunity is impaired. In 1994, about thirty percent of patients suffering from leukemia or undergoing organ transplants developed a systemic *Candida* infection of which thirty percent have been estimated to have succumbed to the infection.

Only a handful of agents are active against fungi. For life threatening disease caused by any of the pathogenic fungi, amphotericin B is the agent of choice. This drug, however, is associated with numerous severe side effects such as fever, dyspnea and tachycardia, and dosage is limited over the lifetime of the patient because of renal toxicity. An agent frequently used concurrently is flucytosine, a nucleoside analog, which cannot be used independently of other agents because of the rapid appearance of resistance. Untoward effects of treatment with flucytosine include leukopenia, thrombocytopenia, rash, nausea, vomiting, diarrhea, and severe enterocolitis.

In conditions where the patient's life is not threatened, ketoconazole can be used as a long-term therapy for blastomycosis, histoplasmosis, or coccidioidomycosis. Fluconazole also has a significant role in the treatment of superficial fungal infections. Both compounds are from the same class, the triazoles, and are cytostatic. The emergence of resistance and hepatic toxicity limits the use of triazoles such as fluconazole and ketoconazole. The newest triazole, itraconazole, has similar pharmacokinetics and spectrum of activity as fluconazole. None of the azoles can be used for life threatening or deep seated fungal infections. They are only effective in reducing colonization of fungi such as *Candida* species and for treating superficial mycoses.

All major antifungal agents function by attacking, either directly or

indirectly, ergosterol, a component of the cell wall. Amphotericin B and other polyene macrolide compounds like nystatin interact with ergosterol in the cell membrane and form pores or channels that increase the permeability of the membrane. Resistance to amphotericin B in mutant strains is accompanied by decreased concentrations of ergosterol in their cell membranes. Imidazoles and triazoles inhibit sterol 14 α -demethylase, a microsomal cytochrome P₄₅₀-dependent enzyme system. Imidazoles and triazoles thus impair the biosynthesis of ergosterol for the cytoplasmic membrane, leading to the accumulation of 14 α -methyl sterols, which impair certain membrane-bound enzyme systems (see, *The Pharmacological Basis of Therapeutics, Eighth Edition*, Goodman and Gilman, Pergamon Press, 1990).

Nystatin, amphotericin B, flucytosine and the various azoles have all been used to treat oral and systemic *Candida* infections. However, orally administered nystatin is limited to treatment within the gut and is not applicable to systemic treatment, and resistance to flucytosine is so widespread that it is only used in combination with other drugs. Some life-threatening systemic infections are susceptible to treatment with the azoles or amphotericin B. Azoles have been the most successful drugs used for treatment of such infections in the last few years but they work relatively slowly, have to be taken for months, and are fungistatic rather than fungicidal. While such azole antifungal agents exhibit significantly lower toxicity compared to amphotericin B, their mechanism of action and inactivation of cytochrome P₄₅₀ prosthetic groups in certain enzymes preclude their use in patients that are simultaneously receiving other drugs that are metabolized by the body's cytochrome P₄₅₀ enzymes.

Widespread use of azoles has also resulted in an important change in the spectrum of *Candida* infections. Whereas *C. albicans* used to be the common cause of *Candidosis*, 50% of these infections are now caused by non-*albicans* species which tend to be less susceptible to azole treatment. In addition, a quickly rising percentage of *C. albicans* isolates obtained from infected patients have been found to be resistant to azoles.

There is thus an immediate need for an effective treatment of opportunistic infections caused by *C. albicans* and other fungi. Although the majority of life-threatening fungal infections are caused by *C. albicans*, infections caused by other less common fungi as discussed above, e.g., *Aspergillus fumigatus* have a worse prognosis. In large part this is due to the absence of diagnosis until a very late stage of infection, usually post-mortem.

Therefore it is desirable that novel compounds be able to act against all pathogenic fungi, preventing the need for precise, time-consuming diagnosis.

Development of an effective method and composition for treatment of fungal infections is a critical goal of the pharmaceutical industry. The industry has made numerous efforts to identify fungal-specific drugs, with only limited success. It would be of great value to identify a new class of antifungal drugs that block a fungal target other than ergosterol. This target should be fungal-specific and should lead to development of a drug that is effective in preventing or inhibiting the growth of, and preferentially killing, the organisms that are resistant to current therapy.

Antifungal drug development often relies on the screening of a large number of compounds before one or more lead compounds are found that are effective against the target fungi. Thus, it is critical for the development of these screens to define proteins essential for survival or growth of the target fungi and to discover means of purifying or producing such proteins. Therefore, there is a need in the art to identify essential fungal structural or functional elements that can serve as targets for drug intervention, and for methods and compositions for identifying useful anti-fungal agents that interact with or inhibit essential fungal elements that can be used to treat fungal infections by preventing or inhibiting the growth of, and preferentially killing, the fungi.

SUMMARY OF THE INVENTION

The present invention is based on the determination of *Saccharomyces cerevisiae* proteins which are potential targets to kill *S. cerevisiae* cells. The invention provides a screening method for detecting and identifying a compound that binds to a homologous target protein isolated from *C. albicans*, as well as compounds which can inhibit *C. albicans* and other fungal growth. The invention also provides a method for evaluating the toxicity of such a fungal inhibitor in mammalian cells.

The invention utilizes target proteins involved in such processes as DNA synthesis, DNA replication, DNA transcription, mRNA translation, post-translational modification of proteins, and intracellular transport of proteins, as well as target proteins whose exact cellular functions are unknown. In preferred embodiments, the invention provides for the use of *S. cerevisiae* target proteins listed in Table 1 together with *C. albicans* and human homologs, depicted therein by their respective amino acid sequences

which are provided in Figure 79. The nucleic acid sequences corresponding to these amino acid sequences are depicted in Figure 80.

Each of the *S. cerevisiae* DNA sequences, and their predicted target protein sequences, which are utilized in practicing the invention are publicly available. The
5 essentiality of each of such *S. cerevisiae* genes may already be known or may be determined and/or corroborated through the analysis of the ability to knock out the gene's function in *S. cerevisiae*. The present invention thus provides a method of determining and/or validating the essentiality of the *S. ceriviseae* gene and the target protein encoded by that gene. More specifically, the invention is directed to the determination of the *S.*
10 *ceriviseae* protein as a cidal target to be used in the determination and isolation of a homologous target in *C. albicans*. The *C. albicans* target may then be used in the screening of compounds which can inhibit *Candida albicans* and other fungal growth.

Following the determination of the essentiality of the *S. cerevisiae* gene, the *S. ceriviseae* DNA sequence may be used to isolate a homologous fungal gene. Thus,
15 in another aspect, the invention is based on the determination of a *C. albicans* nucleic acid encoding the *C. albicans* protein as a target which is essential for the growth of *C. albicans*.

In a still further aspect, the invention provides for producing a recombinant target *C. albicans* target protein, comprising culturing a host cell transformed with a
20 nucleic acid encoding the *C. albicans* target protein under conditions sufficient to permit expression of the nucleic acid encoding the *C. albicans* target protein and isolating the *C. albicans* target protein to be used in assays described below.

Sequence alignments utilizing the *S. cerevisiae* nucleic acid or protein sequences and/or the *C. albicans* nucleic acid or protein sequences in combination with
25 known sequences available in Genbank may be carried out in order to demonstrate any similarity or differences between different fungi, *i.e.*, *S. cerevisiae*, *C. albicans*, and *Aspergillus*, and mammals. In this manner, homologous genes can be isolated. One example of such analysis would be BLAST™ analysis.

In a further embodiment, following the determination that the target protein
30 in *Saccharomyces cerevisiae* is a cidal target, and that the homologous protein in *Candida albicans* is essential for growth, the *C. albicans* protein may be used as a target to isolate candidate inhibitors of fungal growth and/or infection. Detection and identification of

compounds that bind to the essential protein may be performed in the presence of a plurality of candidate inhibitor compounds. In carrying out the screening methods of the invention which involve screening a plurality of candidate inhibitor compounds, the plurality of inhibitor compounds may be screened together in a single assay or individually using multiple simultaneous individual detecting steps.

In another aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in culture, by contacting the culture with an inhibitor compound that selectively inhibits the biological activity of a fungal target protein, particularly a *C. albicans* target protein.

In a further aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in a mammal, comprising administering to the mammal an effective amount of an inhibitor compound that selectively inhibits the biological activity of a fungal, particularly *C. albicans*, target protein.

In a still further aspect, the invention provides a method of preventing or inhibiting fungal, particularly *C. albicans*, growth in a mammal, comprising administering to the mammal an effective amount of an inhibitor compound, wherein the inhibitor selectively inhibits the biological activity of a fungal, particularly *C. albicans*, target protein, but inhibits the biological activity of the homologous mammalian protein to a lesser degree, or not at all.

In yet another aspect, the invention provides a method of preventing or inhibiting fungal growth, comprising administering to a fungal infection an effective amount of an inhibitor compound that selectively inhibits the biological activity of a fungal target protein.

In still another aspect, the invention provides a method of studying pathogenic mycetes using such nucleic acid and/or protein sequences.

Other features and advantages of the invention will be apparent from the description, preferred embodiments thereof, the drawings, and from the claims.

TABLE 1 – Preferred target proteins

<u><i>S. cerevisiae</i></u>			<u><i>C. albicans</i></u>	<u>Human</u>	
<u>Gene name</u>	<u>ORF name ¹</u>	<u>Sequence</u>	<u>Sequence</u>	<u>Sequence</u>	<u>Genbank Acc# ²</u>
RPC34	YNR003C	SEQ ID NO:1	SEQ ID NO:	SEQ ID NO:3	U93869

			2		
POP3	YNL282W	SEQ ID NO:4	SEQ ID NO: 5	-	n/a
TFA2	YKR062W	SEQ ID NO: 6	SEQ ID NO: 7	SEQ ID NO: 8	NP_002086
NAB2	YGL122C	SEQ ID NO: 9	SEQ ID NO: 10	SEQ ID NO: 11	AAD42873
MPT1	YMR005W	SEQ ID NO: 12	SEQ ID NO: 13	SEQ ID NO: 14	CAA72189
MTR2	YKL186C	SEQ ID NO: 15	SEQ ID NO: 16	-	n/a
BOS1	YLR078C	SEQ ID NO: 17	SEQ ID NO: 18	SEQ ID NO: 19	NP_003560
POL30	YBR088C	SEQ ID NO: 20	SEQ ID NO: 21	SEQ ID NO: 22	P12004
RSA2	YMR131C	SEQ ID NO: 23	SEQ ID NO: 24	SEQ ID NO: 25	NP_005601
SQT1	YIR012W	SEQ ID NO: 26	SEQ ID NO: 27	SEQ ID NO:28	NP_001078
MTW1	YAL034W-A	SEQ ID NO: 29	SEQ ID NO: 30	-	n/a
TFB1	YDR311W	SEQ ID NO: 31	SEQ ID NO: 32	SEQ ID NO: 33	W19128
SPC98	YNL126W	SEQ ID NO: 34	SEQ ID NO: 35	SEQ ID NO: 36	AAC39727
BFR2	YDR299W	SEQ ID NO: 37	SEQ ID NO: 38	SEQ ID NO: 39	NM_000055
RNA1	YMR235C	SEQ ID NO: 40	SEQ ID NO: 41	SEQ ID NO:42	CAA57714
GCD7	YLR291C	SEQ ID NO: 43	SEQ ID NO: 44	SEQ ID NO: 45	AAC42002
SKI6	YGR195W	SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 48	BAA91279
NIP1	YMR309C	SEQ ID NO: 49	SEQ ID NO: 50	SEQ ID NO: 51	AAD03462
LCP5	YER127W	SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 54	AL050003
NCE103	YNL036W	SEQ ID NO: 55	SEQ ID NO: 56	-	n/a
ECO1	YFR027W	SEQ ID NO: 57	SEQ ID NO: 58	-	n/a
ORC2	YBR060C	SEQ ID NO: 59	SEQ ID NO: 60	SEQ ID NO: 61	Q13416
CNS1	YBR155W	SEQ ID NO: 62	SEQ ID NO: 63	SEQ ID NO:64	NP_004614
YPD1	YDL235C	SEQ ID NO: 65	SEQ ID NO: 66	SEQ ID NO: 67	CAA78727
TIM10	YHR005C-A	SEQ ID NO: 68	SEQ ID NO: 69	SEQ ID NO:70	NP_036588
SRB4	YER022W	SEQ ID NO: 71	SEQ ID NO: 72	SEQ ID NO: 73	BAA88763

¹ ORF = Open Reading Frame² Acc # = Accession number

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1-26 provide sequence alignments and identity determinations for the target proteins presented herein. Each figure refers to one target protein as identified in Table 2, comparing amino acid sequences from *S. cerevisiae*, *C. albicans*, and, if available, human homologs. Sequence alignment was carried out using Clustal W (Thompson *et al.*, Nucleic Acids Res. 1994;22:4673-80), and percentage identities determined using the Genetics Computer Group ("GCG") GAP Program (Madison, Wisconsin) with a gap creation penalty of 12 and a gap extension penalty of 4.

Figures 27-52 provide *S. cerevisiae* inactivation analyses of the target genes/proteins identified in Table 1. These data show the essentiality of each gene for *S. cerevisiae* growth. Each figure refers to one target protein. Inactivation analyses were conducted by placing the *S. cerevisiae* expression of a target gene under the control of a metal-sensitive element and incubating the yeast cells together with a Cu-salt, as described in the Detailed Description below and in Example 1.

Figures 53-78, A and B for each, provide *C. albicans* deletion analyses of the target genes/proteins identified in Table 1. These data indicate the essentiality of each gene for *C. albicans* growth. Each figure refers to one target protein. Deletion analyses were conducted as described in the Detailed Description, and *C. albicans* transformation as described in Example 2 below.

Figure 79 provides amino acid sequences for each of the proteins disclosed herein and depicted in Table 1.

Figure 80 provides nucleic acid sequences corresponding to each of the proteins disclosed in Figure 79.

DETAILED DESCRIPTION OF THE INVENTION

All patent applications, patents, and literature references cited in this specification are hereby incorporated by reference in their entirety.

This invention is directed to essential fungal proteins isolated from *S. cerevisiae* to be used in the determination and/or isolation of a homologous protein from

fungi, particularly *C. albicans*. These fungal proteins, each of which described in more detail below, play essential roles in cell viability and/or growth, and are conserved among fungi. Because these fungal proteins are essential for viability and/or growth of fungal cells, a compound that blocks the biological activity of such a target protein would be expected to have fungicidal and/or fungistatic properties. Since amino acid sequences of any such protein from different fungal sources are likely to be more similar to one another than to the corresponding human protein, it is expected that certain compounds that bind to the fungal protein will not bind to the corresponding human protein, and so will be specific inhibitors of fungal cell growth. Therefore, the invention is also directed to assays to screen for inhibitors of these target proteins which are active against fungi.

In general, nucleic acid manipulations and other related techniques used in practicing the present invention employ methods that are well known in the art, as disclosed in, e.g., *Molecular Cloning, A Laboratory Manual* (2nd Ed., Sambrook, Fritsch and Maniatis, Cold Spring Harbor) and *Current Protocols in Molecular Biology* (Eds. Ausubel, Brent, Kingston, More, Feidman, Smith and Stuhl, Greene Publ. Assoc., Wiley-Interscience, NY, NY, 1997).

Definitions

1. The terms "Prevention" and "Inhibition" as used herein may be used interchangeably. "Inhibition" as used herein refers to a reduction in the parameter being measured, whether it be fungal growth, DNA transcription, or another parameter related to a selected process relating to the biological activity of a target protein. The amount of such reduction is measured relative to a standard (control). Because of the multiple interactions of various fungal protein in cell division, growth regulation, cell cycle regulation, and other growth and/or metabolic processes, the amount of target product needed to produce a detectable inhibition will vary with respect to the particular screening assay employed. "Reduction" is defined herein as a decrease of at least 25% relative to a control, preferably of at least 50%, and most preferably of at least 75%.

2. "Growth" or "multiplication" as used herein refers to the normal growth pattern of fungi, particularly *S. cerevisiae* and/or *C. albicans*, i.e., to a cell doubling time of 60-90 minutes during the log phase of growth. In rich media, wild-type *S. cerevisiae* strains have a doubling time of 90 minutes, while wild type *C. albicans*

doubling time is closer to approximately 60 minutes. Growth of the cells may be measured by following the optical density of cells in liquid media. An increasing optical density indicates growth. Growth can also be measured by colony formation from single cells on solid media plates.

5 3. "Viability" as used herein refers to the ability of the *S. cerevisiae* or *C. albicans* cells to resume growth following a treatment of the cells which results in cessation of growth. Examples of such treatments resulting in cessation of growth include, but are not limited to, transient inactivation of a gene product required for growth or treatment with an antifungal drug. One typical means by which viability is measured
10 is by testing the ability of cells to form colonies on solid media plates following removal of the treatment which resulted in a cessation of growth. Cells that fail to form colonies are considered inviable.

 4. "Cidal" as used herein is defined as a rapid loss in viability. Rapid
15 is defined as a population of cells losing viability with a measured half-life of at least about 2 hours or less.

 5. A "homologous" protein as used herein is defined as any protein which possesses a protein domain with at least about 30% sequence identity or similarity to a given protein, preferably at least about 40% sequence identity, and most preferably at least about 50% sequence identity. Useful sequence comparison algorithms to determine
20 degree of sequence similarity include BLAST™, FASTA, DNA Strider, the GCG pileup program (Wisconsin Package version 10, Genetics Computer Group, Madison, Wisconsin), as well as alignment schemes such as Clustal W (*See Thompson et al., supra*), using, *e.g.*, the default parameters provided with these algorithms. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available
25 in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. (*See "hybridization", below*)

 6. A "protein domain" as used herein is defined as a region of a protein which is at least about 50 amino acids ranging to the full length of the protein.

 7. "Biological activity" as used herein refers to the ability of a protein
30 to promote or sustain cell growth and/or metabolism through a known or unknown cellular mechanism. Biological activity need not be measured in living cells; an *in vitro* system consisting of the protein together with other chosen components, designed to reflect the

ability of the protein to promote or sustain cell growth and/or metabolism, may also be used to evaluate biological activity.

8. "Target protein" or "cidal protein" as used herein refers to an essential protein involved in, *e.g.*, growth and/or metabolism. Inhibition of the biological activity of a fungal target protein results in an inhibition of fungal growth. Target proteins may play essential roles in processes which include, but are not limited to, DNA synthesis, DNA repair, transcription, mRNA transport, mRNA processing, translation, protein transport, protein processing, cell cycle control, cell division, and cell signaling. The term "target protein" also includes fragments and polypeptides, as well as target proteins modified by any means known in the art, *e.g.*, by radiolabeling, conjugation, mutations in amino acid sequence, using chemically modified amino acid residues in the target protein, and so forth.

9. "Mycete" or "fungi" as used herein refers to a eukaryotic organism which carries spores, nutrition of which takes place via absorption, which is deficient in chlorophyll and which reproduces sexually or asexually.

10. "Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, *i.e.*, DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

11. An "isolated" nucleic acid or polypeptide as used herein refers to a nucleic acid or polypeptide that is removed from its original environment (for example, its natural environment if it is naturally occurring). An isolated nucleic acid or polypeptide contains less than about 50%, preferably less than about 75%, and most preferably less than about 90%, of the cellular components with which it was originally associated.

12. A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that is related in nucleotide or amino acid sequence to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative

variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physical and/or chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants of a designated polypeptide also include any polypeptides that have the ability to elicit antibodies specific to the designated polypeptide.

13. Nucleic acids are "hybridizable" to each other when at least one strand of nucleic acid can anneal to another nucleic acid strand under defined stringency conditions. Stringency of hybridization is determined, *e.g.*, by a) the temperature at which hybridization and/or washing is performed, and b) the ionic strength and polarity (*e.g.*, formamide concentration) of the hybridization and washing solutions, as well as other parameters. Hybridization requires that the two nucleic acids contain substantially complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementarity, variables well known in the art.

Hybridizable polynucleotides may be of any length. In one embodiment, such polynucleotides are at least 7, preferably at least 25 and most preferably at least 100 nucleotides long. In another embodiment, the polynucleotide that hybridizes to any of the polynucleotides of the invention is of the same length as the polynucleotide of the invention. Nucleic acids that are hybridizable to other nucleic acids are capable of hybridizing with their complements under the hybridization conditions defined herein as "high stringency" as defined below.

- Prehybridization treatment of the support (nitrocellulose filter or nylon membrane), to which is bound the nucleic acid capable of being hybridized at 65°C for 6 hours with a solution having the following composition: 4 x SSC, 10 x Denhardt (1X Denhardt is 1% Ficoll, 1% polyvinylpyrrolidone, 1% BSA (bovine serum albumin)); 1 x SSC consists of 0.15M of NaCl and 0.015M of sodium citrate, pH 7);

- Replacement of the pre-hybridization solution in contact with the support by a buffer solution having the following composition: 4 x SSC, 1 x Denhardt, 25 mM

- Incubation for 12 hours at 65EC;
- Successive washings with the following solutions: (i) four washings with 2 x SSC, 1 x Denhardt, 0.5% SDS for 45 minutes at 65EC; (ii) two washings with 0.2 x SSC, 0.1 x SSC for 45 minutes at 65EC; and (iii) 0.1 x SSC, 0.1 % SDS for 45 minutes at 65EC.

15. A "candidate inhibitor," as used herein, is any compound with a potential to inhibit *Candida albicans* or other fungal growth and/or metabolism via an activity mediated by any of the target proteins described in Table 1, and throughout the specification.

20 **Target proteins**

14

Ideally, an antifungal compound directs its action against a target that is present in fungi but absent in human cells. Such targets, however, are important for cell function and tend to be conserved in evolution and, thus, be present in both human and fungal cells. In such cases, the target protein is present in both cell types, as noted above, but the human homolog of the target protein has an amino acid sequence that distinguishes it from the fungal target protein.

If a human homolog of the target protein has been identified, such a human sequence is considered distinguishable from the fungal sequence if it has less than about 50%, preferably less than about 40%, and even more preferably less than about 30% sequence identity. The lower the sequence similarity, the higher the chance for identifying compounds that act specifically against the fungal target protein but not its human homolog. However, an important factor is also the sequence similarity between different fungal homologs of the target protein. If homologous proteins derived from two different fungal sources such as, *e.g.*, *S. cerevisiae* and *C. albicans*, display a high sequence similarity such as, *e.g.*, higher than 50%, more preferably 70%, and even more preferably higher than 90%, this allows for a higher chance of identifying an inhibitor specific for the fungal target proteins but not their human homolog. Thus, a higher than optimal sequence similarity between the fungal and human target protein homologs does not preclude finding a substance which only inhibits the biological activity of the fungal protein.

Each preferred target protein is described below. Non-limiting examples of some assays for some of the target proteins are also provided. Such assays are useful in identifying and/or measuring the biological activity of target proteins, *e.g.*, in the presence of a potentially inhibitory compound. Amino acid sequences for each target protein in *S. cerevisiae*, *C. albicans*, and, where relevant, human, can be found in Table 1. Sequence identity determinations between the the *S. cerevisiae*, *C. albicans*, and, if available, human homologs, are provided in Table 2.

RPC34

RPC34 (C34) is an essential and specific subunit of RNA polymerase III complex (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395). RNA polymerase III is responsible for transcription of tRNAs, 5S rRNA, and some other small RNAs. Three RNA polymerase III unique subunits, C34, C82, and C31 form a complex that interacts

with 70-kDa component of transcription factor TFIIB via C34 (Werner, M., *et al.*, J. Biol. Chem., 1993; 268:20721-20724). C34 subunit is a major determinant of pol III recruitment by pre-initiation complex. Interaction between C34 and TFIIB70 is essential for pre-initiation complex formation and later during promoter opening (Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). It has been demonstrated that strains carrying temperature-sensitive or cold-sensitive mutations in RPC34 are impaired in tRNA synthesis (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395; Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). RPC39 human homolog of RPC34 has been identified (Wang, Z. and Roeder, R. Gen. Dev., 1997; 11:327-7949). RPC34 and RPC39 are 27% identical and 50% similar.

RPC34 assays:

(a) ATLAS

(b) Cell-based assays in *S. cerevisiae* and human cells were developed utilizing the information that in the absence/inability to perform, the function of RPC34 tRNA synthesis decreases (Stettler, S., *et al.*, J. Biol. Chem., 1992; 267:21390-21395; Brun, I., *et al.*, EMBO J., 1997; 16:5730-5741). If the compound specifically binds to Rpc34p, a tRNA level decrease can be detected after addition of the compound to the growing media. Similar assay in human cells can be designed based on the same principle. The level of tRNA can be assayed upon addition of a compound to the cells at different time points.

(c) In vitro assays can be developed using purified RNA polymerase III transcription factors, including RPC34, to assess tRNA and 5S rRNA levels in the presence/absence of a compound (Kassavetis, G., *et al.*, EMBO J., 1999; 18:5042-5051).

(d) A reporter-based assay can be developed utilizing a two-hybrid system, knowing that RPC34 physically interacts with C82, C31, and TFIIB70. One of the proteins can be fused with a transcriptional activator and the other with a DNA-binding protein. The ability of the two proteins to interact with each other in the presence or absence of a compound can be measured by monitoring enzymatic activity of a reporter gene expressed from the promoter.

POP3

Saccharomyces cerevisiae POP3 is involved in post-transcriptional processing of the large precursor RNAs into the mature functional forms of tRNA and rRNA (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429; Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). This processing of tRNA and
5 rRNA is carried out by the RNase MRP and RNase P ribonucleoproteins, respectively, but the two complexes are known to have extensive subunit overlap (Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). Mutations in POP3 result in phenotypes identical to loss of RNase MRP, including interference with the complete processing of tRNA and rRNA (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429;
10 Chamberlain, J.R., *et al.*, Genes and Development, 1998; 12:1678-1690). POP3 is essential for cell growth in *Saccharomyces cerevisiae* (Dichtl, B. and D. Tollervey, EMBO Journal, 1997; 16:417-429).

POP3 Assays:

(a) ATLAS: CaPop3 protein could be purified and challenged with an
15 environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaPop3 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaPOP3 and a *Candida albicans* ortholog of another subunit of either the RNase MRP or
20 the RNase P complex could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than those in the RNase MRP or RNase P complex
25 could be used in this format.

TFA2

Saccharomyces cerevisiae TFA2 is a subunit of the general RNA polymerase II transcription initiation factor, TFIIE. The gene product of TFA2 forms a
30 hetero-tetramer with that of TFA1, and both genes are essential for cell viability (Feaver *et al.*, J Biol Chem, 1994, 269:27549-53). The genes for TFA1 and TFA2 were identified from the purified protein shown to have an activity required for accurately initiated

transcription from promoters in vitro, and the gene sequences have significant homology to mammalian TFIIE (Feaver *et al.*, J Biol Chem, 1994, 269:27549-53). The requirement for TFIIE to carry out transcription of a gene varies, depending on the promoter structures, (Sakur *et al.*, J Biol Chem, 1997, 272: 15936-15942). It has been suggested that yeast
5 GAL11 product enhances the interaction between TFIIE and the RNA polymerase II holoenzyme and thus increases transcriptional efficiency (Sakurau *et al.*, PNAS, 1996, 93:9488-9492).

TFA2 Assays:

(a) ATLAS: CaTfa2 protein could be purified and challenged with an
10 environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaTfa2 protein may stabilize the native conformation of the protein.

(b) Two-hybrid interruption screen using another interacting protein: CaTfa2 and CaTfa1 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter
15 gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaTfa1p could be used in this format, notably CaGal11 protein.

NAB2

Nascent RNA polymerase II transcripts associate with nuclear ribonucleoproteins and remain associated during the subsequent RNA processing reactions, such as pre-mRNA polyadenylation and splicing and transport to the cytoplasm.
25 *Saccharomyces cerevisiae* NAB2 is one of the major proteins associated with polyadenylated RNA in vivo and is essential for cell growth (Anderson, J.T., *et al.*, Molecular and Cellular Biology, 1993;13:2730-2741). The NAB2 gene product is localized primarily to the nucleus (Anderson, J.T., *et al.*, Molecular and Cellular Biology, 1993;13:2730-2741). Two different RNA-binding motifs are identifiable in the sequence
30 of NAB2: an RGG box observed in a variety of heterogenous nuclear RNA-binding proteins, and CCCH motif repeats related to the zinc-binding motifs of the largest subunit of RNA polymerases (Anderson, J.T., *et al.*, Molecular and Cellular Biology,

1993;13:2730-2741). NAB2 gene product interacts with the product of yeast KAP104, a gene encoding a karyopherin shown to function in the nuclear import of proteins, and has been shown to interact with human transportin1 (hTRN1), the human homolog of yeast KAP104 (Aitchison, J.D., *et al.*, Science, 1996; 274:624-627; Truant, R., *et al.*,
5 Molecular and Cellular Biology, 1998;18:1449-1458; M.C. Siomi, *et al.*, Molecular and Cellular Biology, 1998; 18:4141-4148).

NAB2 Assays:

(a) ATLAS: CaNab2 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the
10 protein. A compound that binds to CaNab2 protein may stabilize the native conformation of the protein.

(b) Two-hybrid interruption screen using another interacting protein: CaNAB2 and CaKAP104 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a
15 reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaKap104p could be used in this format.

(c) RNA-binding screen: Compounds could be screened for their ability to interfere with the binding of RNA by CaNab2 protein. The binding of RNA and
20 CaNab2 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled RNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when RNA is bound by the protein.

25

MPT1

MPT1 is a target that has been identified in both *S. cerevisiae* and *C. albicans*. MPT1 proteins have not been characterized in detail. ScMPT1 was isolated in a two-hybrid screen using ScPrp9 as bait (Fromont-Racine, M., *et al.*, Nat Genet, 1997; 16:277-82). Prp9 is a subunit of a complex involved in RNA splicing. The fact that
30 ScMPT1 would interact with Prp9 suggests that ScMPT1 would also be involved in RNA splicing. Validation data in *S. cerevisiae* and *C. albicans* indicate that MPT1 is important for fungal cell growth and viability, which may correlate with its putative function in RNA

splicing. A mammalian homolog has been proposed, but the degree of homology is too low to be confident about this. The apparent importance of MPT1 for fungal growth combined with the absence of a highly similar protein in mammalian cells make MPT1 an excellent target for antifungal drug discovery.

5 *MPT1 assays:*

(a) ATLAS. (See above).

(b) Cell-based assays: Various strains of *S. cerevisiae* could be constructed in which ScMPT1 would be replaced with a functional MPT1 gene (*i.e.*, derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These
10 cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains may suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of MPT1.

(c) Protein-protein interaction based assays: (i) Two-hybrid screen
15 (Fromont-Racine, M., *et al.*, Nat Genet, 1997; 16:277-82) using MPT1 and PRP9 (or any other protein found to interact with MPT1); (ii) Direct binding assay: The interacting protein could be fixed onto a carrier and allowed to bind easily detectable MPT1. In the absence of inhibitors, a high signal would result. However, interference with this interaction may reduce signal. The orientation of the assay could also be reversed by
20 fixation of MPT1 and incubation with a interacting protein labeled with a reporter molecule such as, *e.g.*, a radionucleotide or a fluorescent compound.

MTR2

In eukaryotic cells, mRNA transport is an important cellular process for
25 gene expression and regulation. A set of genes were identified through an attempt to isolate *Saccharomyces cerevisiae* temperature-sensitive mutants that accumulate poly(A) RNA in the nucleus. (Kadowaki, T., *et al.*, J Cell Biol, 1994; 126, 649-59) One of the genes, MTR2 encodes a 21 kD nuclear protein that shows a limited homology to a *E. coli* protein implicated in plasmid DNA transfer. (Kadowaki, T., *et al.*, J Cell Biol, 1994; 126, 649-59)
30 It has been shown that Mtr2 protein can interact with a nuclei pore associated protein, Mex67p and their interaction appears to be essential for mRNA export. (Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38) Genetic and biochemical evidence also indicated

that Mtr2p can interact with Nup85p, suggesting that Nup85p might be the target at nuclear pore complex (NPC) to which Mtr2p and Mex67 bind. (Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38) Given all these factors, it was proposed that Mtr2 protein is the key component of mRNA export machinery in yeast. (Santos-Rosa, H., *et al.*, Mol Cell Biol, 1998; 18:6826-38; Schneider, R., *et al.*, Mol Biol Cell, 1995; 6:357-70)

Recently, a human homolog of Mex67, TAP was identified that can interact with poly(A) RNA and human nucleoporin. However, no Mtr2 human homolog was found so far. Katahira *et al* (The Mex67p-mediated nuclear mRNA export pathway is conserved from yeast to human. Embo Journal 18, 2593-2609 (1999)) identified a small human protein, p15 that interact with TAP. Interestingly, co-expression of TAP and p15 in yeast can functionally complement Mex67-Mtr2 complex suggesting the existence of the evolutionarily conserved pathway that is involved in mRNA transport.

MTR2 assays:

(a) ATLAS: Mtr2 protein can be purified to homogeneity. Challenging purified Mtr2 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading protein to the unfolding state. Any compound that binds to Mtr2 will potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Mtr2.

(b) Two hybrid with Mex67. Mtr2 and Mex67 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Mtr2 and Mex67 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupts the interaction of Mtr2p and Mex67p will disrupt the induction of the reporter gene and thus that compound can be identified.

(c) Two hybrid with Nup85p. Mtr2 and Nup85 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Mtr2 and Mex67 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupts the interaction of Mtr2p and Nup85p will disrupt the induction of the reporter gene and thus that compound can be identified.

BOS1

Saccharomyces cerevisiae BOS1 is an essential gene that functions in ER-to-Golgi transport. The protein is a cytoplasmically-oriented type II integral membrane protein of secretory vesicles (Newman *et al.*, *Embo J.*, 1992, 11:3609-3617; Lian *et al.*, *Cell*, 1993, 73:735-745). Depletion of BOS1 results in a block in ER-to-Golgi protein transport and accumulation of small vesicles (Shim *et al.*, *J. Cell Biol.*, 1991, 13:55-64). The gene was originally isolated as a high copy suppressor of BET1 (Newman *et al.*, *Embo J.*, 1992, 11:3609-3617). BOS1 exhibits genetic and physical interactions with several proteins known to be involved in vesicular transport from the ER to the Golgi. In addition to suppressing BET1 defects, BOS1 overexpression can also overcome defects in SEC22 and YPT1 (Newman *et al.* *Embo Journal* 11, 3609-17 (1992)). Bos1p has been shown to pair with Sec22p under the influence of Ypt1. Bos1p, Bet1p and Sec22p are V-SNARE proteins (Lian *et al.*, *Cell* 73, 735-45 (1993); Pfeffer, *Annu. Rev. Cell Dev. Biol.* 12, 441-461 (1996)) that form a complex involved in transport vesicle docking (Ferro-Novick *et al.*, *Cell Biophys* 19, 25-33 (1991)). YPT1 is a Rab protein required for SNARE complex formation (Sogaard *et al.*, *Cell* 78, 937-48 (1994); Lian *et al.*, *Nature* 372, 698-701 (1994); Lazar *et al.*, *Trends Biochem Sci* 22, 468-472 (1997)). The V-SNAREs Bos1p and Sec22p cooperatively interact with the t-SNARE Sed5p prior to membrane fusion (Sacher *et al.*, *J Biol Chem* 272, 17134-8 (1997)).

BOS1 assays:

(a) BOS1 is a good ATLAS assay target. In addition, defects in BOS1 function could be assessed in a reconstituted transport system (Lian, J. P., and Ferro-Novick, S. Bos1p, *Cell*, 1993; 73:735-45) or in a cell-based assay of invertase secretion (Johnson, L.M., *et al.*, *Cell*, 1987; 48:875-885) that monitors the inefficient transport of secreted protein from the ER to the Golgi (Shim, J., *et al.*, *J Cell Biol*, 1991;113:55-64).

(b) In vitro transport system (Lian *et al.*, *Cell* 73, 735-45 (1993)).

(c) Cell-based assay of invertase secretion (Johnson *et al.*, 1987) that monitors the inefficient transport of secreted protein from the ER to the Golgi (Shim *et al.*, 1991).

(d) Protein:protein interactions. BOS1 has multiple protein partners (see above) whose interactions can be monitored by assayed by two-hybrid analysis or in vitro protein binding assays.

5

POL30

References for this section are numbered at the end of the section.

Saccharomyces cerevisiae POL30 is an essential gene and encodes the yeast proliferating cell nuclear antigen (PCNA) (Bauer *et al.*, NAR, 1990, 18: 261-5). The structure of yeast PCNA has been determined, and it appears to function as a trimer that
10 forms a sliding clamp around the DNA double helix (Krishna *et al.*, J Mol Biol, 1994, 241: 265-8). PCNA can load onto the ends of linear DNA molecules in vitro, but efficient loading of PCNA onto DNA requires ATP and the product of RFC1 (McAlear *et al.*, Genetics, 1996, 142:65-78, Burgers *et al.*, J Biol. Chem., 1993, 268: 19923-19926).

PCNA is required for both DNA synthesis and DNA repair in mammals and
15 yeast. PCNA interacts with DNA polymerase delta or epsilon to enhance processive replication of DNA (Holmes *et al.*, Cell, 1999, 96: 415-424). PCNA interacts with FEN-1, the product of the mammalian homolog of RAD27, a protein required for Okazaki fragment processing (Ishimi *et al.*, J. Biol.Chem., 1988, 263: 19723-19733; Li *et al.*, J. Biol. Chem., 1995, 270:22109-22112; Turchi *et al.*, PNAS, 1995, 91:9803-9807). PCNA
20 is required in vitro for reconstitution of nucleotide excision repair and base excision repair reactions. (Ayyagari *et al.*, Mol Cell Biol, 1995, 15:4420-0; Umar *et al.*, Cell, 1996, 87:65-73; Johnson *et al.*, J Biol Chem, 1996, 271:27987-90; Matsumoto *et al.*, Mol Cell Bio., 1994, 14:6187-97; Nichols *et al.*, NAR, 1992 10:2441-2446; Shivji *et al.*, Cell, 1992, 69:367-374). Transcription silencing may also involve PCNA (Ehrenhofer-Murray
25 *et al.*, Genetics, 1999, 153:1171-82).

POL30 assays:

(a) ATLAS: CaPol30 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaPol30 protein may stabilize the native conformation
30 of the protein.

(b) Two-hybrid interruption screen using CaRad27 protein or another interacting protein: CaPol30 and CaRad27 could be placed into yeast two-hybrid screening

vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaRad27p could be used in this format. A screen could be designed to interfere with the multimerization of CaPol30 by using the gene as both bait and prey.

(c) DNA-binding screen: Compounds could be screened for their ability to interfere with the binding of DNA to CaPol30 protein. The binding of DNA and CaPol30 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled DNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when DNA is bound by the protein.

YMR131C

YMR131C is an essential gene in *C. albicans*. Nearest human match is a 25% identity to human retinoblastoma protein RBBP4. YMR131C protein has WD40 repeats suggesting that it may physically interact with other proteins. Recent report suggests that the protein may be involved in the nucleopore complex formation (Rout, M., *et al.*, J. Cell Biol., 2000; 148:635-652).

YMR131C assays:

(a) ATLAS

(b) If a mammalian YMR131C Homolog is found that complements *C. albicans* YMR131C, a cell-based assay could be set up to measure cell growth in the presence/absence of a compounds comparing strains with *C. albicans* YMR131C and human YMR131C Homolog.

(c) If proteins that physically interact with YMR131C are identified, two-hybrid system based assay can be developed to monitor interaction between YMR131C and another protein.

(d) If YMR131C is essential for nuclear pore transport, an assay can be set up to monitor efficiency of transport through nuclear pores.

SQT1

Saccharomyces cerevisiae SQT1 is an essential gene, which encodes a 60S ribosomal subunit protein required for joining of 40S and 60S subunits (Eisinger *et al.*, MCB, 17:5146-5155, 1997). SQT1 was isolated as a suppressor of dominant-negative
5 truncation mutations of ribosomal protein QSR1 (Eisinger *et al.*, MCB, 17:5136-5145, 1997; Eisinger *et al.*, MCB, 17:5146-5155, 1997). The loss of SQT1 function results in the formation of half-mer polysomes whereby the 40S and 60S subunits fail to join. SQT1 may be required for the assembly of QSR1 onto the 60S ribosomal subunit (Eisinger *et al.*, MCB, 17:5146-5155, 1997). The protein may be part of an oligomeric complex and is
10 localized to the cytoplasm where it is loosely associated with ribosomes (Eisinger *et al.*, MCB, 17:5146-5155, 1997).

SQT1 assays:

(a) SQT1 is a good candidate for an ATLAS assay. In addition, polysome and ribosome subunit analysis could be carried out in a low-throughput secondary assay.
15 Interference with SQT1 function should result in half-mer polysome profiles. This type of assay would involve isolation and fractionation of ribosomal subunits, 80S ribosomes and polysomes on sucrose velocity gradients (Eisinger *et al.*, MCB, 17:5136-5145, 1997).

(b) Polysome and ribosome subunit analysis could be carried out in a low-throughput secondary assay. Interference with SQT1 function should result in half-mer
20 polysome profiles. This type of assay would involve isolation and fractionation of ribosomal subunits, 80S ribosomes and polysomes on sucrose velocity gradients (Eisinger *et al.*, 1997a).

MTW1

25 MTW1 is an essential protein in *C. albicans* with unknown function. Mtw1p (Mis twelve-like protein) is 33% identical to *S. cerevisiae* Mis12p. The published data suggests that *S. pombe* Mis12p is required for centromere structure maintenance and correct spindle morphogenesis during chromosomal segregation (Goshima *et al.*, Gen. Dev., 13:1664-1677, 1999). It is possible that *C. albicans* Mtw1p has DNA-binding
30 motifs. No true human homolog has been identified so far.

MTW1 assays:

(a) ATLAS

(b) If MTW1 binds to DNA, an assay for DNA-binding activity can be set up.

(c) If a mammalian MTW1 homolog is found which complements *C. albicans* MTW1, a cell-based assay can be set up to measure cell growth in the presence/absence of a compound, comparing strains with *C. albicans* MTW1 and the human MTW1 homolog.

(d) If proteins that physically interact with MTW1 are identified, two-hybrid system based assays can be developed to monitor interaction between MTW1 and other proteins.

10

TFB1

RNA polymerase II needs five additional general transcription factors for promotor dependent transcription, one of which is TFIIF (Svejstrup *et al.*, J Biol Chem, 269:28044-8, 1994). TFIIF contains DNA-dependent ATPase activity and protein kinase activity directed against the C-terminal Repeat Domain of RNA polymerase II. TFB1 is one of the subunits of TFIIF and is needed for both transcription and nucleotide excision repair.

TFB1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approximately 40% vs. 20%). This difference combined with the importance for fungal cell viability makes TFB1 an excellent target for antifungal drug discovery.

15

TFB1 assays:

(a) ATLAS

(b) RNA polymerase II promotor-dependent transcription assay

(c) Cell-based assay: Various strains of *S. cerevisiae* would be constructed in which ScNIP1 would be replaced with a functional TFB1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of TFB1.

30

(d) Protein-protein/DNA interaction based assay: (i) Two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 16:277-82, 1997) using TFB1 and any protein (or DNA) found to interact with TFB1 (*e.g.* other TFIID subunits); (ii) Direct binding assay: The interacting protein or DNA would be fixed onto a carrier and allowed to bind easily detectable TFB1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be reversed by fixation of TFB1 and incubation with labeled interacting protein/DNA.

SPC98

Saccharomyces cerevisiae SPC98 encodes an essential protein that has a role at the spindle pole body (SPB), the fungal equivalent of the centrosome. SPC98 was identified as a high copy suppressor of a mutation in TUB4, the yeast gene for gamma-tubulin. A conditional mutation in SPC98, when shifted to restrictive conditions, results in a cell-cycle arrest with defective mitotic spindles (Geissler, *et al.*, Embo Journal, 15:3899-911, 1996). SPC97, a gene that has regions of sequence similarity to SPC98, was identified as a high copy suppressor of a mutation in SPC98 (Knop *et al.*, Embo Journal, 16:1550-64, 1997). The products of both SPC97 and SPC98 have been shown to form a complex with gamma tubulin and to be responsible for microtubule nucleation (Knop, M., *et al.*, 1997; Pereira *et al.*, Embo Journal, 18:4180-4195, 1999; Chen *et al.*, J Cell Biol, 141:1169-1179, 1998). The human homologs of SPC97 and SPC98 are also in a complex with gamma-tubulin and appear to have the same functions (Tassin *et al.*, J Cell Biol, 141:689-701, 1998; Murphy *et al.*, J Cell Biol, 141:663-74, 1998).

SPC98 Assays:

(a) ATLAS: CaSp98 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaSp98 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaSp98 and CaSp97 could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the binding of the two proteins should disrupt the

induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than CaSpc97 could be used in this format.

BFR2

5 *Saccharomyces cerevisiae* BFR2 is an essential gene that was isolated as a high copy suppressor of the growth defects induced by Brefeldin A (BFA), a fungal metabolite that disrupts Golgi structure and function (Chabane *et al.*, Curr. Genet, 33:21-8, 1998; Takatsuki *et al.*, Agric. Biol. Chem., 49:899-902, 1995; Klausner *et al.*, J. Cell Biol., 116:1071-1080, 1992). In addition, BFR2 overproduction was shown to partially
10 suppress the growth defects of four mutants involved in the secretory pathway (Chabane *et al.* 1998). The mutants, sec13-1, sec16-1, sec23-1 and ypt1-1, are each involved in budding and or docking of small vesicles en route to the Golgi. Thus, it was suggested that BFR2 is involved in protein transport (Chabane *et al.* 1998).

BFR2 assays:

- 15 (a) BFR2 can be screened in an ATLAS assay format; and
 (b) Based on the proposed function of BFR2, compound interference with BFR2 would make cells more highly sensitive to BFA. Therefore, increased cellular sensitivity to BFA is an additional assay that could be used as a secondary screen.

RNA1

20 *Saccharomyces cerevisiae* RNA1 gene encodes the Rna1 protein, which is involved in nuclear export of all types of RNA (Sarkar *et al.* Mol Biol Cell, 1998, 9:3041-55). It is required for export of assembled 60S ribosomal subunits from the nucleus to the cytoplasm (Hurt *et al.*, J Cell Biol, 1999, 144:389-401). Rna1p plays a direct role in the
25 import of proteins into the nucleus (Corbett *et al.*, J Cell Biol, 1995, 130:1017-26). GST-Rna1p catalytically stimulates GTP hydrolysis by purified Gsp1p (Corbett *et al.*, J Cell Biol, 1995, 130:1017-26). It does not stimulate GTPase activity of ras or Rab7 (Becket *et al.*, J Biol Chem, 1995, 270:11860-5). RNA1 has extensive homology to *S. pombe* Rna1p and to the mammalian Ran/TC4 GTPase activating protein (Corbett *et al.*,
30 J Cell Biol, 1995, 130:1017-26; Bischoff *et al.*, PNCAS USA, 1995 92:1749-53; Melchior *et al.*, Mol Biol Cell, 1993 4:569-81). The rna1-1 mutant is complemented by *S. pombe* rna1. It is a member of superfamily of proteins that have leucine-rich repeat motifs, which

can be up to 29 amino acids in length (Melchior *et al.*, Mol Biol Cell, 1993 4:569-81; Schneider *et al.*, Mol Gen Genet, 1992, 233: 315-8). Cytosolic extracts made from *rna1-1* mutants are completely devoid of Rna1p and the protein was found to be localized within the nucleus (Traglie *et al.*, PNCAS USA, 1996, 93:7667-72). The mutant affects

5 RNA processing and export from nucleus although Rna1p is cytoplasmic (Hopper *et al.*, J Cell Biol, 1990, 111:309-21). *rna1-1* mutant accumulates intron-less and intron-containing tRNA in the nucleus at the nonpermissive temperature (Sarkar *et al.* Mol Biol Cell, 1998, 9:3041-55). It shows altered export of RNA from nucleus to cytoplasm with RNA accumulating at the nuclear periphery (Amberg *et al.*, GAD, 1992 6:1173-89).

10 The temperature-sensitive mutant has accumulation of 35S pre-rRNA (Venema *et al.*, Yeast, 1995, 11:1629-50). The *rna1-1* mutant abolishes nuclear pore complex localization of Cse1p-GFP, which becomes distributed throughout the cell (Hood *et al.*, J Biol Chem, 1998, 273:35142-35146). When the 11 amino acids from the carboxy terminal are removed, the protein retains its function (Traglia *et al.*, Mol Cell Biol, 1989, 9:2989-99).

15 In *rna1-1* mutant, export of the small ribosomal subunit from the nucleus is directly inhibited with accompanying secondary defects in processing of pre-rRNA (Moy *et al.*, GAD, 1999, 13:2118-2133).

RNA1 assays:

- (a) ATLAS
- 20 (b) Mutants of RNA1 accumulates intron-less and intron-containing tRNA
- (1). This information may be useful in assaying such tRNA in presence/absence of compounds that bind and disrupt Rna1p activity.
- (c) The defects in processing of ³⁵S pre-rRNA may be monitored by probing with oligonucleotides near the pre-rRNA cleavage sites by Northern Hybridization and
- 25 primer extension analysis.
- (d) There is accumulation of ³⁵S pre-rRNA in temperature sensitive mutants
- (11). This effect may be studied in a cell-based assay. Levels of ³⁵S-labeled pre-rRNA may be assayed in presence/absence of a compound.

30

GCD7

Eukaryotic protein translation is initiated by acquisition of mRNA and Met-tRNA^{iMet} by the 40S ribosomal subunit. These changes are mediated by Initiation

Factors (eIF's). eIF2 forms a complex with Met-tRNAⁱMet and GTP, which binds to 40S ribosomes (Pavitt *et al.*, Mol Cell Biol, 1997, 17:1298-313). After subsequent binding of mRNA to these 40S ribosomes and recognition of the AUG codon by Met-tRNAⁱMet, GTP hydrolysis releases eIF2-GDP. eIF2-GDP is converted to eIF2-GTP by eIF2B, a guanine nucleotide exchange factor, as a result of which protein translation can continue. Starvation for amino acids leads to phosphorylation of eIF2, reduction of recycling of eIF2-GDP by eIF2B and preferential translation of GCN4, a transcriptional activator of amino acid biosynthetic enzymes. eIF2B is composed of 5 subunits of which 4, including GCD7, are essential for growth. GCD7 seems to form part of the binding site for phosphorylated-eIF2 thereby mediating inhibition of eIF2B.

GCD7 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approximately 50% vs. 35%). This difference combined with the importance for fungal cell viability makes GCD7 an excellent target for antifungal drug discovery.

GCD7 assays:

- (a) ATLAS
- (b) Protein translation assay (Colthurst, *et al.*, J Gen Microbiol, 1991, 137:851-857)
- (c) Cell-based assays: (i) Various strains of *S. cerevisiae* could be constructed in which ScGCD7 would be replaced with a functional GCD7 gene (*i.e.*, derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of GCD7; (ii) Instead of measuring growth dependent on the presence of inhibitory compounds a more specific assay aimed at expression of GCN4 could be performed. Histidine starvation would be induced with AT thereby making expression of GCN4 required for growth. Alternatively, cells could be grown to higher densities prior to addition of AT and GCN4 activation could be monitored by transcriptional (or translational) fusions of the GCN promoter (plus (part

of) Gcn4p) to a suitable reporter gene/protein (Pavitt *et al.*, Mol Cell Biol, 1997, 17:1298-313).

(d) GDP exchange assays (Cigan *et al.*, PNAS, 1993, 90:5350-5354): eIF2 and eIF2B would be isolated from an appropriate host. eIF2 would complexed
5 with labeled GDP. Incubation of this complex will release labeled GDP, which would be separated from the complex. Compound interference with this liberation would leave high amounts of label.

(e) Protein-protein interaction based assays: (i) A two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using GCD7 and any protein
10 found to interact with GCD7 (*e.g.* other eIF2 subunits); (ii) A direct binding assay. The interacting protein would be fixed onto a carrier and allowed to bind easily detectable GCD7. In the absence of inhibitors, a high signal would result. However, interference with this interaction would reduce the signal. Orientation of the assay could also be reversed by fixation of GCD7 and incubation with labeled interacting protein.

15

SKI6

Most strains of *Saccharomyces cerevisiae* carry one or more dsRNA viruses. Yeast harboring these viruses are called killer strains and secrete toxin which is lethal to most of the ones that carry no viruses. Derepression of toxin expression
20 results in superkiller phenotype (Ridley *et al.*, Mol Cell Biol, 1984, 4:761-70).

SKI6 is one of the many genes that were identified by the superkiller phenotype of mutants. (Masison *et al.*, Mol Cell Biol, 1995, 15:2763-71) It encodes an essential protein that is homologous to bacterial tRNA-processing enzyme, RNase PH. (Lussier *et al.*, Genetics, 1997, 147:435-450; Mitchell *et al.*, Cell, 1997, 91:457-466)
25 Benard *et al.* discovered that ski6 mutation bypassed the requirement of polyA tail for efficient mRNA translation, allowing better translation of non-polyA mRNA, including L-A virus mRNA. (Benard *et al.*, Mol Cell Biol, 1998, 18:2688-2696) Later experiments suggested that SKI6 plays an important role in 3'-5' mRNA decay which is consistent with the fact the ski6 mutant derepresses the virus mRNA
30 translation. (Mitchell *et al.*, Cell, 1997, 91:457-466; vanHoof *et al.*, Cell, 1999, 99:347-350)

SKI6 also functions in ribosomal RNA processing. (Allmang *et al.*, GAD, 1999, 13:2148-58) It is a part of exosome complex that functions as 3'-5' exoribonuclease that is required for 5.8S rRNA maturation. (Mitchell *et al.*, Cell, 1997, 91:457-466)

5 SKI6 Ski6p can be screened by 3'-5' exoribonuclease activities. RNA substrate will be radiolabeled with P-32 and incubated with recombinant purified Ski6p. Loss of TCA precipitable radiolabeled RNA substrate is due to the activity of Ski6 protein, and inhibitors of Ski6p can thereby be screened.

10 (a) ATLAS: Ski6 protein can be purified to homogeneity. Challenging purified Ski6 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading to the unfolding state. Any compound that binds to Ski6 can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Ski6p.

15 (b) Luciferase assay. Luciferase messenger RNA with or without PolyA tails can be prepared and transfected into yeast through electroporation. Since Ski6p blocks translation of non-polyA mRNA, Luciferase activity will be high with mRNA that contains polyA tails and about 40 times lower with mRNA that has no polyA tails. In the presence of compound that block the activity of Ski6p, luciferase activity in the
20 presence of mRNA that contains polyA tails should remain relatively the same while activity in the absence of polyA tail should increase about 10 times.

NIP1

Eukaryotic protein translation is initiated by acquisition of mRNA and
25 Met-tRNA^{iMet} by the 40S ribosomal subunit (Hanachi *et al.*, J Biol Chem, 1999, 274:8546-8553). These changes are mediated by Initiation Factors (eIF's). eIF3 is composed of approximately 8-10 subunits, one of which is NIP1. No specific, enzymatic function of NIP1 within eIF3 has been described. However, validation of this gene in *C. albicans* and *S. cerevisiae* indicates that the protein is important for cell
30 growth and viability.

NIP1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi

and mammalian (approx. 40% vs. 25%). This difference combined with the importance for fungal cell viability makes NIP1 an excellent target for antifungal drug discovery.

NIP1 assays:

(a) ATLAS

5 (b) Protein translation assay (Colthurst *et al.*, J Gen Biol, 1991, 137:851-857)

(c) Cell-based assays: Various strains of *S. cerevisiae* would be constructed in which ScNIP1 would be replaced with a functional NIP1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and
10 mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of NIP1.

(d) Protein-protein interaction based assays: (i) A two-hybrid screen
15 (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using NIP1 and any protein found to interact with NIP1 (*e.g.* other eIF3 subunits); (ii) Direct binding assay: The interacting protein would be fixed onto a carrier and allowed to bind easily detectable NIP1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be
20 reversed by fixation of NIP1 and incubation with labeled interacting protein

LCP5

LCP5 is an essential *Saccharomyces cerevisiae* gene which encodes a 40.8 Kd protein. LCP5p immunolocalizes to the nucleolus and participates in the early
25 cleavage events at sites A0 to A2 in the pathway of pre-rRNA processing (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). Depletion leads to reduced levels of 18S ribosomal subunits with concomitant accumulation of 60S ribosomal subunits and a sharp reduction in polysomes (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). An *lcp5-1* mutant shows increased sensitivity to the aminoglycoside antibiotics paromomycin and
30 neomycin, and to cycloheximide, indicating a defect in translation (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). *lcp5-1* mutant, or depletion of Lcp5p, shows sharp

reduction of 18S rRNA, with accumulation of an aberrant 23S pre-rRNA species (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372).

LPC5 assays:

(a) ATLAS

5 (b) Lcp5 mutant shows predominant processing at site A3 and reduced cleavage at sites A0 and A2 in the 35S pre-rRNA (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372). The defects in processing of ³⁵S pre-rRNA may be monitored by probing with oligonucleotides near the pre-rRNA cleavage sites by Northern Hybridization and primer extension analysis.

10 (c) The rRNA metabolism may be affected by LCP5 specific compounds and this may be monitored by looking at the total RNA which will show a decrease in the steady state amounts of 18S rRNA (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372).

(d) Compounds may be assayed in presence/absence of aminoglycoside antibiotics paromomycin and neomycin, and to cycloheximide. Since mutant shows an
15 increased sensitivity to these antibiotics (Wiederkehr *et al.*, RNA, 1998, 4:1357-1372), a synergistic effect may be observed.

NCE103

In a search for components of protein export machinery, Cleves et al (Cleves
20 *et al.*, J Cell Biol., 1996, 133(5):1017-26) discovered NCE103 gene that is involved in non-classic export pathway that functions independent of the classical pathway through ER and the Golgi compartments. (Cleves *et al.*, J Cell Biol., 1996, 133(5):1017-26) Even though NCE103 gene appeared to be essential under normal conditions, experiments by Gotz et al suggested that it grew like wild-type under anaerobics conditions. (Gotz, *et al.*,
25 Yeast, 1999, 15:855-864) The predicted amino acid sequence of Nce103p shows high levels of identities to carbonic anhydrase of both prokaryotes and eukaryotes. (Gotz, *et al.*, Yeast, 1999, 15:855-864) Expression of *Medicago sativa* carbonic anhydrase gene in a high-copy number plasmid complement the growth defects caused by nce103 deletion. (Gotz, *et al.*, Yeast, 1999, 15:855-864) Given that nce103 deletion strain grow like wild-type under
30 anaerobic conditions and null deletion can be complemented by *Medicago sativa* carbonic anhydrase gene, it was proposed that nce103 functions as an authentic carbonic anhydrase and

is required for protection against certain products of oxidative metabolites under aerobics condition. (Gotz, *et al.*, Yeast, 1999, 15:855-864)

NCE103 assays:

- (a) ATLAS: Nce103 protein can be purified to homogeneity. Challenging
5 purified Nce103 protein with different environment conditions such as higher temperature or reduced pH will result in the protein conformation change leading protein to the unfolding state. Any compound that binds to Nce103p can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Nce103p.

10

ECO1

- Saccharomyces cerevisiae* ECO1 (also called CTF7) is an essential gene that is required to establish cohesion between sister chromatids during DNA replication. It was isolated as a mutant that can separate sister centromeres in the presence of Pds1p, an anaphase inhibitory protein (Toth *et al.*, Genes and Dev., 13:320-333, 1999; Skibbens *et al.*, Genes and Dev., 13:307-319, 1999). The protein is essential during S phase to establish
15 sister chromatid cohesion but not during mitosis to maintain it (Skibbens *et al.*, 1999). Cells harboring temperature-sensitive alleles of ECO1 arrest at restrictive temperature predominately as large budded cells with elongated spindles. There is a defect in separation of DNA such that mother cells often contain all the DNA (Skibbens *et al.*, 1999). Some
20 temperature-sensitive mutants display increased chromosome fragment loss at permissive temperature (Toth *et al.*, 1999; Skibbens *et al.*, 1999). The POL30 (DNA replication processivity factor or PCNA) gene in high copy can suppress ctf7 temperature sensitivity and chromosome loss thus lending further support of the hypothesis that CTF1/ECO1 functions in the establishment of sister chromatid cohesion (Skibbens *et al.*, 1999).

25

ECO1 assays:

- (a) ECO1 can be screened in an ATLAS format. Chromosome fragment loss can be assessed in a secondary assay. In this assay, faithful maintenance of a reporter chromosome fragment yields white colonies whereas loss of the reporter chromosome yields red sector colonies (Toth *et al.*, 1999; Skibbens, *et al.*, 1999). In addition, the DNA
30 content of cells can be analyzed by flow cytometry and in micrographs of cells stained with the nuclear dye, DAPI. (Toth *et al.*, 1999).

(b) Chromosome fragment loss. Faithful maintenance of a reporter chromosome fragment yields white colonies whereas loss of the reporter chromosome yields red sector colonies (Toth *et al.*, 1999; Skibbens, *et al.*, 1999).

(c) DNA content of cells can be analyzed by flow cytometry and in micrographs of
5 cells stained with the nuclear dye, DAPI. (Toth *et al.*, 1999).

ORC2

Saccharomyces cerevisiae ORC2 is a component of the 6-subunit origin
10 recognition complex (ORC) that acts at the origins of DNA replication distributed throughout the length of chromosomes (Bell *et al.*, Nature, 1992, 357:128-134). ORC2 is required for viability, and temperature sensitive mutations in ORC2 result in cell cycle arrest consistent with defects in DNA replication (Micklem *et al.*, Nature, 1993, 366:87-89; M. Foss *et al.*, Science, 1993, 262:1838-1844; Bell *et al.*, Science, 1993, 262:1844-1849).
15 ORC has been demonstrated to bind origins of replication by DNase footprinting, and this activity is dependent on ORC2 (Bell *et al.*, Science, 1993, 262:1844-1849; Lee *et al.*, Mol Cell Bio, 1993, 262:1844-1849). The gene has also been shown to be required for transcriptional silencing and telomere silencing (Micklem *et al.*, Nature, 1993, 366:87-89; M. Foss *et al.*, Science, 1993, 262:1838-1844; Bell *et al.*, Science, 1993, 262:1844-1849).
20 These appear to be separable functions for the ORC2 gene product, since the role of ORC2 in silencing can be complemented in yeast by expression of *Drosophila* ORC2, but its role in replication is not complemented (Ehrenhofer-Murray *et al.*, Science, 1995, 270:1671-1674).

ORC2 assays:

25 (a) ATLAS: CaOrc2 protein could be purified and challenged with an environmental condition, such as higher temperature or reduced pH, that unfolds the protein. A compound that binds to CaOrc2 protein may stabilize the native conformation of the protein.

(b) Two hybrid interruption screen using another interacting protein: CaOrc2
30 and a *Candida albicans* ortholog of another member of the ORC could be placed into yeast two-hybrid screening vectors, one as the bait and one as the target. Binding by the two proteins will induce expression of a reporter gene. A compound that interferes in the

binding of the two proteins should disrupt the induction of the reporter gene, allowing such compounds to be identified in a screening format. Interacting proteins other than those in the ORC could be used in this format.

- (c) DNA-binding screen: Compounds could be screened for their ability to interfere with the binding of DNA to CaOrc2 protein. The binding of DNA and CaOrc2 protein could be assessed in a variety of ways: 1) through capture on a filter or capture by antibodies; 2) in homogeneous solution using fluorescently-labeled DNA and detection of a change in fluorescence polarization; or 3) detection of a gel shift when DNA is bound by the protein. These screens may be done with other proteins in the ORC present during the assay.

CNS1

- Hsp90 chaperone complexes maintain or restore activity in both heat-denatured proteins and signaling proteins prone to deactivation (Dolinski *et al.*, Mol Cell Biol, 1998, 18:7344-7352). In present day models of Hsp90 complex interaction with signaling proteins (*e.g.*, hormone receptors), a cycle is assumed to occur of construction and degradation of an Hsp90-signaling protein complex into its subunits. When construction of the protein complex is complete, signaling can occur. However, if Hsp90 removal does not occur the signaling protein is degraded.

- CNS1 is one of the Hsp90 chaperone complex subunits and is presumably bound via a Tetratricopeptide Repeat (TPR) domain. CNS1 genes have been found in both mammalian and fungal cells. However, the degree of conservation between fungi is higher than that between fungi and mammalian (approx. 55% vs. 30%). This difference combined with the importance for fungal cell viability makes CNS1 an excellent target for antifungal drug discovery

CNS1 assays:

(a) ATLAS

- (b) Cell-based assays: Various strains of *S. cerevisiae* could be constructed in which ScCNS1 would be replaced with a functional CNS1 gene (*i.e.* derived from cDNA when necessary) from different organisms, in particular fungi and mammals. These cells would be grown in individual wells containing defined number and mixtures of compounds, which potentially could inhibit growth. Differences in degrees of inhibition by compounds

between above-mentioned strains suggest that a compound may inhibit growth by preferentially inhibiting activity of a class of CNS1.

- (c) Protein-protein interaction based assays: (i) Two-hybrid screen (Fromont-Racine *et al.*, Nat Genet, 1997, 16:277-82) using CNS1 and any protein found to interact with CNS1 (*e.g.* other Hsp90 complex subunits); (ii) Direct binding assay: The interacting protein would be fixed onto a carrier and allowed to bind easily detectable CNS1. In the absence of inhibitors a high signal would result. However, interference with this interaction would reduce signal. Orientation of the assay could also be reversed by fixation of CNS1 and incubation with labeled interacting protein.

10

YPD1

- Saccharomyces cerevisiae* YPD1 is an essential gene that functions in a two-component regulatory system in the high-osmolarity sensing MAP kinase pathway. The protein mediates a transfer of a phosphate from Sln1p to Ssk1p under normal osmolarity to inhibit the MAP kinase kinase kinases Ssk2p and Ssk22p (Posas *et al.*, Cell, 86:865-875, 1996). Ypd1 lethality is due to constant activation of the HOG1 pathway (Posas *et al.*, 1996). The structure of Ypd1p has been solved and consists of a four-helix bundle that makes up the central core and contains the active site residue, His64. Residues around the active site are exposed to solvent and are important for phosphotransfer activity (Xu *et al.*, J. Mol. Biol., 292:1039-1050, 1999).

20

YPD1 assays:

- (a) YPD1 is a good candidate for an ATLAS screen. In addition, as a secondary in vitro assay, transfer of radiolabeled phosphate from Sln1p to Ypd1 can be monitored (Li *et al.*, 1998).
- (b) Transfer of radiolabeled phosphate from Sln1p to Ypd1 can be monitored in vitro (Li *et al.*, EMBO J., 17:6952-6962, 1998).

25

TIM10

- Tim10 was originally isolated as a suppressor of *mrs2* mutant that is defect in mitochondria RNA splicing and respiration. (Jarosch *et al.*, Mol Gen Genet, 1997, 255:157-65) Tim10 belongs to a group of evolutionary conserved protein called TIM family and shares extensive homology with another Tim protein, Tim9. (Bauer, *et al.*, GEBS Lett,

30

1999, 464:41-47) Located in the mitochondria intermembrane space, it functions to transfer metabolic carrier proteins from cytoplasm to mitochondria. Tim10 is a soluble protein that forms a complex with Tim9 and Tim12 to bind to the precursor protein that is destined to the mitochondria and transfer them to another Tim complex, Tim 54-22-18. (Koehler *et al.*,
5 Science, 279:369-373, 1998; Sirrenberg *et al.*, Nature, 391:912-915, 1998; Adam *et al.*, Embo Journal, 18:313-319, 1999; Koehler *et al.*, Embo J., 17:6477-6486, 1998; Endres *et al.*, Embo J., 18:3214-3221, 1999). Tim 10 is essential for the biogenesis of mitochondria, as well as for viability of yeast cells. (Jarosch *et al.*, Mol Gen Genet, 1997, 255:157-65) As
10 a result of Tim10 depletion, mitochondria undergo dramatic changes in morphology and are unable to assemble cytochrome complexes. (Kubrich *et al.*, J Biol Chem, 1998, 273:16374-16381)

TIM10 assays:

(a) ATLAS: Tim10 protein can be purified to homogeneity. Challenging purified Tim10 protein with different environment conditions such as higher temperature or
15 reduced pH will result in the protein conformation change leading to the unfolding state. Any compound that binds to Tim10p can potentially stabilize protein in the native state. Using ATLAS can help identify compound that binds to Tim10p.

(b) Two-hybrid with Tim9. Even though, Tim10 has been shown to form a complex with Tim9 and Tim 12, only Tim10p direct interaction with Tim9p has been fully
20 addressed. Screening compound that block Tim10 interaction with Tim9 using Two-hybrid will help identify compound that hit Tim10 protein. Tim10 and Tim9 can be used as a pair of genes in yeast with one of them as the bait and the other used as target. Binding of Tim10 and Tim9 protein in yeast will result in the induction of a reporter gene that can be detected. Any compound that interrupt binding of Tim10 protein and Tim9 protein will
25 disrupt the induction of the reporter gene and thus that compound can be identified.

SRB4

SRB4 is an essential component of RNA polymerase II multisubunit complex (Thompson *et al.*, Cell, 1993, 73:1361-75). SRB is known in the art to stand for Suppressor
30 of RNA Polymerase B. SRB4 is required for RNA polymerase II transcription at most of the promoters (Thompson *et al.*, PNAS, 1995, 92:4587-90). It has been recently demonstrated that SRB4 is dispensable for transcriptional activation of some genes

depending on activation mechanism of a particular activator (Lee *et al.*, Gen. Dev., 1999, 13:2934-9). DNA-crosslinking immunoprecipitation assay was used to show that activator-dependent stimulation of TBP binding requires Srb4 (Li *et al.*, Nature, 1999, 399:605-9). *C. albicans* Srb4 protein has an intron and it is about 30% identical to its *S.*

5 *cerevisiae* Homolog. SRB4 has a potential human homolog which is 20% identical.

SRB4 assays:

(a) ATLAS

(b) Cell-based assays can be set up to monitor transcriptional activation of a reporter gene in wild type strain and SRB4 temperature-sensitive strain.

10 (c) A two-hybrid system based assay can be developed to monitor interaction between Srb4p and other SRB proteins or RNA polymerase II CTD.

(d) *In vitro* transcription assay (Thompson *et al.*, Cell, 1993, 73:1361-75, Koleske *et al.*, Nature, 1994, 368:466-469).

15 Sequence identities

The degree of sequence identity between the above *S. cerevisiae* (sc) genes and their *C. albicans* (ca) and, if available, human (hs) homologs are provided in Table 2. (See below). Multiple alignments were created using Clustal W (See Thompson *et al.*, *supra*), and percentage identities calculated using the GCG GAP program with a gap creation penalty of 12 and a gap extension penalty of 4. The sequence alignment results are

20 also presented in the figures referred to in Table 2.

Table 2 – Sequence Identities

S. cerevisiae					C. albicans	Human	Sequence identities (%)			FIG.
Nominated targets										
half-life	gene name	orf name	genbank DNA	genbank protein	source	genbank #	ca v sc	sc v hs	ca v hs	
0.11	RPC34	YNR003C	Z71618	CAA96279.1	stan-4-1929	U93869	50.4	28.3	27.3	1
0.34	POP3	YNL282W	Z71558	CAA96194.1	gtc5417	n/a	26.1	-	-	2
0.35	TFA2	YKR062W	Z28287	CAA82141.1	stan-4-2738 / gtc	NP_002086	40.8	23.2	19.4	3
0.36	NAB2	YGL122C	Z72644	CAA96830.1	stan-4-2144	AAD42873	32.2	22.5	22.8	4
0.37	MPT1	YMR005W	Z48613	CAA88520.1	stan-4-2743 / gtc	CAA72189	36.7	23.3	19.2	5
0.39	MTR2	YKL186C	Z28186	CAA82029.1	stan-4-3102	n/a	28.7	-	-	6
0.44	BOS1	YLR078C	X57792	CAA97636.1	stan-4-2841 / gtc	NP_003560	37.9	16.8	18.1	7
0.49	POL30	YBR088C	Z35957	CAA85038.1	gtc2521	P12004	54.5	35.7	41.3	8
0.54	RSA2	YMR131C	NC_001145	CAA88556.1	stan-4-2117	NP_005601	63	24	26.1	9
0.68	SQT1	YIR012W	U75717	AAB69630.1	stan-4-3094	NP_001078	44.5	22.9	25.1	10
0.81	MTW1	YAL034W-A	AB027473	BAA77792.1	stan-4-2532 / gtc	n/a	31.8	-	-	11

5	0.83	TFB1	YDR311W	M95750	AAB64747.1	stan-4-2961	W19128	32.4	23.3	23	12
	0.84	SPC98	YNL126W	Z71402	CAA96007.1	stan-4-2821	AAC39727	30	21.5	19.9	13
	0.85	BFR2	YDR299W	D84656	AAB64735.1	stan-4-3108	NM_000055	42.1	20.7	22.5	14
	1.05	RNA1	YMR235C	Z49939	CAA90206.1	stan-4-2003 / gtc	CAA57714	51.5	32.1	33.7	15
	1.06	GCD7	YLR291C	L07116	AAB67337.1	stan-4-2913	AAC42002	52.2	34.5	35.6	16
10	1.27	SKI6	YGR195W	L36940	CAA97221.1	stan-4-3104	BAA91279	62.5	34.8	39.1	17
	1.28	NIP1	YMR309C	L02899	A46417	stan-4-2825	AAD03462	42.7	30	26.7	18
	1.32	LCP5	YER127W	U18916	AAC03225.1	stan-4-2982	AL050003	34.7	18.6	18	19
	1.63	NCE103	YNL036W	Z71312	CAA95901.1	stan-4-2981	n/a	34.7	-	-	20
	1.67	ECO1	YFR027W	D50617	BAA09266.1	stan-4-2722 / gtc	n/a	34.8	-	-	21
15	1.86	ORC2	YBR060C	Z35929	CAA85003.1	stan-4-3102 / gtc	Q13416	26.7	21	22	22
	1.93	CNS1	YBR155W	Z36024	CAA85114.1	stan-4-3053 / gtc	NP_004614	51.8	26.8	25.6	23
	1.96	YPD1	YDL235C	Z74283	CAA98815.1	stan-4-2907	n/a	33.3	-	-	24
	0.88*	TIM10	YHR005C-A	Z80875	AAB68435.1	stan-4-3104	NP_036588	68.1	36.6	36.6	25
	1.30*	SRB4	YER022W	L12026	AAB64555.1	stan-4-3098	BAA88763	28.4	18	18	26

* half-life determined using temperature-sensitive strain

Production and Isolation of Target Proteins

The invention is also based on the generation of fungal target protein to be used in analysis as an antifungal target. Such generation requires the use of vectors comprising sequences encoding for *S cerevisiae*, *C. albicans* and/or human target proteins, in particular those listed in Table 1, cells comprising the vectors, and methods for producing the *S cerevisiae*, *C. albicans* and/or human target protein homologs that involve culturing the cells.

A large number of vectors, including plasmid and fungal vectors, have been described for expression in a variety of eukaryotic and prokaryotic hosts. Such vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, *e.g.* antibiotic resistance, and one or more expression cassettes. The inserted target protein encoding sequences may be synthesized, isolated from natural sources, prepared as hybrids, etc. Ligation of the coding sequences to the transcriptional regulatory sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected by any suitable method including electroporation, CaCl_2 mediated DNA uptake, fungal infection, microinjection, microprojectile, or other established methods.

A wide variety of host/expression vector combinations may be employed in expressing DNA sequences encoding the target proteins, in particular those listed in Table 1. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of

SV40 and known bacterial plasmids, *e.g.*, *E. coli* plasmids col E1, pCR1, pBR322, pMal-C2, pET, pGEX (Smith *et al.*, Gene 67:31-40, 1988), pMB9 and their derivatives, plasmids such as RP4; phage DNAs, *e.g.*, the numerous derivatives of phage λ , *e.g.*, NM989, and other phage DNA, *e.g.*, M13 and filamentous single stranded phage DNA; yeast plasmids
5 such as the 2 micron plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

Appropriate host cells for expressing protein include bacteria,
10 Archaeobacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *E. coli*, *B. subtilis*, *S. cerevisiae*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation
15 and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under the appropriate expression conditions, host cells can be used as a source of recombinantly produced target proteins. Advantageously, vectors may also include a
20 promoter sequence operably linked to the *S. cerevisiae*, *C. albicans*, and/or human target protein encoding portion. The encoded *S. cerevisiae*, *C. albicans*, and/or human target protein may be expressed by using any suitable vectors and host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not altogether critical to the invention.

25 For the purposes of this invention, the promoter sequence in the vector is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with
30 nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

Expression of *S. cerevisiae*, *C. albicans*, and/or human target protein may be controlled by any promoter/enhancer element known in the art, but these regulatory elements must be functional in the host selected for expression. Promoters which may be used to control *S. cerevisiae*, *C. albicans*, and/or human target protein gene expression include, but are not limited to, Cytomegalovirus immediate early promoter (CMV promoter; US Patent Nos. 5,385,839 and 5,168,062) the SV40 early promoter region (Benoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, Nature 296:39-42); prokaryotic expression vectors such as the β -lactamase promoter (Villa-Kamaroff, *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the *tac* promoter (DeBoer, *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Ornitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adames *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 235:53-58), alpha 1-antitrypsin gene control region which is active in the liver (Kelsey *et al.*, 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogram *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987,

Cell 48:703-712), myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason *et al.*, 1986, Science 234:1372-1378).

Nucleic acids encoding wild-type or variant *S. cerevisiae*, *C. albicans*,
5 and/or human target proteins/polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods, such as non-homologous recombinations or deletion of endogenous genes by homologous recombination,
10 may also be used.

The invention is also based on the generation of isolated and purified *S. cerevisiae*, *C. albicans*, and/or human target proteins/polypeptides, including, *e.g.*, a polypeptide having any of the amino acid sequences depicted in Table 1, as identified by their SEQ ID NOS, as well as function-conservative variants of these polypeptides,
15 including fragments that retain transcriptional and/or other growth regulatory activity as described above.

S. cerevisiae, *C. albicans*, and/or human-derived target proteins/polypeptides according to the present invention, including function-conservative variants, may be isolated from wild-type or mutant *S. cerevisiae* and/or *C. albicans* cells,
20 respectively, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which a *S. cerevisiae*, *C. albicans*, and/or human-derived target protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins. Alternatively, polypeptides may be chemically synthesized by commercially available automated
25 procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis.

"Purification" of a *S. cerevisiae*, *C. albicans*, and/or human target protein/polypeptide refers to the isolation of the polypeptide in a form that allows its transcription and/or growth regulatory activity to be measured without interference by other
30 components of the cell in which the polypeptide is expressed. Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion

exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude
5 lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against *S. cerevisiae*, *C. albicans*, and/or human target protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The polypeptides of the present invention obtained by expression of the
10 polynucleotides of the present invention can be purified from transformed cell cultures by methods known to those of ordinary skill in the art, such as precipitation with ammonium sulphate or ethanol, extraction under acid conditions, anion or cation exchange chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and high performance liquid chromatography (HPLC).
15 Techniques well-known to those of ordinary skill in the art can be used to regenerate the protein if it is denatured during its isolation or purification.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, *i.e.*, a reporter molecule, either directly or
20 indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

Antibodies Directed To Target Proteins

The present invention also encompasses antibodies that bind with high affinity to the *C. albicans* target proteins or fragments identified as described above. As
25 used herein, antibodies with high affinity include without limitation antibodies that bind to any *C. albicans* target protein identified herein in its native or denatured, *i.e.*, folded or unfolded, conformation, particularly preferred antibodies are those which recognize either unfolded or folded target protein to be used in assays as described below. Thus, in one embodiment, the antibodies of the invention are those that are antibody preparations with
30 high affinity for the target protein in its native conformation but not in its denatured, unfolded form, or *vice versa*.

Antibodies which specifically recognize a *C. albicans* target protein in either its native or non-native conformation, may advantageously be used in screens for potential antifungal compounds which bind or otherwise inhibit the biological activity of, the *C. albicans* target protein. In such a screen, antibodies specific for the *C. albicans* target protein in its native conformation may be used to test whether potential antifungal compounds prevent denaturation of the target protein, thus indicating a strong interaction with the target.

Following the binding of the potential antifungal compound to the *C. albicans* target protein, the *C. albicans* target protein is subjected to denaturing conditions, such as, for example, high temperature, pH, denaturing solvents, and denaturants such as, *e.g.*, urea. Following the application of these denaturation conditions, the sample containing the *C. albicans* target protein and a potential antifungal compound is reacted with an antibody specific for the *C. albicans* target protein in either its native or non-native conformation. Binding of this antibody type indicates that the binding of the potential antifungal compounds in the screen protected the target protein from denaturation. Thus, the antibodies of the invention which are specific for either the native or the non-native target protein are useful in the screening of antifungal compounds with any *C. albicans* target protein.

Examples of such types of screens can be found in U.S. Patent No. 5,585,277, issued December 17, 1996, and U.S. Patent No. 5,679,582, issued October 21, 1997, each of which are incorporated herein by reference. The antibodies of the invention may be polyclonal or monoclonal, but most preferably monoclonal. The antibodies may be elicited in an animal host by immunization with a *C. albicans* target protein, or fragments derived therefrom which carry epitopes of the *C. albicans* target protein, or may be formed by *in vitro* immunization of immune cells. The immunogens used to elicit the antibodies may be isolated from *C. albicans* cells or produced in recombinant systems. The antibodies may also be produced in recombinant systems programmed with appropriate antibody-encoding DNA. Alternatively, the antibodies may be constructed by biochemical reconstitution of purified heavy and light chains. The antibodies include hybrid antibodies (*i.e.*, containing two sets of heavy chain/light chain combinations, each of which recognizes a different antigen), chimeric antibodies (*i.e.*, in which either the heavy chains, light chains, or both, are fusion proteins), and univalent antibodies (*i.e.*, comprised of a heavy chain/light

chain complex bound to the constant region of a second heavy chain). Also included are Fab fragments, including Fab' and F(ab)₂ fragments of antibodies.

Methods for the production of all of the above types of antibodies and derivatives are well-known in the art and are discussed in more detail below. For example, techniques for producing and processing polyclonal antisera are disclosed in Mayer and Walker, 1987, *Immunochemical Methods in Cell and Molecular Biology*, Academic Press, London. Such antibodies are conveniently made using the methods and compositions disclosed in Harlow and Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, as well as immunological and hybridoma technologies known to those of ordinary skill in the art. Where natural or synthetic peptides derived from any *C. albicans* target protein are used to induce an specific immune response directed against the *C. albicans* target protein, the peptides may be conveniently coupled to a suitable carrier such as KLH and administered in a suitable adjuvant such as Freund's. Preferably, selected peptides are coupled to a lysine core carrier substantially according to the methods of Tam (Proc. Natl. Acad. Sci. USA 1988; 85:5409).

In one embodiment, a purified recombinant *C. albicans* target protein is used to immunize mice, after which their spleens are removed, and splenocytes used to form cell hybrids with myeloma cells and obtain clones of antibody-secreting cells according to techniques that are standard in the art. The resulting monoclonal antibodies are screened using *in vitro* assays such as those described herein for binding to the *C. albicans* target protein or inhibiting its biological activity. The antibodies are tested for specificity of binding to the *C. albicans* target protein in its native conformation by screening the antibodies for target protein binding before and after subjecting the *C. albicans* target protein to denaturing conditions.

Antibodies specific to a target protein in an unfolded conformation are also useful in screening methods as described below.

In addition to their use in the antifungal compound screens described above, the anti-target protein antibodies of the invention, may be used to quantify a selected undenatured *C. albicans* target protein, using immunoassays such as, but not limited to, ELISA. The antibodies may also be used to block the native function of the chosen *C. albicans* target protein by inhibiting its biological activity, immunodepleting cell extracts, or interfering with other reactions related to the function of the target protein. In addition,

these antibodies can be used to identify, isolate, and purify *C. albicans* target proteins from different sources, and to perform subcellular and histochemical localization studies as well as diagnostic analyses to determine the presence of an antigenic *C. albicans* target protein in a tissue, blood or serum sample.

5

Methods for Determining the Essential Nature of a Putative Essential Gene

Various methods can be used to determine whether the product of a gene is essential to the survival of a mycete or essential to the establishment or maintenance of an infection. The identification of the essential character of a gene provides additional information regarding its function and allows selection of genes for which the product constitutes a target of interest for an antifungal substance. Examples of these methods are summarized briefly below. These methods are described in the following works, each of which are hereby incorporated by reference herein: Guthrie C. and Fink G.R. (eds.), *Methods in Enzymology*, Vol. 194, 1991, 'Guide to Yeast Genetics and Molecular Biology', Academic Press Inc.; Rose A.H., A.E. Wheals and J.S. Harrison (eds.), *The Yeasts*, Vol. 6, 1995, 'Yeast Genetics', Academic Press Inc.; Ausubel F. *et al.* (eds.), *Short Protocols in Molecular Biology*, 1995, Wiley; and Brown A.J.P. and Tuite M.F. (eds.), *Methods in Microbiology*, Vol. 26, 1998, 'Yeast Gene Analysis' Academic Press Inc.

Depending on the circumstances, one of the methods described will be used, depending on the desired result. In particular, it is possible to proceed by a method of either direct inactivation of the gene or transitory inactivation of the gene. Below, we exemplify assays useful for determining the essentiality of *S. cerevisiae* and *C. albicans* genes.

S. cerevisiae Inactivation Analysis

In the yeast *S. cerevisiae*, the method used most generally comprises inactivation of the gene of interest at its site within the chromosome of the yeast. The wild type allele is inactivated by insertion of a genetic marker (for example a gene for auxotrophy or a resistance marker). This insertion is in general obtained by the method of gene conversion with the aid of linear deletion cassettes prepared by known methods, as described in Guthrie C. and Fink G.R. (eds.), *Methods in Enzymology*, or in Gultner *et al.* *Nucleic Acid Research*, 1996, 24: 2519-2524.

Preferred methods, yeast cells and vectors for determining if an *S. cerevisiae*

gene and/or protein is essential for growth and viability are described in U.S. Provisional Patent Application 60/056,719, filed August 22, 1997, U.S. Patent Application No. 09/138,024, filed August 21, 1998, now allowed and awaiting issue, and U.S. Patent Application No. 09/573,322, filed May 18, 2000, each of which are incorporated herein by
5 reference.

Briefly, an *S. cerevisiae* strain in which expression of a particular gene can be tightly regulated is generated. To do this the wild-type allele of the gene of interest is replaced with an allele that can be regulated by exogenous metal. The replacement is generally carried out utilizing a double-crossover strategy with a linear piece of DNA
10 prepared by known methods as described in U.S. Patent and Application Nos. cited above.

The recombinant cells comprise, for example:

(i) a first gene encoding a transcriptional repressor protein, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the repressor protein is stimulated by the addition of a metal ion to the
15 growth medium of the cells;

(ii) a second gene encoding a selected target protein, wherein expression of the target protein is controlled by a promoter, the activity of which is inhibited by the repressor protein; and

(iii) a third gene encoding a biomineralization protein, wherein the third
20 gene is inactivated and wherein inactivation of the third gene enhances the transcriptional response of the metal-responsive element to added metal ions.

In a preferred embodiment, the first gene is ROX1; the second gene is a gene encoding for a target protein described herein, controlled by an ANB1 promoter; and the third gene is SLF1.

25 In a particularly preferred embodiment, the recombinant cells comprise an additional gene such that the cells comprise:

(i) a first gene encoding a transcriptional repressor protein, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the repressor protein is stimulated by the addition of a metal ion to the
30 growth medium of the cells;

(ii) a second gene encoding a target protein, wherein expression of the target protein is controlled by a promoter, the activity of which is inhibited by the repressor protein;

(iii) a third gene encoding a protein that targets ubiquitin-containing
5 polypeptides for degradation, the expression of which has been placed under the control of a metal ion-responsive element, wherein expression of the ubiquitin targeting protein is stimulated by the addition of a metal ion to the growth medium of the cells, wherein the stability of the target protein is controlled by the ubiquitin targeting protein; and

(iv) a fourth gene encoding a biom mineralization protein, wherein the
10 fourth gene is inactivated and wherein inactivation of the fourth gene enhances the transcriptional response of the metal-responsive element to added metal ions.

Thus, in a particularly preferred embodiment, the first gene is ROX1; the second gene, encoding for a target protein according to the invention, is controlled by an ANB1 promoter; the third gene is UBR1; and the fourth gene is SLF1.

15 Utilizing this preferred system, expression of the target protein gene is carried out in the absence of added metal ion. When it is desired to decrease or eliminate expression of the target protein gene, metal ions are added to the medium, which stimulate expression of the repressor and ubiquitin targeting protein to a degree that is dependent upon the concentration of added metal ions and represses transcription of the target protein gene
20 and reduces the stability of the protein. In the preferred system, expression of Rox1 and Ubr1 protein is induced by the addition of copper to the growth media, and thus, expression of the target protein is shut off. If the engineered *S. cerevisiae* strain containing the target protein gene under control of this repressible system stops growing and loses viability in the presence of copper, the target protein is shown to be essential and a cidal target.

25 *S. cerevisiae* inactivation analyses of the target proteins described in Table 1 were conducted as described herein and in Example 1, and the results are presented in FIGS. 27-52.

Once the *S. cerevisiae* target protein has been shown to be both essential for growth and viability, and a cidal target in *S. cerevisiae*, the homologous *C. albicans* gene
30 and/or protein must then be analyzed to determine if either are essential for growth and can act as a potential cidal target in *C. albicans*. The *C. albicans* gene is identified by comparative sequence analysis. When a DNA fragment is required for some type of analysis

(gene inactivation or protein expression) it is preferably obtained by PCR cloning using methods well known in the art (See for example, Eds. C.W. Dieffenbach and E.F. Dvekfler, PCR Primer: A Laboratory Manual Cold Spring Harbor Laboratory Press, Plainview, New York, 1995.)

5

C. albicans Deletion Analysis

Determining if a particular gene or protein is essential for growth is carried out by determining if, when the gene or protein is inactivated in *C. albicans*, the cells will survive. Because *C. albicans* is a diploid fungus which, largely due to the absence of a sexual phase in its life cycle, is resistant to a considerable number of genetic techniques that are applicable to *S. cerevisiae*, DNA constructs are used to inactivate, or delete all, or a portion, of the gene of interest in *C. albicans*. Such constructs provide for the inactivation or deletion of the wild type allele by insertion of a genetic selection marker (for example a gene for auxotrophy or a resistance marker). This insertion is in general obtained by the method of gene conversion with the aid of linear deletion cassettes prepared by known methods of DNA manipulation as described above.

In one embodiment, in order to assess whether the target protein gene is essential for growth in *C. albicans*, plasmids can be used to construct a double disruptant strain according to the methods outlined in Figures 53-78. If a double disruptant strain can be produced, then the gene is determined to be non-essential. Methods used in these constructions employ common techniques employed in the genetic manipulation and screening of *C. albicans*.

One commonly used approach utilizes *C. albicans* strain CAI4 (Fonzi and Irwin, 1993) to generate a uridine auxotrophic strain of *C. albicans* transformed with linearized DNA fragments containing the *CaURA3* gene (able to confer uridine prototrophy upon transformants) flanked by identical *HisG* sequences. This *HisG-CaURA3-HisG* cassette is flanked by sequences upstream of the gene of interest on one side and downstream of it on the other side.

Prototrophic transformants have undergone replacement of one copy of the gene of interest with the *HisG-CaURA3-HisG* cassette. Auxotrophic, uridine requiring derivatives can be isolated by selecting for 5' fluoro-orotic acid (FOA) resistance in the presence of uridine. The *URA3* gene product converts FOA into fluorouracil which is toxic.

FOA selection therefore allows one to select cells that have lost the *URA3* gene upon *cis*-recombination of the two identical *hisG* flanking regions.

To determine if the gene of interest is essential for growth, a second disruption plasmid is used in order to attempt to inactivate the second copy of the gene. The *CaURA3* gene, as described above, is able to confer uridine prototrophy upon transformants, and is flanked by identical *HisG* sequences. This *HisG-CaURA3-HisG* cassette is flanked by sequences upstream of the gene of interest on one side and downstream of the gene of interest on the other side. Generation of prototrophic transformants can occur by integration of the cassette into the non-disrupted allele of the gene of interest, by replacement of the *hisG* cassette with the *CaURA3* cassette, or by non-homologous recombination events. Transformants that disrupt the second copy of the gene is proof that the gene of interest is not essential. In order to establish that a gene in *C. albicans* is essential for growth, at least 20 second round transformants should be analyzed. If analysis of 20 transformants demonstrates that the second copy of the gene is still present, this indicates that the gene is essential. All transformants are analyzed by Southern blotting. *Candida albicans* transformations are performed as described (Elble R., *Biotechniques* 1992;13:18-20).

A second commonly used approach utilizes *C. albicans* strain CAI8 (Fonzi and Irwin, 1993). CAI8 is a uridine and adenine auxotrophic strain that can be converted to uridine and adenine prototrophy by transformation with *C. albicans* *URA3* (*CaURA3*) and *C. albicans* *ADE2* (*CaADE2*), respectively.

Deletion of the first allele of the gene of interest is accomplished by transformation of CAI8 to adenine prototrophy with a linearized DNA fragment containing the *CaADE2* gene flanked by sequences upstream of the gene of interest on one site and downstream of it on the other site.

To determine if the gene of interest is essential for growth, a second disruption plasmid is used in order to attempt to inactivate the second copy of the gene. The *CaURA3* is flanked by sequences upstream of the gene of interest on one site and downstream of it on the other site. Generation of adenine/uridine prototrophic transformants can occur by integration of the cassette into the non-disrupted allele of the gene of interest, or by non-homologous recombination events. Transformants that disrupt the second copy of the gene is proof that the gene of interest is not essential. In order to establish that a gene in *C. albicans* is essential for growth at least 20 second round transformants should be

analyzed. If analysis of 20 transformants shows that the second copy of the gene is still present and could not be deleted, which indicates that the gene is essential. All transformants are analyzed by Southern blotting. *Candida albicans* transformations are performed as previously described (Elble, 1992).

5 URA3 can be used for either of the selectable markers as described above with the CAI8 strain.

These types of analytical procedures can also be carried out by transitory inactivation of the gene of interest with adjustable promoters other than that described above with the Rox1 repressor protein. To achieve this, the native promoter of the gene is replaced
10 by an adjustable promoter directly on the chromosome or on an extra chromosomal plasmid. One example of another adjustable promoter for use in this method is the CAL promoter or its derivatives, or the tetO promoter (Mumberg *et al.* 1994, *Nucleic Acid Research*, 22: 5767-5768; Belli *et al.* 1998, *Yeast*, 14: 1127-1138). The essential character of the gene studied can thus be observed, while the promoter used is repressed, either in the haploid
15 strains in the yeast *S. cerevisiae*, or after inactivation of the second allele in the diploid microorganism (for example *C. albicans*).

C. albicans deletion analyses were carried out for each of the target genes identified in Table 1, as described in this section and in Example 2. The results are presented in FIGS. 53-78, each figure representing a single target gene.

20

Methods for Identifying Homologous Genes

From a known essential gene in a species, genes which are homologous or have the same function in another species of mycete can be identified. The methods known to those of ordinary skill in the art can be used to identify a homolog to a gene studied in
25 another species of mycete (so-called "orthologous" genes) or genes having the same function as the gene studied. Examples of methods which can be used are given below. These methods are described in the following works which are hereby incorporated by reference herein: Sambrook *et al.* 1989, Molecular Cloning, Cold Spring Harbor Laboratory Press; Ausubel F. *et al.* eds. Short Protocols in Molecular Biology, 1995, Wiley; and Guthrie C.
30 and Fink G.R. eds. Methods in Enzymology, Vol. 194, 1991, 'Guide to Yeast Genetics and Molecular Biology', Academic Press Inc.

Such methods include screening for homology or gene complementation to

genomic or cDNA libraries of pathogenic mycetes, or PCR amplification of such library DNA using specific primers selected by virtue of their homology to the nucleotide sequence of interest.

The homologous DNA sequences of other mycetes as defined above can be
 5 isolated, in particular, by the PCR amplification methods known to those of ordinary skill in the art. A non-limiting of such PCR technique is carried out using degenerate nucleotide primers to amplify these homologous DNAs from genomic or cDNA libraries of the corresponding mycetes. The cDNAs can also be prepared from mRNAs isolated from mycetes of various species studied in the context of the present invention, directed to
 10 *Saccharomyces cerevisiae* and *Candida albicans*, namely *Candida stellatoidea*, *Candida tropicalis*, *Candida parapsilosis*, *Candida krusei*, *Candida pseudotropicalis*, *Candida quilliermondii*, *Candida glabrata*, *Candida lusitanae* or *Candida rugosa*, or also mycetes of the type *Aspergillus* or *Cryptococcus*, and in particular, for example, *Aspergillus fumigatus*, *Coccidioides immitis*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, *Blastomyces*
 15 *dermatitidis*, *Paracoccidioides brasiliensis* and *Sporothrix schenckii*, or also mycetes of the classes of *Phycomycetes* or *Eumycetes*, in particular the sub-classes of *Basidiomycetes*, *Ascomycetes*, *Mehiascomycetales* (yeast) and *Plectascales*, *Gymnascales* (fungus of the skin and hair) or of the class of *Hyphomycetes*, in particular the sub-classes *Conidiosporales* and *Thallosporales*, and among these the following species: *Mucor*, *Rhizopus*, *Coccidioides*,
 20 *Paracoccidioides* (*Blastomyces*, *brasiliensis*), *Endomyces* (*Blastomyces*), *Aspergillus*, *Menicillium*, (*Scopulariopsis*), *Trichophyton* (*Ctenomyces*), *Epidermophyton*, *Microsporon*, *Piedraia*, *Hormodendron*, *Phialophora*, *Sporotrichon*, *Cryptococcus*, *Candida*, *Geotrichum*, *Trichosporon* or also *Toropsulosis*.

Homologous polynucleotides can thus be obtained using the usual methods of
 25 cloning and screening, such as those of cloning and sequencing from fragments of chromosomal DNA extracted from cells. For example, to obtain such homologous polynucleotides, it is possible to start from a library of chromosomal DNA fragments. A probe corresponding to a radiolabeled oligonucleotide, preferably made up of 17 nucleotides or more and derived from a partial sequence, can be prepared. The clones containing a DNA
 30 identical to that of the probe can thus be identified under stringent conditions. By sequencing individual clones identified in this way using sequencing primers resulting from the original sequence, it is then possible to prolong the sequence in both directions to determine the

sequence of the complete gene. Such sequencing can usually be carried out effectively using a double-stranded denatured DNA prepared from a plasmid. Such techniques are described by Maniatis, T., Frisch, E.F., and Sambrook as indicated above. (Laboratory Manual, Cold Spring Harbor, New York (1989), in particular in 1.90 and 13.70 in the chapters on
5 screening by hybridization and sequencing from double-stranded denatured DNA).

The genomic DNA or cDNA libraries can be prepared by known methods and the polynucleotide fragments obtained are integrated into an expression vector, for example a vector such as pRS423 or its derivatives, which can be used both in the bacterium *E. coli* and in *S. cerevisiae*. Screening of the library will be carried out by conventional
10 methods of *in situ* hybridization on a replica of bacterial colonies. The hybridization conditions will be adapted to the stringency required for the reaction so that fragments more or less homologous with the gene studied are identified. The genes of other species of mycetes can also be identified by known so-called "gene complementation" methods. For example, a strain of *S. cerevisiae* in which an identified essential gene has been placed under
15 the control of an adjustable promoter can be transformed by a representative sample of a DNA or cDNA library corresponding to the mycete studied. When yeasts are cultured under conditions such that the promoter is repressed, the only yeasts that can survive are the ones that carry a recombinant vector containing a sequence of the mycete studied which is functionally equivalent to the initial essential gene. The gene sequence in the mycete studied
20 is then identified by isolating the recombinant vector and sequencing it by known methods. In the same way, the so called "plasmid shuffle" method allows selection of yeasts which have lost expression of the initial essential gene and contain a functionally equivalent sequence originating from another mycete.

This type of study can be performed on various species: the genes which are
25 functionally equivalent or homologous in sequence to an essential gene can be isolated in other mycetes, and in particular in the various mycetes which are pathogenic to humans. For this, it is possible to use, in particular, mycetes belonging to the classes *Zygomycetes*, *Basidiomycetes*, *Ascomycetes* and *Deuteromycetes*. More particularly, the mycetes will belong to the sub-classes *Candida* spp., in particular *Candida albicans*, *Candida glabrata*,
30 *Candida tropicalis*, *Candida parapsilosis* and *Candida krusei*. The mycetes will also belong to the sub-classes *Aspergillus fumigatus*, *Coccidioides immitis*, *Cryptococcus neoformans*, *Histoplasma capsulatum*, *Blastomyces dermatidis*, *Paracoccidioides brasiliensis* and

Sporothrix schenckii.

Inhibition of Fungal Growth

The present invention provides for a number of strategies to inhibit fungal growth by inhibiting the biological activity of the target proteins provided herein. As described above, these fungal target proteins are involved in a wide range of activities related to growth and viability, such as, but not limited to, DNA transcription, mRNA translation, mRNA and protein processing and transport, cell division, growth regulation, cell cycle regulation, and other processes. Although the exact function of some target proteins is not yet known, the target proteins provided by the invention all have the common feature of being involved in fungal growth. In the section below, transcription is exemplified as one potential mechanism through which growth can be affected, but it is to be understood that other mechanisms not specifically described below can be used for studying and/or implementing growth inhibition using the methods described herein.

Transcription

The present invention provides methods of modifying gene transcription by contacting a *S. cerevisiae* and/or *C. albicans* target protein with substances that bind to, or interact with, such a protein or the DNA/RNA encoding such a protein. These substances may modify the influence of the *S. cerevisiae* and/or *C. albicans* target protein on transcription, chromatin remodeling or other processes essential to gene transcription. Substances that bind to, or interact with, the *S. cerevisiae* and/or *C. albicans* target protein or the DNA/RNA encoding such a protein can prevent or enhance its biological activity, which may directly or indirectly inhibit fungal growth.

For example, anti-sense or non-sense nucleotide sequences that hybridize with the *S. cerevisiae* and/or *C. albicans* target protein DNA or RNA and either completely inhibit or decrease their translation or transcription can prevent and inhibit the transcription of other fungal genes. Alternatively, compounds that can bind to or interact with the *S. cerevisiae* and/or *C. albicans* target protein can prevent or enhance the function of the protein in the transcription process. These substances include antibodies that are reactive with and bind to either or both of the *S. cerevisiae* and/or *C. albicans* target proteins.

Candidate Inhibitors

Once it has been determined that the target protein is a cidal target in *Saccharomyces cerevisiae* and essential for growth *Candida albicans*, the protein may be used as a cidal target in order to isolate candidate inhibitors of fungal growth and/or infection.

5 As noted above, a "candidate inhibitor," as used herein, is any compound with a potential to inhibit, in *Candida albicans* or other fungal species, the biological activity of a target protein. Candidate inhibitor compounds are first identified in a primary screen against the *C. albicans* target protein. This primary screen may be affinity based, mechanistic (*e.g.*, *in vitro* transcription assay), or cell-based (*e.g.*, reporter assay). Such
10 assays are described further below. A candidate inhibitor is tested in a concentration range that depends upon the molecular weight of the molecule and the type of assay. For example, for inhibition of protein/protein or protein/DNA complex formation or transcription elongation small molecules (as defined below) may be tested in a concentration range of 1pg - 100 ug/mL, preferably at about 100 pg - 20 ug/mL; large molecules, *e.g.*, peptides, may
15 be tested in the range of 10 ng - 100 ug/mL, preferably 100 ng - 10 ug/mL.

Inhibitors of *Candida albicans* growth or viability may target the *C. albicans* target proteins described herein, or it may target a protein or nucleic acid that interacts with the *C. albicans* target protein to prevent the natural biological interaction that occurs *in vivo*. An inhibitor identified as described herein must possess the property that at some
20 concentration it will inhibit *Candida albicans* growth or viability, most preferably at the same concentration it will not significantly affect the growth of mammalian, particularly human, cells.

Candidate inhibitors include peptide and polypeptide inhibitors having an amino acid sequence based upon the *C. albicans* target protein sequences described herein.
25 For example, a fragment of the *C. albicans* target protein may act to prevent the growth of wild type *Candida albicans* cells because it acts as a competitive inhibitor with respect to the *C. albicans* target protein binding to other proteins involved in *Candida* growth, *e.g.*, chromatin binding, cell division, transcription, or another essential activity.

Inhibitory compounds to be tested are screened from large libraries of
30 synthetic or natural compounds. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from Maybridge Chemical Co. (Trevillet,

Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from *e.g.* Pan Laboratories (Bothell, WA) or
5 MycoSearch (NC), or are readily producible. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Compounds useful as inhibitors may be found within numerous chemical classes, though typically they are organic compounds, and preferably small organic
10 compounds. Small organic compounds have a molecular weight of more than 50 yet less than about 2,500 daltons, preferably less than about 750, more preferably less than about 350 daltons. Exemplary classes include heterocycles, peptides, saccharides, steroids, and the like. The compounds may be modified to enhance efficacy, stability, pharmaceutical compatibility, and the like. Structural identification of an agent may be used to identify,
15 generate, or screen additional agents. For example, where peptide agents are identified, they may be modified in a variety of ways to enhance their stability, such as using an unnatural amino acid, such as a D-amino acid, particularly D-alanine, by functionalizing the amino or carboxylic terminus, *e.g.* for the amino group, acylation or alkylation, and for the carboxyl group, esterification or amidification, or the like. Other methods of stabilization
20 may include encapsulation, for example, in liposomes, etc.

Primary Inhibitor Screening

High-Throughput Methods For Screening Inhibitors

In a preferred embodiment, a high-throughput screening protocol, also
25 referred to as ATLAS, is used to survey a large number of test compounds for their ability to bind or otherwise interact with a *C. albicans* target protein. High-throughput screening methods are described in U.S. Patent Nos. 5,585,277 and 5,679,582, in U.S.S.N. 08/547,889, and in the published PCT application PCT/US96/19698, and may be used for identifying a ligand that binds the target proteins described herein. According to these
30 methods, a ligand, or a plurality of ligands for a *C. albicans* target protein is identified by its ability to influence the extent of folding or the rate of folding or unfolding of the target protein. Experimental conditions are chosen so that the target protein unfolds to a

measurable extent, whether reversible or irreversible. If the test ligand binds to the target protein under these conditions, the relative amount of folded:unfolded target protein or the rate of folding or unfolding of the target protein in the presence of the test ligand will be different, *i.e.* higher or lower, than that observed in the absence of the test ligand. Thus,

5 the method encompasses incubating the *C. albicans* target protein in the presence and absence of a plurality of test ligands under conditions in which (in the absence of ligand) the target protein would partially or totally unfold. This is followed by analysis of the absolute or relative amounts of folded vs. unfolded target protein or of the rate of folding or unfolding of the target protein.

10 An important feature of this method is that it will detect any compound that binds to any sequence or domain of the *C. albicans* target protein, and not only to sequences or domains that are intimately involved in a biological activity or function. The binding sequence, region, or domain may be present on the surface of the target protein when it is in its folded state, or may be buried in the interior of the protein. Some binding sites may only
15 become accessible to ligand binding when the protein is partially or totally unfolded.

Briefly, to carry out this method, the test ligand or ligands are combined with the *C. albicans* target protein, and the mixture is maintained under appropriate conditions and for a sufficient time to allow binding of the test ligand. Experimental conditions are determined empirically. When testing test ligands, incubation conditions are chosen so that
20 most ligand:target protein interactions would be expected to proceed to completion. The test ligand is present in molar excess relative to the target protein. The target protein can be in a soluble form, or, alternatively, can be bound to a solid phase matrix. The matrix may comprise without limitation beads, membrane filters, plastic surfaces, or other suitable solid supports.

25 In a preferred embodiment, binding of test ligand or ligands to the target protein is detected through the use of proteolysis. This assay is based on the increased susceptibility of unfolded, denatured polypeptides to protease digestion relative to that of folded proteins. In this case, the test ligand-target protein combination, and a control combination lacking the test ligand, are treated with one or more proteases that act
30 preferentially upon unfolded target protein. After an appropriate period of incubation, the level of intact *i.e.* unproteolysed target protein is assessed using one of the methods described below *e.g.* gel electrophoresis and/or immunoassay.

There are two possible outcomes that indicate that the test ligand has bound the target protein. Either 1) a significantly higher, or 2) a significantly lower absolute amount of intact or degraded protein may be observed in the presence of ligand than in its absence.

5 Proteases useful in practicing the present invention include without limitation trypsin, chymotrypsin, V8 protease, elastase, carboxypeptidase, proteinase K, thermolysin, papain and subtilisin (all of which can be obtained from Sigma Chemical Co., St. Louis, MO). The most important criterion in selecting a protease or proteases for use in practicing the present invention is that the protease(s) must be capable of digesting the target protein
10 under the chosen incubation conditions, and that this activity be preferentially directed towards the unfolded form of the protein. To avoid "false positive" results caused by test ligands that directly inhibit the protease, more than one protease, particularly proteases with different enzymatic mechanisms of action, can be used simultaneously or in parallel assays. In addition, co-factors that are required for the activity of the protease(s) are provided in
15 excess, to avoid false positive results due to test ligands that may sequester these factors.

In a typical embodiment of this method, purified target protein is first taken up to a final concentration of about 1-100 g/mL in a buffer containing 50 mM Tris-HCl, pH 7.5, 10% DMSO, 50 mM NaCl, 10% glycerol, and 1.0 mM DTT. Proteases, such as, for example, proteinase K or thermolysin (proteases with distinct mechanisms of action), are
20 then added individually to a final concentration of 0.2-10.0 g/mL. Parallel incubations are performed for different time periods ranging from 5 minutes to one hour, preferably 30 minutes, at 4°C, 15°C, 25°C, and 35°C. Reactions are terminated by addition of an appropriate protease inhibitor, such as, for example, phenylmethylsulfonyl chloride (PMSF) to a final concentration of 1mM (for serine proteases), ethylenediaminetetraacetic acid
25 (EDTA) to a final concentration of 20 mM (for metalloproteases), or iodoacetamide (for cysteine proteases). The amount of intact protein remaining in the reaction mixture at the end of the incubation period may then be assessed by any method, including without limitation polyacrylamide gel electrophoresis, ELISA, or binding to nitrocellulose filters. It will be understood that additional experiments employing a narrower range of temperatures
30 can be performed to establish appropriate conditions. This protocol allows the selection of appropriate conditions (*e.g.*, protease concentration and digestion temperature) that result in

digestion of approximately 70% of the target protein within a 30 minute incubation period, indicating that a significant degree of unfolding has occurred.

In another embodiment, the relative amount of folded and unfolded target protein in the presence and absence of test ligand is assessed by measuring the relative amount of the protein that binds to an appropriate surface. This method takes advantage of the increased propensity of unfolded proteins to adhere to surfaces, which is due to the increased surface area, and decrease in masking of hydrophobic residues, that results from unfolding. If a test ligand binds the *C. albicans* target protein (*i.e.*, is a ligand), it may stabilize the folded form of the target protein and decrease its binding to a solid surface. Alternatively, a ligand may stabilize the unfolded form of the protein and increase its binding to a solid surface.

Surfaces suitable for this purpose include without limitation microtiter plates constructed from a variety of treated or untreated plastics, plates treated for tissue culture or for high protein binding, nitrocellulose filters and PVDF filters.

In another embodiment, the extent to which folded and unfolded target protein are present in the test combination is assessed through the use of antibodies specific for either the unfolded state or the folded state of the protein *i.e.* denatured-specific ("DS"), or native-specific ("NS") antibodies, respectively. (Breyer, *J. Biol. Chem.* 1989; 264(5):13348-13354). Polyclonal or monoclonal antibodies are prepared as described above. The resulting antibodies are screened for preferential binding to the *C. albicans* target protein in its denatured state. These antibodies are used to screen for inhibitors of these interactions.

In another embodiment, molecular chaperones are used to assess the relative levels of folded and unfolded protein in a test combination. Chaperones encompass known proteins that bind unfolded proteins as part of their normal physiological function. In this embodiment, a test combination containing the test ligand and the *C. albicans* target protein is exposed to a solid support *e.g.* microtiter plate or other suitable surface coated with a molecular chaperone, under conditions appropriate for binding the target protein with its ligand and binding of the molecular chaperone to unfolded target protein. The unfolded target protein in the solution will have a greater tendency to bind to the molecular chaperone-covered surface relative to the ligand-stabilized folded target protein. Thus, the ability of the test ligand to bind target protein can be determined by determining the amount

of target protein remaining unbound, or the amount bound to the chaperone-coated surface. Alternatively, a competition assay for binding to molecular chaperones can be utilized.

Once conditions are established for high-throughput screening as described above, the protocol is repeated simultaneously with a large number of test ligands at
5 concentrations ranging from, *e.g.*, 20 to 200 M. Observation of at least a two-fold increase or decrease in the extent of digestion of the target protein signifies a "hit" compound, *i.e.*, a ligand that binds the target protein. Preferred conditions are those in which between 0.1 % and 1 % of test ligands are identified as "hit" compounds using this procedure.

In yet another embodiment, the test and control combinations described
10 above can be contacted with a conformation-sensitive probe containing a reporter molecule such as, *e.g.*, a fluorescent molecule or radionucleotide, *i.e.*, a probe that binds preferentially to the folded, unfolded, or molten globule state of the *C. albicans* target protein or whose reporter-mediated properties are in any way affected by the folding status of the *C. albicans* target protein.

15 Phage Display Technology Screening

In addition to the high-throughput screening techniques described above, technologies for molecular identification can be employed in the identification of inhibitor molecules. One of these technologies is phage display technology (U.S. Patent No. 5,403,484. Viruses Expressing Chimeric Binding Proteins). Phage display permits
20 identification of a binding protein against a chosen target. Phage display is a protocol of molecular screening which utilizes recombinant bacteriophage. The technology involves transforming bacteriophage with a gene that encodes an appropriate ligand (in this case, a candidate inhibitor) capable of binding to the target molecule of interest. For the purposes of this disclosure, the target molecule may be a *C. albicans* target protein. The transformed
25 bacteriophage (which preferably is tethered to a solid support) express the candidate inhibitor and display it on their phage coat. The cells or viruses bearing the candidate inhibitor which recognize the target molecule are isolated and amplified. The successful inhibitors are then characterized.

Phage display technology has advantages over standard affinity ligand
30 screening technologies. The phage surface displays the microprotein ligand in a three dimensional conformation, more closely resembling its naturally occurring conformation. This allows for more specific and higher affinity binding for screening purposes.

Biospecific Interaction Analysis Screening

Another relatively new screening technology which may be applied to the inhibitor screening assays of this invention is biospecific interaction analysis (BIAcore, Pharmacia Biosensor AB, Uppsala, Sweden). This technology is described in detail by Jonsson *et al.* (Biotechniques 11:5, 620-627 (1991)). Biospecific interaction analysis utilizes surface plasmon resonance (SPR) to monitor the adsorption of biomolecular complexes on a sensor chip. SPR measures the changes in refractive index of a polarized light directed at the surface of the sensor chip.

Specific ligands (*i.e.*, candidate inhibitors) capable of binding to the target molecule of interest (*i.e.*, a *C. albicans* target protein or a protein-protein or protein-DNA complex containing the *C. albicans* target protein) are immobilized to the sensor chip. In the presence of the target molecule, specific binding to the immobilized ligand occurs. The nascent immobilized ligand-target molecule complex causes a change in the refractive index of the polarized light and is detected on a diode array. Biospecific interaction analysis provides the advantages of; 1) allowing for label-free studies of molecular complex formation; 2) studying molecular interactions in real time as the assay is passed over the sensor chip; 3) detecting surface concentrations down to 10 pg/mm²; detecting interactions between two or more molecules; and 4) being fully automated (Biotechniques 11:5, 620-627 (1991)).

Screening Through Use Of A Transcription Assay

In cases where the target protein has been identified as being required for transcription *per se* and/or elongation, the present invention encompasses the identification of agents useful in modulating fungal gene transcription, particularly the transcription of genes by RNA polymerase II in a target protein-dependent manner. Thus, if the target protein has been identified as being essential for transcription and/or elongation, inhibitors of *Candida albicans* growth and viability may also be screened either by measuring inhibition of any of the activities described above, or by assaying formation of a protein/DNA complex or inhibition of sporulation when cells are contacted with *Candida albicans* inhibitors.

In Vitro Transcription Assay

If an essential target protein has been identified as being required for transcription, and it has been identified according to any of the screening methods described above, its activity and effect on transcription can be confirmed by adding it to an *in vitro* transcription reaction, and measuring its effect on the target protein-mediated activated transcription, using an *in vitro* transcription assay. For example, DNA of interest (*i.e.*, DNA to be transcribed) can be admixed with (i) purified RNA polymerase II, (ii) the SRB proteins, (iii) transcription factors b, e, g or a, (iv) the *C. albicans* target protein and (v) the substance (ligand) to be tested. The mixture is maintained under conditions sufficient for transcription to occur. The resulting combination is referred to as a test mixture. DNA transcription can be assessed by determining the quantity of mRNA produced. Transcription is determined in the presence of the substance being tested and compared to DNA transcription in the absence of the test substance taking place under identical conditions (*e.g.*, a control mixture). If transcription occurs to a lesser extent in the test mixture, (*i.e.*, in the presence of the substance being evaluated) than in the control mixture, the substance may have interacted with one or more SRB proteins, or with the *C. albicans* target protein, preferably in such a manner as to inhibit transcription. If transcription occurs to a greater extent in the test mixture than in the control mixture, the substance has interacted in such a manner as to stimulate transcription.

Transcription of DNA sequences, or translation of mRNA sequences encoding the *C. albicans* target protein can also be inhibited or decreased by inhibitor compounds, resulting in decreased production of, or the complete absence of the *C. albicans* target protein. Gene transcription can be modified by introducing an effective amount of a substance into a cell that inhibits transcription of the gene encoding the *C. albicans* target protein, or that inhibits translation of mRNA encoding the *C. albicans* target protein. For example, antisense nucleotide sequences can be introduced into the cell that will hybridize with the gene encoding the target protein and inhibit transcription of the gene. (*See, Current Protocols in Molecular Biology*, Eds. Ausubel *et al.* Greene Publ. Assoc., Wiley-Interscience, NY, NY, 1997). Alternatively, an antisense sequence can be introduced into the cell that will interfere with translation of the mRNA encoding the *C. albicans* target protein.

Secondary Screens - Measurement of Inhibition of *Candida albicans* Growth in Culture

Once a putative inhibitor has been identified in the primary screen or screens, it may be desirable to determine the effect of the inhibitor on the growth and/or viability of *Candida albicans* in culture. Methods for performing tests on fungal growth inhibition in
5 culture are well-known in the art.

Non-limiting examples of such procedures test the candidate inhibitor compounds for antifungal activity against a panel of three strains: *C. albicans*, *S. cerevisiae*, and *A. nidulans*. One such procedure is based on the NCCLS M27A method (The National Committee for Clinical Laboratory Standards, Reference Method for Broth Microdilution
10 Antifungal Susceptibility Testing of Yeasts; approved standard, 1997) to measure minimum inhibitory concentrations (MICs) and minimum fungicidal concentrations (MFCs). An overview of this of this protocol follows.

Media

- 15 1. *Sabouraud dextrose agar* (SDA): 10 g Bacto Neopeptone; 40 g Bacto Dextrose; 15 g Bacto Agar. Suspend contents in 1 liter of water and boil while stirring to dissolve completely. Autoclave for 15 minutes. SDA is conveniently sold as a powdered mix by DIFCO (Cat #0109-17-1).
2. *Potato dextrose agar* (PDA): 4 g Potato extract; 20 g Bacto
20 Dextrose; 15 g Bacto Agar. Suspend contents in 1 liter of water and boil while stirring to dissolve completely. Autoclave for 15 minutes. PDA is conveniently sold as a powdered mix by DIFCO (Cat #0013-17-6).
3. *RPMI-1640*: 10.4 g powdered media (Sigma R-6504, w/ glutamine & w/o bicarbonate); 2.0 g NaHCO₃ (Sigma S-6297); 34.53 g MOPS buffer (Sigma M-6270).
25 Dissolve powdered media and NaHCO₃ in 900 ml distilled water. Add MOPS and stir until dissolved. Adjust pH to 7.0 using 1N NaOH. Bring final volume to 1 liter, filter sterilize, and store at 4°C.
4. *RPMI-1640 with 12.5 % mouse serum*: 10.4 g powdered media
(Sigma R-6504, w/ glutamine & w/o bicarbonate); 2.0 g NaHCO₃ (Sigma S-6297); 34.53 g
30 MOPS buffer (Sigma M-6270); 50 ml mouse serum (Sigma S-7273). Dissolve powdered media and NaHCO₃ in 750 ml distilled water. Add MOPS and stir until dissolved. Adjust pH to 7.0 using 1N NaOH and bring volume to 875 ml. Remove 350 ml and add to it 50 ml

of mouse serum. Bring remaining volume of media (525 ml) to 600 ml with the addition of 75 ml of distilled water. Filter sterilize each solution and store at 4°C.

Inoculum Preparation

1. *Yeasts:* Yeasts (*Saccharomyces cerevisiae* and *Candida albicans*) are
5 cultured on Sabouraud dextrose agar (SDA) plates in a 35°C incubator. Strains on SDA plates are stored at 4°C and used as working stock cultures. Working stock plates are prepared once a month from frozen stocks of cells. Inoculum for susceptibility testing is prepared from fresh 24 hour cultures. 5-10 colonies are scraped from the plate and suspended in three milliliters of sterile 0.85% saline (8.5 g/liter NaCl). The cell density of
10 the solution is determined by measuring the absorbance in a spectrophotometer (Shimadzu UV-1201S UV-VIS Spectrophotometer) set at 600 nm. An absorbance value between 0.1 and 0.4 is required for an accurate reading.

For *C. albicans*, e.g., strain ATCC 10231, 1.0 OD₆₀₀ unit is approximately 10⁷ cells per ml while for *Saccharomyces cerevisiae* strain CTY552 1.0 OD₆₀₀ unit is slightly
15 less than 10⁷ cells per ml. Dilute the cell suspension with the appropriate medium (typically RPMI-1640) to OD₆₀₀=0.0003 for *Candida* and OD₆₀₀=0.0004 for *Saccharomyces*. The diluted suspension should contain approximately 3 X 10³ cells per ml (this is a 2X concentration inoculum). Two 100 ul aliquots of this dilution should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming
20 units. An acceptable range for the inoculum (2X) is 1-5 X 10³ cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be 0.5-2.5 X 10³ per ml. The inoculum should be kept at 4°C and used within a few hours.

2. *Filamentous fungi:* Filamentous fungi (*Aspergillus* spp.) should be
25 cultured on Potato dextrose agar (PDA) plates in a 35°C incubator. A fresh plate should be started from frozen cell stocks once a month. Inoculum of *Aspergillus* for susceptibility testing is prepared from plates incubated at 35°C for 5 days. Colonies are covered with five ml of sterile 0.85% saline (8.5 g/liter NaCl) and gently rocked for 10-15 minutes. To dislodge the conidia, use an automatic pipettor to gently wash over the colonies. The saline
30 solution is removed from the plate and the heavy particles allowed to settle for 3-5 minutes. The upper suspension is removed and vortexed for 15 sec. The turbidity of the solution is determined by measuring the absorbance in a spectrophotometer (Shimadzu UV-1201S UV-

VIS Spectrophotometer) set at 600 nm. An absorbance value between 0.1 and 0.4 is required for an accurate reading.

Dilute the cell suspension with the appropriate medium (typically RPMI-1640) to $OD_{600}=0.0004$. The final suspension should contain approximately 3×10^3 cfu per ml (this is a 2X concentration inoculum). Two 100 ul aliquots of this dilution should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming units. An acceptable range for the inoculum (2X) is $1-5 \times 10^3$ cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be $0.5-2.5 \times 10^3$ per ml. The inoculum should be kept at 4°C and used within a few hours.

Compound Preparation

Stock solutions and concentrations tested will vary from compound to compound. In general, though, stock solutions of 12.8 mg/ml in DMSO (Sigma D-8779) should be prepared. This will allow for a 128 ug/ml starting test concentration containing 1% DMSO. Stock solutions should be stored at -20°C and dilutions for antifungal testing should be freshly prepared before each assay.

For compounds of unknown activity or ones with MIC values of >4 ug/ml, a range of concentrations from 128 ug/ml to 0.125 ug/ml should be used. More active compounds, such as Amphotericin B (Sigma A2411) and Itraconazole (Research Diagnostics Inc. cat# 30.211.44), require a lower range of concentrations (16 ug/ml to 0.016 ug/ml). Stock solutions of Amphotericin B and Itraconazole should be prepared at 1.6 mg/ml in DMSO. Amphotericin B is sold as a powder that is approximately 80% Amphotericin B. Stock solutions should be made accordingly (2.0 mg of powder for a 1 ml solution of 1.6 mg/ml Amphotericin B).

Stock solutions of control compounds (1.6 mg/ml, Amphotericin B or Itraconazole) are initially diluted in medium to a concentration of 32 ug/ml while stock solutions of test compounds (typically 12.8 mg/ml) are diluted to 256 ug/ml. Both of these (control and test compounds) represent 1:50 dilutions. For an assay with three fungal strains, 40 microliters of a stock solution should be diluted to 2.0 ml with room temperature medium. If a stock solution of a test compound is not at 12.8 mg/ml, the appropriate

dilution must be calculated. Serial dilutions will be produced (see below) using these initial dilutions. Addition of cells to compound will produce an additional two-fold dilution.

Natural product extracts are tested at concentrations ranging from 200 to 204,800 fold dilution of the extract based upon the initial culture volume. The extract
5 should first be diluted 100 fold then serial dilutions produced as directed below.

Assay Setup

Antifungal susceptibility tests should be setup in polystyrene, 96-well, flat bottom plates (Costar 9017). To every well in columns 2-12 is added 100 microliters of media. An electronic multichannel (12) pipettor with no tip on channel one makes this job
10 simple. To every well in column one is added 200 microliters of diluted compound (32 ug/ml for Amphotericin B and Itraconazole controls, 256 ug/ml for test compounds, 100-fold dilution for natural product extracts). A manual multichannel (8) pipettor is then used to set up a series of 2-fold dilutions. 100 microliters is removed from each well of column one and mixed with 100 microliters in column 2. This is done successively (column two to
15 column three etc.) to produce a set of 11 serial dilutions (column 12 is a drug free control).

To every well in two rows, 100 ul of inoculum (2X) of a single strain is added. To the final two rows on the plate (G & H), only media is added. Addition of inoculum is best accomplished using an electronic multichannel (12) pipettor. This setup
20 (see below) creates a starting cell density of 500-2500 per ml (100-500 per well) and drug concentration ranging from 16 ug/ml to 0.016 ug/ml for controls (Amphotericin B and Itraconazole), 128 ug/ml to 0.125 ug/ml for pure test compounds, and 200 to 204,800-fold dilutions for natural product extracts.

It is important to determine the number of colony forming units (CFUs)
25 present in each strain inoculum (2X). Two 100 ul aliquots of each inoculum (2X) should be spread on SDA plates and incubated at 35°C for 1-2 days to determine the precise number of colony forming units. An acceptable range for the inoculum (2X) is $1-5 \times 10^3$ cfu/ml (100-500 for 100 ul). Following two-fold dilution of the inoculum with compound, the final concentration of cells will be $0.5-2.5 \times 10^3$ per ml. The plates should then be placed in a
30 dark, 35°C incubator for 48 hours.

Modified Assay Setup for Low Solubility Compounds

Some compounds are not very soluble in aqueous media even at low

concentrations and dilution artifacts can result from precipitation of the compounds. To avoid such problems a series of two fold dilutions at 100 times the final concentration is prepared from the stock solution in the same solvent (typically DMSO). Each intermediate solution is then diluted to final strength with 1X inoculum.

5 This type of assay setup involves making a series of 11, 2-fold dilutions in DMSO ranging from 12,800 ug/ml to 12.5 ug/ml for test compounds and 1600 ug/ml to 1.6 ug/ml for control compounds (Amphotericin B and itraconazole). Two microliters of diluted compound are placed into each well of the appropriate column (12,800 ug/ml in column 1, down to 12.5 ug/ml in column 11, and DMSO to column 12). To every well in two rows,
10 200 ul of inoculum (1X) of a single strain is added. To the final two rows on the plate (G & H), only media (200 ul) is added. Addition of inoculum is best accomplished using an electronic multichannel (12) pipettor. Final concentrations of cells and compounds are the same as described above for the standard assay setup. Please note that the inoculum in this assay is at 1X concentration, while the inoculum for the assay described above is a 2X
15 concentrate. The 1X inoculum is made by adding an equal volume of media to the 2X inoculum.

NCCLS recommends using this type of assay setup for insoluble compounds, including Amphotericin B and Itraconazole. While we are able to obtain reasonably consistent results for Amphotericin B and Itraconazole using the standard assay setup, some
20 test compounds may benefit from doing the serial dilutions in DMSO. Compounds that form heavy precipitates upon dilution to media should be considered for this assay, particularly if the compound seems to be a promising candidate or inconsistent results are obtained in the standard assay.

Reading the Results

25 *Minimum Inhibitory Concentration (MIC)*: The MIC is the lowest concentration of an antifungal agent that inhibits growth of the organism. For Amphotericin B, the lowest drug concentration which gives no visible growth is the MIC. For Itraconazole (and other azoles), the lowest drug concentration which reduces growth to \leq 20% of the growth control (column 12) is the MIC.

30 For test compounds that give a sharp endpoint (like Amphotericin B), the lowest drug concentration which gives no visible growth is the MIC. For test compounds that give a trailing effect on inhibition of cell growth (like the azoles), the lowest drug

concentration which reduces growth to $\leq 20\%$ of the growth control (as determined by measurement of turbidity) is the MIC.

The turbidity of each well is determined by measuring the absorbance at 415 nm on a plate reader (BIO-RAD Model 3550-UV). The rows containing no cells (G & H) serve as a control for absorbance. Column 12, containing no compound, serves as the growth control.

Minimum Fungicidal Concentration (MFC): The MFC is the lowest concentration of an antifungal agent that results in an inviable culture. Two slightly different standards and assays are applied, depending on the circumstances. For each of the two methods, though, culture viability should be determined beginning with the drug dilution immediately below the MIC and continuing through to the highest drug concentration.

The first and more rigorous standard considers a culture to be inviable if it contains $\leq 1\%$ of the colony forming units of the starting culture. This is determined by completely removing the cells from a well of the microtiter plate and placing them in a microfuge tube containing 1.3 ml of RPMI media. The cells are spun for 2 minutes, supernatant poured off, cells resuspended in the remaining media, and spread on an SDA plate. The plate is incubated at 35°C for 1-2 days, and the colonies counted. These numbers are compared to the original cfu count from day 1 of the assay.

A second, simpler method is more practical for processing a large number of samples and is the method that we routinely use. Following resuspension of the cells by pipetting, 15 microliters is spotted directly to an SDA plate and incubated for 2 days at 35°C. A culture is considered inviable if no colonies form on the plate. While this method is much simpler than the one above, it is less quantitative and no efforts are made to wash the compound away from the cells before plating. One may observe inhibition of growth on the agar plate if a compound is still present at high enough concentrations

The control compound Amphotericin B is a cidal drug and the MIC is typically equal to the MFC. Itraconazole, in contrast, is a static drug and viable cells should be recovered from wells containing compound at concentrations well above the MIC.

Quality Control

Cell density of the inoculum (2X) must be between 1 and 5 X 10³ cfu/ml (100-500 cfu per 100 microliters). Starting cell concentration in the assay will be 0.5 to 2.5

X 10³ cfu/ml.

Acceptable MIC range values (ug/ml):

	<u>Am B</u>	<u>Itraconazole</u>
<i>Candida albicans</i> , e.g., ATCC 10231	0.25-1.0	0.25-1.0
5 <i>Saccharomyces cerevisiae</i> , e.g., CTY552	0.25-1.0	0.25-1.0
<i>Aspergillus nidulans</i> , e.g., NRRL 194 (ATCC 38163)	0.5-2.0	0.25-1.0

If the starting cell density or MIC values do not fall within the acceptable range, all results in the assay for the particular strain in question are considered invalid and
10 the assay should be repeated.

Secondary Screens - Mechanistic Assays

The preferred inhibitor compounds of the invention are those which possess antifungal activity, although compounds with significant activity in an *in vitro* mechanism-based assay may be considered for further development. Such secondary assays
15 are performed to determine the mechanism of action of these compounds. Such secondary mechanistic assays include *in vitro* experiments, as well as and *in vivo* experiments in fungi, to determine the mechanistic inhibitory activity of these compounds. The precise nature of these assays will depend on the target.

Compounds that prevent cell growth through inhibition of the target protein
20 are considered for further development.

Counterscreening in Other Species

In parallel to secondary screen assays, counterscreens are performed to determine if the compounds inhibit the activity of any human homolog. The precise nature of the counterscreen(s) will depend on the nature of the target protein. These counterscreens
25 may include an affinity assay to determine if the compound binds the human homolog or an *in vitro* or cell-based mechanistic assay to determine if the compound inhibits the activity of the human protein.

Cytotoxicity studies on mammalian cells are also performed to determine if the compound is toxic to mammalian cells in culture. Compounds that do not bind to and/or
30 inhibit the activity of the human homolog will be considered for further development.

Transcription Inhibition Counterscreen Using Human Homolog

When the essential target protein has been identified as being required for growth and as an inhibitor of *Candida albicans* according to one or more of the assays described herein, it may be tested further in order to determine its effect on the host organism. In the development of useful antifungal compounds for human therapeutics, it is desirable that such compounds act as effective agents in inhibiting the viability of the fungal pathogen while not significantly inhibiting human cell systems. Specifically, inhibitors of *Candida albicans* identified in any one of the above described assays may be counterscreened for inhibition of a human homolog of the target protein.

If available, the human gene encoding for the target protein can be expressed and purified utilizing published methods and its homology to the yeast target protein homolog(s). The human homolog can be contacted with candidate inhibitor in assays such as those described above using a human cell culture system. The effectiveness of a *C. albicans* inhibitor as a human therapeutic is determined as one which exhibits a low level of inhibition against its human homolog relative to the level of inhibition with respect to the *C. albicans* target protein. For example, it is preferred that the amount of inhibition by a given inhibitor of the human homolog in a human system be no more than 20% with respect to the amount of inhibition of the *C. albicans* target protein.

Such inhibitors are "selective inhibitors" of the *C. albicans* target protein which "selectively inhibit" *C. albicans* biological activity. The lack of effect of a test compound on mammalian transcription or other growth-related mechanisms is tested by replacing yeast components with an analogous human *in vitro* transcription system as in *e.g.* Manley *et al. Proc.Natl.Acad.Sci. USA* 77:3855, 1980.

An example of one such mammalian cytotoxicity screening method is described in Example 3.

Chemical Analoging

It is important to note that some compounds may prove to be cytotoxic, but not inhibitory of the activity of the human homolog. Compounds that exhibit such non-target based cytotoxicity are still considered for further development. Chemical analoging efforts may be used to separate the target-based antifungal activity from the non-target-based cytotoxicity activity.

Chemical analoging is also used to identify compounds with improved antifungal activity and reduced cytotoxicity. The secondary assays and counterscreens described above are used in parallel with antifungal assays to ensure that compounds remain active against the appropriate target, *i.e.*, remain inhibitory with the same mechanism of
5 action.

Antifungal testing against a broad spectrum of fungal species and a large number of isolates is also performed at this point. The broad spectrum of fungal species will include those resistant to existing therapeutics, *e.g.*, Amphotericin B and various azoles such as, for example, intraconazole and fluconazole. Compounds which inhibit growth of fungi,
10 particularly *Candida* and *Aspergillus* species, at a concentration of 4 ug/ml or less, exhibit minimal cytotoxicity, and have a confirmed mechanism of action are considered for further development..

Preclinical Development of Candidate Drugs

15 Subsequent preclinical development of compounds includes, but is not limited to: formulation, toxicology, pharmacokinetics, animal efficacy studies, and medicinal chemistry. Compounds with the desired characteristics are selected for clinical trials in human subjects.

Dosage and Pharmaceutical Formulations

20 For therapeutic uses, inhibitors identified as described herein may be administered in a pharmaceutically acceptable/biologically compatible formulation. The compositions of the present invention can be administered in dosages and by techniques well known to those skilled in the medical, veterinary, and agricultural arts taking into
25 consideration such factors as the age, sex, weight, species and condition of the particular patient, and the route of administration. The compositions of the present invention can be administered alone or in combination, or can be co-administered or sequentially administered with additional antifungal agents, such as, *e.g.*, nystatin, amphotericin B, flucytosine and the various antifungal azoles.

30 Such pharmaceutical compositions can be used in particular for treatment of topical and systemic fungal infections and can be administered buccally, rectally, parenterally or locally by topical application to the skin and the mucous membranes, or by intravenous or

intramuscular injection. These compositions can be solid or liquid and can be in any of the pharmaceutical forms generally used in human medicine, such as, for example, simple or coated tablets, capsules, granules, suppositories, injectable preparations, ointments, creams, gels and aerosol preparations. The pharmaceutical compositions of the invention are

5 prepared by the usual methods known to those of ordinary skill in the art. The active principle can be incorporated in them with excipients usually employed in pharmaceutical compositions, such as talc, gum arabic, lactose, starch, magnesium stearate, cacao butter, aqueous or non-aqueous vehicles, fatty substances of animal or plant origin, paraffin derivatives, glycols, various wetting, dispersing or emulsifying agents and preservatives.

10 Liquid preparations are useful for 1) mucosal administration, *e.g.*, oral, nasal, anal, vaginal, peroral, intragastric administration and the like, in the form of solutions, suspensions, syrups, elixirs; and 2) topical administration *e.g.*, in the form of a cream, ointment, lotion or spray. Further, liquid pharmaceutical formulations comprising the inhibitors to be used for parenteral, subcutaneous, intradermal, intramuscular, 15 intravenous administrations, and the like, such as sterile solutions, suspensions or emulsions, *e.g.*, for administration by injection, can be formulated without undue experimentation.

In order for a composition to be administered to an animal or human, and for any particular method of administration, it is preferred to determine the toxicity, such as by determining the lethal dose (LD) and LD₅₀ in a suitable animal model, *e.g.*, mouse; the 20 dosage of the composition(s), and the concentration of components in the composition; and the timing of administration in order to maximize the antiviral and/or antimicrobial response. Such factors can be determined without undue experimentation by such methods as titrations and analysis of sera for antibodies or antigens, *e.g.*, by ELISA and/or EFFIT analysis. Such determinations do not require undue experimentation from the knowledge of 25 the skilled artisan, the present disclosure and the documents cited herein.

The formulations can be administered in a pharmaceutically effective amount and/or an antifungal effective amount, taking into account such factors as the relative activity and toxicity for the target indication, *e.g.*, antifungal activity, as well as the route of administration, and the age, sex, weight, species and condition of the particular patient.

30 As discussed above, the pharmaceutical compositions of the present invention can be solutions, suspensions, emulsions, syrups, elixirs, capsules, tablets, creams, lotions and the like. The compositions may contain a suitable carrier, diluent, or excipient, such as

sterile water, physiological saline, glucose, or the like. Moreover, the compositions can also be lyophilized, and/or may contain auxiliary substances, such as wetting or emulsifying agents, pH buffering agents, adjuvants, gelling or viscosity enhancing additives, preservatives, flavoring agents, colors, and the like, depending upon the route of administration and the preparation desired. Standard texts, such as "Remington's Pharmaceutical Science", 17th Ed., 1985, incorporated herein by reference, may be consulted to prepare suitable preparations, without undue experimentation.

The amount of inhibitor administered will be determined according to the degree of pathogenic infection and whether the infection is systemic or localized, and will typically be in the range of about 1ug - 100 mg/kg body weight. Where the inhibitor is a peptide or polypeptide, it will be administered in the range of about 100 - 500 ug/mL per dose. A single dose of inhibitor or multiple doses, daily, weekly, or intermittently, is contemplated according to the invention.

The route of administration will be chosen by the physician, and may be topical, oral, transdermal, nasal, rectal, intravenous, intramuscular, or subcutaneous.

The following examples are intended as non-limiting illustration of the present invention.

EXAMPLE 1: S. cerevisiae Inactivation Analysis

Yeast genomic DNA preparation

This protocol can be used to prepare genomic DNA from *Candida albicans* cultures as well as *Saccharomyces cerevisiae*. Streak a yeast stock culture from a glycerol stock to a YPD (Bio101 Cat# 4001-242) plate and incubated for 48 hours at 30°C. Pick a single, distinct colony into 5 ml of YPD media (Bio101 Cat# 4001-042), and incubate overnight at 30°C in a roller drum. Cells from 1 ml of this culture are pelleted with a 5 second spin in a microcentrifuge. The cells are washed one time with 1 ml TE (10 mM Tris-Cl, pH 8.0, 1 mM EDTA) and respun. Resuspend the pellet in 0.2 ml Extraction Buffer (2% TritonX100, 1% SDS, 100mM NaCl, 10mM Tris pH 7.5 and 1mM EDTA) and add 0.2 ml phenol/chloroform/isoamyl (25:24:1, v:v:v). Add 0.3 g acid washed 400 micron glass beads. Vortex for 5 minutes. Add 0.2 ml TE; spin in a microcentrifuge for 10 minutes at 10-13 krpm. Remove the aqueous phase to a fresh tube. Precipitate with 2.5

volumes absolute ethanol. Spin and resuspend the pellet in 400 μ l TE plus 3 μ l of a 10 mg/ml RNase A stock. Incubate at 37°C for 5 minutes. Add 10 μ l 4 M ammonium acetate and 1 ml absolute ethanol. Mix by inversion and centrifuge for 8 minutes in a microcentrifuge. Air dry the pellet and resuspend in 50 μ l TE. Store at 4°C. The solution
5 may appear somewhat cloudy. Before diluting this stock for use in PCR reactions or Southern blotting, vortex the stock sample briefly.

Alternately, the YeaStar Genomic DNA Kit is available from Zymo Research (Cat. # D2002). It has the advantage of avoiding the use of glass beads and phenol:chloroform mixtures, and produces very clean genomic DNA, although in some
10 cases it has proven to be a somewhat less reproducible method than that detailed above.

Transformation of *S. cerevisiae*

Streak strain to a rich media plate (such as YPD) and incubate at 30°C for 48 hours. Pick a single distinct colony to 2-5 ml YPD media and incubate overnight on a roller drum. Dilute to $A_{600} = 0.2$ in 200 ml YPD and incubate at 30°C until $A_{600} = 0.8$ (about 4
15 hours growth under normal circumstances). Divide the culture into 4 sterile 50 ml tubes. Centrifuge at medium low speed, for instance in a Beckman JT-6 at 3000 rpm for 5 minutes. Resuspend and combine the pellets in 20 ml H_2O . Re-centrifuge. Resuspend the pellet in 10 ml TEL (10mM Tris pH 7.5, 1 mM EDTA, 0.1 M lithium acetate). Recentrifuge again and resuspend in 2 ml TEL. Competent cells are stable at room temperature for up to four
20 hours. If you wish to make frozen stocks, you may add sterile glycerol (from a 50% stock) to a final concentration of 15%, then freeze by placing in a -80°C freezer (do not quick freeze in liquid nitrogen or dry ice/ethanol bath). The frozen competent cells can be expected to be 3-5 fold less competent than freshly made competent cells.

Add 100 μ g well sheared single stranded carrier DNA and the 30 μ l digested plasmid
25 DNA to a clean eppendorf tube. Add 100 μ l competent cells and mix. Add 0.8 ml PLATE (40% PEG-3350 10mMTris pH7.5, 1 mM EDTA, 0.1 M lithium acetate) and mix well. Incubate 30 minutes at 30°C. Heat shock 20 minutes at 42°C. Centrifuge for 5 seconds in a microcentrifuge and remove the supernatant. Wash the pellet with 1 ml TE, spin again and plate the pellet in a minimal volume (< 50 μ l) onto selective media such as (-)HIS
30 plates.

TEL and PLATE solutions are available commercially (SIGMA Cat. T-0809 and P-8966), and seem to be stable at room temperature. We have found that for TEL and

PLATE made in the laboratory, the solutions work best if made fresh the day of the transformation from stock solutions of Tris-Cl , EDTA , PEG-3350 and lithium acetate.

After 48 to 72 hours incubation at 30°C, depending on the growth rate of the specific strain, individual colonies are coordinately struck with a sterile toothpick to two
5 identically arrayed plates, one of which is (-)HIS and one of which is (-)HIS (+)Cu. Pick at least 12 colonies in this manner and incubate the resultant plates for 48-72 hours (again, depending on the strain growth rate) at 30°C. Be sure to pick a colony or two of CUY106 as a positive control for growth on the (-) HIS (+) Cu plate. After incubation, the plates are scored for growth. In the case of true copper sensitive strains, there will be a clear lack
10 of growth on the (-) HIS (+) Cu plates, and clear growth on the (-)HIS plates.

Copper titration

Single colonies from a selective plate (see above) are picked to CSM media (Bio101 Cat. # 4500-022) and grown overnight at 30°C in a roller drum. The use of Bio101 CSM appears to be critical to the reproducibility of the titrations. Cultures are
15 diluted to A600 = 0.2 and are 2 ml portions are aliquoted to sterile capped culture tubes. From a 500 mM stock, copper sulfate is added to each tube to final concentrations of 0 uM ((-) copper control), 10 uM, 20 uM, 50 uM, 100 uM, 200 uM, 500 uM 1.0 mM, 1.5 mM and 2.0 mM. The ten tubes are incubated at 30°C on a roller drum for 16-20 hours. The A600 of each aliquot is measured, and the results are graphed on a semi-log plot: Y axis =
20 A600 of sample normalized to the A600 of the (-)copper control (linear scale). X axis = concentration of CuSO₄ (log scale).

Copper time course

Single colonies from a selective plate (see above) are picked to CSM media (Bio101 Cat. # 4500-022) and grown overnight at 30°C in a roller drum. As is the case for
25 the copper titrations, the use of Bio101 CSM appears to be critical to the reproducibility of the copper time courses. Cultures are diluted in 25 ml of CSM to A600 = 0.02 - 0.1. the cultures are split evenly between two sterile 50 ml tubes and allowed to grow in a shaker/incubator for 1 hour at 30°C. Addition of 1 mM copper sulfate (from a 500 mM sterile stock) to one of the cultures defines the 0 time point. At each time point, a 1.2 ml
30 aliquot is taken from each culture for analysis, and the cultures are quickly returned to incubation at 30°C with shaking. The exception to this is the 0 time point, at which time only the culture which does not receive added copper is assayed as the data point for both

10 Appropriate dilutions to plate to YPD:

At 0 time point: $10^3, 10^4, 10^5$

At time points less than 10 hours: 10^3 , 10^4 , 10^5

At time points greater than 10 hours: 10^4 , 10^5 , 10^6

At 0 time point: $10^3, 10^4, 10^5$

At time points less than 10 hours: 10^1 , 10^3 , 10^5

At time points greater than 10 hours: 10^0 , 10^2 , 10^4 , 10^6

78

Results from *S. cerevisiae* inactivation analyses for the target genes described in Table 1 are shown in FIGS. 27-53.

EXAMPLE 2: *C. albicans* Transformation

5 From a single colony on a plate, grow up a 1 ml overnight culture of *Candida albicans* in YPD supplemented with 20 μ g/ml uridine. at 30°C with agitation. Dilute the culture into 50 ml uridine-supplemented YPD and grow at 30°C with agitation. When the A₅₄₀ of the culture reaches 2, cool the cells on ice for 10 minutes, then Centrifuge at 5000 rpm for 10 minutes at 4°C. Wash the pellet two times with 10 ml TE and
10 recentrifuge each time. Resuspend the pellet in 1 ml TELD (10 mM Tris-Cl, 1 mM EDTA, pH 7.5, 0.01 M lithium acetate, 0.01 M DTT). It is important to make TELD fresh from 10X stocks of each of the components (10X DTT should be stored frozen). Spin briefly in a microcentrifuge. Resuspend the pellet in 200 μ l TELD. This is sufficient competent yeast for 4 transformations. To a fresh tube add: 50 μ l competent yeast preparation, 5 μ l 10
15 mg/ml carrier DNA (Clontech) , 1-2 μ l of digested and gel purified plasmid fragment (at 1-2 μ g/ml), 300 μ l of PEG Solution TELD (10 mM Tris-Cl, 1 mM EDTA, pH 7.5, 0.01 M lithium acetate, 0.01 M DTT, 40% PEG4000 (VWR Cat. # 9727-2)). Mix by inversion. Incubate 30 min at 30°C, then heat shock 20 minutes at 42°C. Spin 15 seconds in a microcentrifuge. Resuspend the pellet in 200 μ l TE and spread on (-)URA plates.

20

EXAMPLE 3: Mammalian Cell Cytotoxicity Screen

Reagents

From ATCC: CV-1 fibroblast cell line originated from a male African monkey kidney. Cat. No.: CCL-70

25 From Gibco BRL:

Dulbecco's modified Eagle's Medium ("DMEM") 1X liquid.	Cat. No.: 11965-065
Dulbecco's modified Eagle's Medium without Phenol red.	Cat. No.: 11054-020
Fetal bovine serum	Cat. No.: 26140-079
Gentamicin reagent solution	Cat. No.: 15710-015
30 Trypsin-EDTA	Cat. No.: 25300-54

From Sigma:

In vitro toxicology assay kit, XTT based.	Cat. No.: TOX-21.
---	-------------------

(XTT is 2,3-bis(2-Methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxyanilideinn salt)

Procedure

1. Split CV-1 cell at 1:20 using DMEM medium supplemented with 10% FBS and 10 g/ml gentamycin.
- 5 2. Three days after the splitting, CV-1 cell should reach about 80-90% confluency.
3. Aspirate the medium out and add 5 ml of PBS.
4. Add 3 ml of trypsin and let stand for 3 minutes. Add 2 ml of DMEM to inactivate the trypsin.
- 10 5. Take 0.5 ml of cell and diluted with 10 ml of DMEM. This should make the cell concentration in the range $0.5-1.5 \times 10^5$ cells / ml.
6. Add 100 μ l cell suspension to row 2-8 of 96 well plates. Add medium only to row 1.
7. Incubate cells for 24 hours.
- 15 8. Make 1:50 dilution of the compound to be tested with concentration of 12.8 mg/ml.
9. Add 300 μ l to column 1 from row 4 to row 8.
10. Row 1 and row 2 of column 1 should be filled with 300 μ l medium only. Row 3 of column 1 should be filled with 300 μ l medium with 2 % DMSO so that
- 20 final concentration of DMSO will start with 1%.
11. Fill columns 2, 3, 4, 5 and 6 with 200 μ l DMEM medium.
12. Make a 1 to 3 serial dilution from column 1 to column 6.
13. Take out 100 μ l of each different conc of compound into the cell plate from column 1 to 6 and duplicate with 7- 12.
- 25 14. Incubate the cells for another 24 hours.
15. Dissolve 5 mg of XTT into 25 ml of DMEM medium without phenol red.
16. Take out the compound solution by aspiration.
17. Wash the 96 well plate with 300 μ l PBS and sit for 3 minutes.
- 30 18. Add 100 μ l XTT solution to column 1-6 and add DMEM medium (without phenol red) to column 7-12.
19. Measure O.D.⁴⁵⁰ and subtract O.D.⁶⁵⁰ at the plate reader. Also, take

time points at 1 hr intervals for 4 hours.

20. Split the CV-1 cells 1:20 using DMEM medium supplemented with 10% FBS and 10% genamycin.

XTT is a measure of mitochondrial activity and, therefore, is considered a reasonable measure of cell growth and viability. After subtracting the OD₆₉₀ from OD₄₅₀, each compound-treated datapoint shall be compared with that of no-compound treatment and this determines the percentage of growth. The percentage of inhibition is defined as one minus the percentage of growth. Percentage of inhibition is plotted vs compound concentration. TC₅₀ is defined as the compound concentration that inhibits cell growth by 50%. The data from the cytotoxicity assay together with the results of the antifungal assays can be used to calculate a therapeutic ratio (TC₅₀/MIC). The higher this ratio, the more attractive the compound. Analoging and medicinal chemistry can be used to improve this ratio.

15

*

*

*

All of the references identified hereinabove, are hereby expressly incorporated herein by reference to the extent that they describe, set forth, provide a basis for or enable compositions and/or methods which may be important to the practice of one or more embodiments of the present inventions.

20

WE CLAIM:

1 1. A method of screening or testing a candidate anti-fungal compound for interaction
2 with an essential protein, comprising;
3 a) providing an essential protein selected from the group consisting of RPC34,
4 POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1,
5 SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1,
6 TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said essential protein with said one or more test compounds; and
9 d) determining the interaction of the test compound with said essential protein.

1 2. The method of claim 1, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of the essential protein. [

1 3. A method of screening or testing a candidate anti-fungal compound for modulation of
2 activity of an essential protein, comprising;
3 a) providing an essential protein selected from the group consisting of RPC34,
4 POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1,
5 SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1,
6 TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said essential protein with said one or more test compounds; and
9 d) determining the modulation of activity of said essential protein in the
10 presence of said test compound.

1 4. The method of claim 3, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of the essential protein.

1 5. A method of screening or testing a candidate anti-fungal compound for interaction
2 with an essential protein in a culture of cells, comprising;
3 a) providing an essential protein within a culture of cells that express said

- 1 essential protein is selected from the group consisting of RPC34, POP3, TFA2, NAB2,
2 MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1,
3 GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;
4 b) providing one or more test compounds;
5 c) contacting said culture of cells with said one or more test compounds;and
6 d) determining the interaction said test compound with said essential protein.
- 1 6. The method of claim 5, wherein said culture of cells comprises bacterial cells, fungal
2 cells, yeast cells or mammalian cells.
- 1 7. The method of claim 5, wherein said culture of cells comprises recombinant cells.
- 1 8. The method of claim 5, wherein when expression or function of said essential protein
2 is reduced or blocked, growth rate of a fungus expressing said essential protein is inhibited.
- 1 9. The method of claim 5, wherein when expression or function of said essential protein
2 is reduced or blocked, viability of a fungus expressing said essential protein becomes
3 reduced.
- 1 10. The method of claim 5, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of the essential protein.
- 1 11. A method of screening or testing a candidate anti-fungal compound for effects on
2 growth or viability of a culture of cells, comprising;
3 a) providing an essential protein within a culture of cells that express an
4 essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1,
5 MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7,
6 SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said culture of cells with said one or more test compounds;and
9 d) determining the effects on the growth or viability of said culture of cells.

- 1 12. The method of claim 11, wherein said culture of cells comprises fungal cells or yeast
2 cells.
- 1 13. The method of claim 11, wherein said culture of cells comprises recombinant cells.
- 1 14. The method of claim 11, wherein when expression or function of said essential
2 protein is reduced or blocked, the growth rate of a fungus expressing said essential protein is
3 inhibited.
- 1 15. The method of claim 11, wherein when expression or function of said essential
2 ~~protein is reduced or blocked, viability of a fungus expressing said essential protein is~~
3 reduced.
- 1 16. The method of claim 11, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of said essential protein.
- 1 17. A method of screening or testing a candidate anti-fungal compound for interaction
2 with an essential protein in a non-human animal, comprising;
3 a) providing a non-human animal with a cell or group of cells expressing an
4 essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1,
5 MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7,
6 SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said non-human animal with said one or more test compounds; and
9 d) determining the interaction of said test compound with said essential protein.
- 1 18. The method of claim 17, wherein when the interaction of said test compound with
2 said essential protein reduces or blocks expression or function of said essential growth rate
3 of a fungus expressing said essential protein is inhibited.

1 19. The method of claim 17, wherein when the interaction of said test compound with
2 said essential protein reduces or blocks expression or function of said essential, viability of a
3 fungus expressing said essential protein is reduced.

1 20. The method of claim 17, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of the essential protein.

1 21. A method of screening or testing the effects of a candidate anti-fungal compound on
2 growth or viability of a cell or group of cells expressing an essential protein in a non-human
3 animal, comprising;

4 a) providing the non-human animal with the cell or group of cells expressing an
5 essential protein selected from the group consisting of RPC34, POP3, TFA2, NAB2, MPT1,
6 MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7,
7 SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4;

8 b) providing one or more test compounds;

9 c) contacting said test animal with said one or more test compounds;and

10 d) determining the effects on the growth or viability of said cell or group of
11 cells.

1 22. The method of claim 21, wherein when expression or function of said essential
2 protein is reduced or blocked growth rate of a fungus expressing said essential protein is
3 inhibited.

1 23. The method of claim 21, wherein when expression or function of said essential
2 protein is reduced or blocked, viability of a fungus expressing said essential protein becomes
3 reduced.

1 24. The method of claim 21, wherein said essential protein comprises a fragment, a
2 function-conservative variant, a fragment or an active fragment of said essential protein.

1 25. The method of claim 3, wherein the modulation of activity comprises modulation of
2 fungal gene transcription.

1 26. The method of claim 5, wherein the interaction is assessed by binding of said test
2 compound with said essential protein or activity of said essential protein in the presence of
3 said test compound.

1 27. The method of claim 17, wherein the interaction is assessed by binding of said test
2 compound with said essential protein or activity of said essential protein in the presence of
3 said test compound.

1 28. A method of screening or testing a candidate anti-fungal compound for binding with
2 an essential protein, comprising;

- 3 a) providing an essential protein selected from the group consisting of RPC34,
4 POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C, SQT1, MTW1, TFB1,
5 SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1,
6 TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said essential protein with said one or more test compounds;and
9 d) determining the binding of the test compound with said essential protein.

1 29. A method of screening or testing a candidate anti-fungal compound for modulation
2 transcription of a gene encoding an essential protein, comprising;

- 3 a) providing a gene encoding an essential protein selected from the group
4 consisting of RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, YMR131C,
5 SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1,
6 ORC2, CNS1, YPD1, TIM10 and SRB4;
7 b) providing one or more test compounds;
8 c) contacting said gene with said one or more test compounds; and
9 d) determining the modulation of transcription of said gene of said essential
10 protein in the presence of said test compound

Rpc34p (YNR003C)

Comparison	Identity
Sac-Can	50.4%
Sac-Hum	28.3%
Can-Hum	27.3%

CARPC34 1 -----MSEMLVSDKARHLYKREYPTSKLFDO-----DELOTFEDKKGSFMEYFOELY
 SCRPC34 1 MCGMENGQSDNKTTHSOMSKGICALFTQ-----OELCKOMGIGSLHPLMSIYQELL
 HSRPC39 1 -MGEVKVKQPPDADPVEIENRIIECHQEPHGHITDQVTONEMPHIEAQQRAVAKNRLI

CARPC34 52 NGKYVKISKMGDOLKFQTVAEERAKKSSMSDDEAVHYYSYIEASGREGIWKTKIKAKTNL
 SCRPC34 57 DKNLHKLKONDELKFGVLESEAKKKAIVSADEALVYSYIEASGREGIWKTKIKAKTNL
 HSRPC39 59 SMGQDLERSNTGLLYRIKDSQNAKKKSGSDNOEKLVYQIIEADGNKGIWSRDLKYKSNL

CARPC34 112 HOHHVOKCLKNLENNRYIKSKSVKHPTRKIYMLYNLOPSDVTGGPWFTDSELDIEETE
 SCRPC34 117 HOHMLVKCLKSLESRYKSVKSVKFPTRKIYMLYSLOPSDVTGGPWFTDSELDIEETIN
 HSRPC39 119 PLTEENKILKNLESKELIKAVKSVAAASKKYYMLYNLOPDRSVTGGAMKSDQEFESCFVE

CARPC34 172 VLEEMCMRFIVGKTYMIKDEEADNEDINPLQTTYNHHPG--VNLDQVYEFINNSNIESV
 SCRPC34 177 SLLTIVVRFSSENTFPNGFKNFEN---GPKNVFYAPNVKNYSTQOELIEFITAAQVANV
 HSRPC39 179 VLNQOCERFFQSKAETAR---ES-----KONPMIOENSS-PASSHEVWKYICELGISKV

CARPC34 230 EIGINDIRSLCHVLIYDPRHEEVGGNQENSGEERATWOSTHDKENTILQNNYQDLKNNVS
 SCRPC34 234 ELLPSKIRSLCEVLYDDKHEKKT-HD--C--KRYTLESILQMN-----QGEGE
 HSRPC39 229 ELSMEDIEELNLTLYDCKMNTIIAAKEGTGSGVDGHMKLYEY-----VNPFI

CARPC34 290 EDCENYQQNQSSVESVFSYKSTIQDQDSSPVIYIDSWNE
 SCRPC34 278 PEAGNKALEDEEESFNFYFMFPASKHDEKVVYEDWTI-
 HSRPC39 278 PPTG-LVRAPCGLCPFVDDCHGGGHS-PSNCTIYTEMIEF

Figure 1

Pop3p (YNL282w)

Comparison	Identity
Sac-Can	26.1%

CAPOP3	1	MNKS	NKVK	KKPS	VAKV	STKA	ASSL	KSQEA	KRQV	TPIL	DN	SFT	-QSNQ	MPFE	PT	IANDI															
SCPOP3	1	MSG	SLK	SLD	KKHAK	-----	-----	-----	ERQV	TPIL	DN	PFT	NEAH	MPRY	HD	QPLIWQ															
CAPOP3	60	VDL	LEV	LK	QDST	EK	YR	GFNP	TV	SALE	KQAA	NR	GI	HNAC	VQIKY	VEVCKYD-ISPAT															
SCPOP3	46	LQSS	HNK	IHIQ	SKEN	YP	WE	LYT	DFNE	I	VQYL	SGA	HGNS	--DPVC	LEV	CNKD	PDVPLV														
CAPOP3	119	LTNV	FPT	LC	FTAS	KA	ED	RVKL	QOL	PRGS	ERLS	KAL	GVDR	VGH	FGL	TKD	TEGAQPLFDL														
SCPOP3	104	LLQ	QIPL	LC	MAP	MT	----	VKL	VOL	PKSA	MT	TFKS	---	VSKY	GM	LL	LRCD	DRVDK	KKFVSQ												
CAPOP3	179	INEN	VKD	TEA	PWL	DCI	IFRE	EM	VFN	Q	PNTK	HV	ASTV	G	KK	KK	KK														
SCPOP3	157	IQKN	V	DL	Q	F	P	W	L	N	A	I	K	Y	R	P	T	S	V	K	--LLK	T	T	V	P	I	V	S	KK	R	K

Figure 2

Tfa2p (YKR062W)

Comparison	Identity
Sac-Can	40.8%
Sac-Hum	23.2%
Can-Hum	19.4%

YKR062w_SAC	1	MSKNRDP	LLANLN	NAFKSKYKSP	VIAPAKV	QCKKND	TVITID	GNTRKR	TASERA	QEN
YKR062w_CAN	1	MSD	LSAQL	SAFKNKUKSP	SVIVPR	KATFTQS		P		SSPLSSST
gi 4504195_HUMAN	1	MDPSLR	ERER	ELFKRALSTP	WVEKRS	ASSES				SSSSSKKK
YKR062w_SAC	59	TLNSAKN	PVLVD	TKKEAGS	NSSNAIS	LD	DDDD	DEDE	FGSSPS	KKVRPGSIAAAALQANOTD
YKR062w_CAN	42	TTTTSKN		DAN	KKRST	DSVTRV	LKK		OK	ANMGE
gi 4504195_HUMAN	40	KTKVEHG		GSSGSK	QNSD	HNGSFN	LKALS			GSSGY
YKR062w_SAC	119	TSKSHD	SSKLLW	ATEYIQ	KGKPK	PVLV	NELD	YLS	WKKDDK	VAIELKKHEDRIEDPK
YKR062w_CAN	75	MGSHLS	LOHFA	VEYIK	EHDP	PTSV	EKLON	YLS	FDISHT	ILPLNEIDRVKNDDES
gi 4504195_HUMAN	74	KFCVLA	KIVNYK	TRHQ	RGDT	HP	THHE	ELDE	TOHMDIGL	KOKOWLMTALVANNPKIEVI
YKR062w_SAC	175	KGTEK	YEST	MDVH	SPSELL	KILRS		QVTF	KGISCK	DLKDGWPQCOETINQLEEDSKILV
YKR062w_CAN	131	KGTELY	WSLH	NRSSD	YLEELRR		QTF	KGTS	MEKELK	DGMAGVAAIDEL
gi 4504195_HUMAN	134	DGKTA	KEPKY	NVRDK	KALL	ILID	QHD	ORG	IGGIL	EDIEEALPNSQKAKALG-DQIEFV
YKR062w_SAC	233	LRTKK	DKTP	RYVM	YNSGN	KCK	ID	EEFV	KMMEN	VQLPQFA--ELPRKIQDLGLKPAS-VD
YKR062w_CAN	189	LRNKK	ENAP	RIYV	ANNGE	LG	ID	TEF	KDMM	DOVKLEPD--VLYQKLDDQGLKPTG-AD
gi 4504195_HUMAN	193	NRPD	KK--	K	EEEN	DKSC	QFS	YD	EEFQ	KTRSVTQDSMDEEKIEEYILKRQGLSSMQESG
YKR062w_SAC	290	PAT	TKRO	TKR	VEVKKK	QR	KKI	TN	THMT	GILKDYSHRV---
YKR062w_CAN	246	PNL	IKKQ	POQ	KEK	QK	ARR	GK	ITN	THMKGILKDYSOIV---
gi 4504195_HUMAN	250	PKK	APIQ	ERR	KPKASQ	KRR	EK	TH	NEHLAG	YLKDYSDITSSK

Figure 3

Nab2p (YGL122C)

Comparison	Identity
Sac-Can	32.2%
Sac-Hum	22.8%
Can-Hum	22.5%

CANAB2 1 MOPAPDNQIGKELQONITQBIQRRFNKPAPDAVDPAVYIYLVIAKKSEQEVAVAKMDID
 SCNAB2 1 ----MSQEQYTENLKVIAEKLIGINENEDIKYVAVIYLVINGGIVESVDELASF
 HS_PART 1 -----

CANAB2 61 ISIDVGFIS-----DYLEIRKBEVKYN-PPAAVEEASPPQBP
 SCNAB2 57 DMSRDTFNVVQFAFFALEALQOGSAENIVSKIRMAQSLGSDIAQQQQQQQ0000
 HS_PART 1 -----

CANAB2 100 -----0000SASVJAPQPIPIGPKKOLTEEEKIALRSORFGTT-----T
 SCNAB2 117 PDIAQQQP000PQLQPEQPOEGTONAMOTDAPATPSPIAFSGVVNAAPPOFAPVDSQ
 HS_PART 1 -----

CANAB2 138 RLSGRGRCSTRTTDFRNGHN---NKNFLDPKKIDQIUSGANNGAIKEVPLPPKSRCP
 SCNAB2 177 RFTORG-GLVGRNRGRCGRGNRNNSTRNPLAKAGMAGESNNETPTKKEGRCH
 HS_PART 1 -----POOLILLSRLEDE---FNGSFS-NAEMSELSVACK---BEKLLERCH

CANAB2 195 DFFYCKN-ONCEMAHPTKNCNVPFCNPPPGTONELHPDQOELIAKIJETSKKEFEERCK
 SCNAB2 236 LEPCPLGRSCPIAHPTKVCEVPNCBPPPGTCELHPNEDEELKEVERTUREEFOKKA
 HS_PART 41 YLPAACKNGDECAHHHISPCKAEPNC-KEAERCLFHPN-----

CANAB2 254 NQAVKQG-----SKYGLKCAKENCPPFAHPTPANPECKIETEMCPQGNQODRNC
 SCNAB2 296 DLAAARKKPVOTGIVLCGALCSNPSPPFCHPTPAN-EDAKVIDLWCDKNLTCDNPC
 HS_PART 79 -----CRYDAKCKPDCPFTHVSRRI-----OLCRYFPA CKMEC

CANAB2 307 TRSHH-----PPPTANSEKLLSAAALALEQCKEGEQCTNLKCPRHATSAVPCPAEAE
 SCNAB2 355 RKAUSSLSKIKEVKPLSKKAAPPVPSKLEQCKEGTCTNKKCKKHARSHIMCRECAN
 HS_PART 114 PFYHB-----KHCRENTOCTRPDCTEYHPTIINVEPRHALK

CANAB2 360 CRVDCIFSHPTKCPREGTKCTNKVYVYCHPEGRTASHTWTGSGNNNSTEN-RSFA
 SCNAB2 415 CTREDCLECHPINE DREGVNCNIIYCHIRHPGRVLP---EKGGAPNSNVETNERPFA
 HS_PART 149 WIRPQISE-----

CANAB2 419 VSDQIVQVQAQ-----
 SCNAB2 472 LPENALJENAPPQTSETHQEQDTEMN
 HS_PART -----

Figure 4

Mpt1p (YMR005W)

Comparison	Identity
Sac-Can	36.7%
Sac-Hum	23.3%
Can-Hum	19.2%

CAMPT1	1	-----MSKSW
SCMPT1	1	-----JANSPKPSDGTGVSASDTPKYCHRP
HSTFIID	661	ALRQLTPDSAAFIQSQOQPPPTSQATTALTAUVLSSVQRTLGKTAALVTSALQPPYL
CAMPT1	7	ISTPOESSNKKOLE-NSESSSPN--KRKTEUTENQSSWESDENSIP-----VELLO
SCMPT1	28	EYKPAFMSPEKASE-LSHSPSPSOIKSTALVSESTHDAAGNDDSVLPKNVSPPTNLR
HSTFIID	721	SLTQPTXGVGKGQOPTPLVQOQPKPGALIBPQVLTLOPMVALRQPHNRIMLTBQ
CAMPT1	59	TEUNG-----HSPAPAPAPPIQ--TINAASSE--RD-----DTSKIND
SCMPT1	87	VEBNGDNNMFSSPAGLALPKDDKKNKESKADSKDGKASNSGONAQOQSDPKKOD
HSTFIID	781	LOLNPLQPVVVKPAVLEPKALSASVSAQAAAKNKLKEPGGSEPR-----DDDDIND
CAMPT1	95	AIAAGVDIQQEEELILQOQNRKSAEGTASNKKSVIRSSKLPPELHNYHIAAFIDKVKAK
SCMPT1	147	VLFSAQDVR-EEEALESINAKSQVQTNMKIPN---HLPEHPEQVSNMYKVGK
HSTFIID	835	VASWAGVNES--EESARILATINSELVGTIRSKDET-----GLQAPLORRILEIGK
CAMPT1	155	QNGIQNFLMDGEMLEWISACETILSNLANTHPSRHRRCHEVIN-KKSGSSSVERS
SCMPT1	202	EONFLTPTKNPEHLEWISSACENYRQUTNALISRHRKAVKIN---SGR-----RS
HSTFIID	886	KHGITEHP--DMSYSHATQORLONLEKISETQOQNFYSQDDDRYEQNSDVRQOL
CAMPT1	214	EUSKEERSALKOKEBEGRVNRKMMGLEKSTKDASKNDENESKAGAEETLHRANAT
SCMPT1	254	EVSAAARALAIIOKKEERRVKRRLGLEK-----EDYENKIDS EETLHRASNVT
HSTFIID	943	KFFEQDQIEKORKIEEBEELMRAAKSRSQ-----EPEQLRLKOKAKEMOQJEL
CAMPT1	274	ANMTMNPGRKKYSMTSSATAGGSDFKSSGSSSKDSKHOQPTISVRGDNELRREI
SCMPT1	305	ACTRAGS--KQYEMTSSVNRP-TSLGKSSCKVAISD-----HARGESULGREA
HSTFIID	995	QOMORDANLITALAIGPRKKK-KVDCPSPGSGAEGSGPS--SVVPGSSGVGTPRQFTR
CAMPT1	334	RSNGSITMMDLLGAEFEKMGTRNAVAKGVAKIKD
SCMPT1	354	REEPGLMRDLLFALENBRNSVQTIHSGVAKIERD
HSTFIID	1051	QRITRNHRLHFCLENERE-TNSHGLLYKAECK-

Figure 5

Mtr2p (YKL186c)



CAMTR	1	--MNQDPTQQL	E	P	F	L	K	R	F	L	A	S	L	D	L	L	Y	T	Q	P	T	S	Q	P	F	P	N	V	E	S	Y	A	T	O	I	G	S	N	L	K	R	S	A	I	I	V	N	G	Q	P
SCMTR	1	MNTNSNTMVMN	D	A	N	Q	A	I	T	A	F	T	K	K	I	L	A	H	L	D	D	P	D	S	N	K	L	A	Q	F	V	O	L	E	N	--P	N	N	C	R	L	I	E	N	A	T	P			

CAMTR	59	IIPSP	OEDCK	L	Q	F	Q	K	K	W	L	Q	T	P	L	S	S	H	Q	L	T	S	Y	D	G	H	L	I	P	G	T	F	V	H	F	S	A	K	V	R	F	D	Q	S	G	R	N	R	L	G	
SCMTR	59	FAQAT	----	V	F	L	Q	M	W	Q	N	V	V	Q	T	Q	H	A	L	T	G	V	D	Y	H	A	I	P	G	S	G	T	L	C	N	V	N	C	K	V	R	E	D	E	S	G	R	D	K	M	G

CAMTR	119	ESAD	I	F	Q	E	-N	N	S	-I	V	S	K	T	N	----	Q	R	P	H	I	N	G	S	M	E	G	M	D	V	N	L	W	D	E	N	V	M	O	D	G	E	--H	I	N	S	M	D	Y	R	F							
SCMTR	114	QDAT	V	P	I	Q	P	N	N	I	G	N	R	N	R	P	N	D	M	N	K	P	R	P	L	W	G	P	Y	E	G	I	S	K	O	L	L	I	D	P	R	I	F	R	N	D	E	N	G	V	I	S	G	F	N	Y	N	M

CAMTR	171	TY	V	P	N	D	S	I	K	V
SCMTR	174	V	K	P	E	D	S	I	K	V

Figure 6

Bos1p (YLR078C)

Comparison	Identity
Sac-Can	37.9%
Sac-Hum	16.8%
Can-Hum	18.1%

CABOS1	1	-----MNSHYNHGCHKOTQTITKBLTQFEKNL-STSPHSLOGATITSLTAFRKTKHK
SCBOS1	1	-----MNALYNHAVKOKNQLQQLARFEKNS-VTAPHSLOGSISATLVLSLEKTVK
HSSTX7	1	MSYTPGVGGDPTQLAQRISNNIQKITQCSVEIORTLNQLGTPQDSPERROQLQKQOQYTN
CABOS1	50	EYSDLLEKNVNDT-----SYTKHENRLNKFNQD--LNEFTLKEDTLKKQORDIQVQEAN-KQ
SCBOS1	50	QYAEHLNFKEDTNAEEIDPKFANRLATITQD--LHFEFTAKFKDLKQS----YNENNSRT
HSSTX7	61	QLAKETPKYHKEFG-SLPTTPSEQRQRKQKDRILVAEFTTSLTNFQKVQR---QAAEREK
CABOS1	103	ELTGRRHISTATAALGSTSSDNPYESSSNPSSQOQOQODEQNTVSYREGLYHEKNSTIE
SCBOS1	104	QLEGGASHVMDSDNPFSTSETIMNKRNVGASANGKGGSSNGGGLPLYQGLQKEQSVFE
HSSTX7	117	EFVARVRASSRVSGSPFEDSSKERNLVSWESQIQPVQVQODEEITDDLRLLHERESSIR
CABOS1	163	RGSEQLDRILEMGQQAEEEDIVEQNEILLRKVQTKFEESLITLGVSCGTIRSVERRAKQDKW
SCBOS1	164	RGNAQLDYILLEMGQOSENIVEQNKILSKVQDRMSNGLRITLGVSEQTIIISINKRVFKDKL
HSSTX7	177	QLEADIMDINEIFKDLGMMIHEQGEVADSIFANVENAEVHVQOQANQOFSRAADYQKKSRK
CABOS1	223	LEWFCVAVMIVVEYIVKKEFER----
SCBOS1	224	VEWIALTILHIGHYVVKWIR-----
HSSTX7	237	TLCIIPLILVIGVAIISLIMWGLNH

Figure 7

Pol30p (YBR088c)

Comparison	Identity
Sac-Can	54.5%
Sac-Hum	35.7%
Can-Hum	41.3%

GTCCAPOL30 1 MLEGKFEAEALLKKVMEALKDCVKKCNFCSEHGITVQAVDDSRVLLVSLLGQTSFSE-
 SCPOL30 1 MLEAKFEEASLEKRIEDGFKDCVQLVNFQCKEDGILAQAVDDSRVLLVSLLEIGVEAFQEX
 HS_PCNA 1 MFEARLVGCSILKKVMEALKDLKNEACWDISSSGVNFOSMSSSHVSLVQLTERSEGEDTY

GTCCAPOL30 60 RCDRDVTGLGHDLSEFSKILKKSANNEDFLTIAEDSPDQIMAILLEEKQKEKISEYSLKLM
 SCPOL30 61 RCDHPVTLCVGLDLSKILKCCNNTDTLTIAEDTPDSIILLFEETKQRIAEYSLKLM
 HS_PCNA 61 RCDRNLAAGVNLTSMSKILKCA GNEDIITLRAEDNADITLALVFEAPNOEKVSDYEMKLM

GTCCAPOL30 120 IDSEELQIDDMVEYDAVVMMPSSDEFAKIVRDKNLSESRVWTKDSVKFTSEGDSGSGSV
 SCPOL30 121 IDADELKIIEELQYDSTISIPSEESKIVRDLSQLSDSINIMTKETTKFVADGDIGSGSV
 HS_PCNA 121 IDVEQLGIPEOEYSCVVKMPSGEFARIQRDLSHIGDAVVISCAKDGVKFSASGEFGNGNI

GTCCAPOL30 180 ILKPYTINLKNERESVTISLDDPVDLTFGCLKYLNDIVKAAALSDVVTITKLADKTPALFEFK
 SCPOL30 181 ILEKPEVDMEHPETSIKHEMDQPVDLTFEGAKYLLDIKESLSLSDRVGIRLSSEAPALFQFD
 HS_PCNA 181 KLSQTSNMDKKEEAVTIEMNEPVQLTFALRYLNFEFTKAHPLSSSTVTSMSADVPLVVEFK

GTCCAPOL30 240 MQSGGMLRFYLAPKFDDEEY-
 SCPOL30 241 EKSG-ELQELAPKENDEE--
 HS_PCNA 241 IADMGHLKXYLAPKIEDEEGS

Figure 8

Ymr131cp (YMR131C)

Comparison	Identity
Sac-Can	63.0%
Sac-Hum	24.0%
Can-Hum	26.1%

CAYMR131C	1	MSKRS	ADDLSGNGSTSHATVKNKDSITTTTNGKBBEPNNDIGBFGPYGDEFPST
SCYMR131C	1	MSKRS	IEVNEEQD---RVVSPKTESHBAIPAS--BEQI-APKNDIEEQLSDEESIE
HSRBBP4	1		
CAYMR131C	60	IEH	ONDEBDCMIDENSQAQIEBEAKBDEQ---EQOSHYLPFKSKPLGDEVLE
SCYMR131C	55	IEH	IGDDEIND-EDGLRKCEBETLVCKDSEBENKEKCEHYLPFPSPPLGDEVLE
HSRBBP4	1		MAKBAFPCCAVEERVINEEYVWKKE---
CAYMR131C	117	ADPTV	YENLHNLEWPCITVDRLPDSLCNGRRSYFVYVDTATQAKAKNDNELIAKKA
SCYMR131C	113	ADPTV	YEMLHNLEWPCITVDRLPDSLCNGRRSYFVYVDTATQAKAKNDNELIAKKA
HSRBBP4	28	-TF	NDLNMTHALFMSLTAQWPLVTRPEGDESIRHVLGTHYS---DECNHNVFAS
CAYMR131C	177	SSLAK	VMKDNE-EDDEEDDDRDVLSDFILSES-IPLRHTTNRNRVSHAPQOTGEVI
SCYMR131C	173	SNLAK	VMKDNEEDDEEDDDRDVLSDFILSES-IPLRHTTNRNRVSHAPQOTGEVI
HSRBBP4	84	VEL	PDDAQDASHYCESEKGEFGFGSISGRKIEIEIKINHEGEVNPARYMIONP---C
CAYMR131C	235	DAMS	ENGVIYIEDLAQYKAFETPGYIPKSKRPHHTTNRHGNVEGYGLDMSPIANTC
SCYMR131C	229	DATMS	ENGVDVIELAEGSKAFSTPGYIPKSKRPHHTTNRHGNVEGYGLDMSPIANTC
HSRBBP4	140	IATK	PSSDVLEFETKHP---SKP---DPSGCNPDLRHGHQ-REGYGISMENTIS-G
CAYMR131C	295	ALLSG	MSGRVLYLNRHTS---SETTDTPPFASQS-SIEDIQSNGEHTVAVVSGCDGY
SCYMR131C	289	ALLSG	CSGOTLYFNRHTS---RVTDRCPFTVSNKNSIEDIQSNGEHTVAVVSGCDGY
HSRBBP4	192	HLSS	DDHTICINDISAVEKEGVDAKTIENGHTAVVEDNSHLLHESIEGSEVDFOK
CAYMR131C	351	ICIND	TRSR-KHKDAMSVTASKSDVRVLSMSKINHLSASGDDSGSGVNDLRNNTT
SCYMR131C	346	IRIND	TRSR-KHKDAMSVTASKSDVRVLSMSKINHLSASGDDSGSGVNDLRNNTT
HSRBBP4	252	IMIND	TRSNNTSKESHVDAHTAEVNGUSNPYSEHLEATGSACTVAVWDLRLDKLKH
CAYMR131C	410	SNPS	PVYDFHNSFITSLFNPLDESIVAVSSDNTVTLVDLAVDDEEISOCRFBQ
SCYMR131C	405	DAVCE	VAQYDFHNSFITSLFNPLDESIVAVSSDNTVTLVDLAVDDEEISOCRFBQ
HSRBBP4	312	S	-----FESHDEIFQOMSPHNEHLSGTRRINDLSKIG-BEQS-----PE
CAYMR131C	470	EIH	IPOLLEHVOR---EVKDVHHPQIPGLVSGCG-GLNWKTKISVE-----
SCYMR131C	465	EIO	IPOLLEHVOR---EVKDVHHPQIPGLVSGCG-GLNWKTKISV-----
HSRBBP4	358	PAED	CEPALLEHGGHTAKESDFSMNENEEVTCVSECTNTEGVAQMAENTYNDEDPES
CAYMR131C			
SCYMR131C			
HSRBBP4	418	VD	ECQGS

Figure 9

Sqt1p (YIR012W)

Comparison	Identity
Sac-Can	44.5%
Sac-Hum	22.9%
Can-Hum	25.1%

CASQT1	1	-----MSHOC--DVVDIQTQEEYINVN---EVAEEVADDDQAPPDDEE
SCSQT1	1	-----MEPQEEF-ITTEVEOEIVPTV---EVEQDVVPDIEGENDDC
HSAAMP	1	MDSGRRLGPEKWRIRLRMESESAGAAATTPLETTSFHDGEFIIEVVELD-PGPPDFC
CASQT1	38	DEEMETIDSEHETLEMDSN--SWTYFDKHTDSHFTIFESH
SCSQT1	39	DE--MNDDEEALGMDSN--SLTYFDKHTDSVEAIGHHP
HSAAMP	60	DLAQEMEDVDFEESEEEGNEEGVLEPQGVVGSMEGPDDESEVTEALHSASVEFCVSLDP
CASQT1	77	KLPWVITEG-DNTAINTHTHQPPFVGEHTGHKESVISSEGTADGKEVVVTDMMGLIQ
SCSQT1	76	NLEIVCIGG-DNLALINTSHQPPFAGTTCYGESVISCFTSEGGFVTDADMSGKVL
HSAAMP	120	KTNTEAVTGGEDDKAEVRLSD--GELLFECACHKESVTCGEFSHPSTLVATGDMSGLEK
CASQT1	136	VEKATKGGEOWKFGCHDEVEEVUEVTVHPHPI-FAFGATDGSMMVQIDESSKLVQI
SCSQT1	135	VHMGOKGGFQMKLASQOEVEEINWTKHTPTAEARTAEAGTDCSMACVOINEQDGSLEOI
HSAAMP	178	VHQVDTKEEVS-----FEAGDIEMWHEWHPRAP-VLLAGTADGNTMMKVPNGD---CKT
CASQT1	195	MSGFSHTLKNGCVPIEG-KQENDTLVSIISRDGTVMNMCETGQVNNKIQPHDQFKGVE
SCSQT1	195	MSGFVHOOCMSGEFNTDKGENTDELVPCSPSTIVAMNGFTGOQDEKIT-QAEIKGLE
HSAAMP	229	FOGPNCPATC-GRVLPDG---K--RAWGY-EDGTIRIMELKQGSPIHVUK---GTEGHQ
CASQT1	254	SPWVIVKH-----GN--LVAIGORDGOLSHVNDTGKRVHTLATEDNVD-----D
SCSQT1	254	PEWISI-SIAPETLTGKSGVACSNNGLLAVNCNNGGAILHISTVIEKPE-----QD
HSAAMP	279	GLTCVPAQND-----GS--LHILTSVDCQAKFUSATTKVGVFSPETVASQPSLGEGE
CASQT1	298	IAELSIERLSNCESKNENLAVGVVSGDXLLHEDTQOVRRLKRLKVDNATKLOEVGETPI
SCSQT1	309	ELDASIESHSNSS--KFSLLAAGVCGEILLYDTSAMRVRHKFVDEDSVTKLVFNDQ--
HSAAMP	333	SESNVSESLGCS--VMPAAVGYEDGTIAHYDLATQTLRHQCQHQSGIVQLWEAGTAV
CASQT1	358	LVGNSMDGKXKMEPRVCEKXFAGVGTNMGSYGLCYFK-----IEVKNWILLVDERCFH
SCSQT1	365	LEASCIINGKVQIENARQOEKVCVGHNMGMVLDHILLHPVANTGTQQRKVUTAGDEGVS
HSAAMP	391	DAITCSIDGIWRLWIAATGRLLLTDVCHTAELLDFALESK-----DASLVVTISGDHAKK
CASQT1	412	WSLFV-----
SCSQT1	425	LVFEVFN--
HSAAMP	444	QFCVQRPDR

Figure 10

Mtw1p (YAL034w-A)



CAMTW1	1	MSDKTIDERTAILTEHLE	EAPETLDDVINAVNEIMYK	GTTAETYLKE	OKQLMKNGIT
SCMTW1	1	MSAPT--RSTSLTEHLG	YPFESLDDHINAVNEIMYK	CTAAVEKYLIS	-KSKIGE---
CAMTW1	61	KVTEDEIEIGMGKLESLL	ESTIDKNFDKFELYCLRN	IFENIPKDL	PIYIQLSHQ
SCMTW1	55	EDYGEIEIKSGVAKLES	LIENSVDKNFDKLELYV	LRNVLRIPEEY	DANVFRLEN---QKD
CAMTW1	121	DNVEQKREFDQQIKNL	QLKIMQELQLRKILK	QLVKVQK	IKAVLIAIDNDFKK
SCMTW1	112	LVIVDENELKKSEEL	REKINDVELAFKKN	ELLKRVTKVKRIL	FTIRGFKQKINELLKC
CAMTW1	181	GGNEESI	PIILKNLOPIDET	TYFLISQ	ERNLINQIEQLSNKVNTNLKT
SCMTW1	172	KDDVOLQ	ILLESUKPIDET	TILTDS	ERKLYVDSESTSSSTEEVEALLQ
CAMTW1	234	LRDKRIDGRTER	VLQQTGFWKDL	EKNDIKILVQGN	DNNNNNNNNTLT
SCMTW1	232	FRTRRIDIRTN	NVLKRLGLGDKE	-----DEK	QSAKPDARTQAGDIVS---ID
CAMTW1	294	IIPQDD	LDVDA	IKKNINAQIF	
SCMTW1	278	EEP	QLDLDDV	-----	

Figure 11

Tfb1p (YDR311w)

Comparison	Identity
Sac-Can	32.4%
Sac-Hum	23.0%
Can-Hum	23.3%

Figure 12

CATBf1 1 MDIIRACSDVIGKGVNRRD-----DGLMPSVETPOEZIPGSPDIPPTTOSPK
 SCTBf1 1 -PSHSGNATKAVSFAKINSD-----SSAEFISTD---GIRVHVVFIFOKQAP
 HUTBf1 1 -MATEEELIKKIRCKKQDGLYKAREDADEGK--DFTTISHYADEKQKTEP

 CATBf1 57 EAGEKMMIRVATSGPPANAVETNDEGGGGEKSEKLFETIRPTIRPKDESLQITV
 SCTBf1 53 RSEKMLNIDEDSKKKNDESNVPS---PPI-HHFEENHRTVNDNUSKMLQDII
 HUTBf1 58 EGKAEQDQIMTPEG-DITTFHFSNESTVVA---EK--NRCC

 CATBf1 117 AERTTEGGA PVLOLOLOHOLMCGSDPADTIRDTSSPEIPPTTSGTSTSSS
 SCTBf1 109 SEKPGDITFE--KRRREESADIT--STEMSSSEVAGDPRFDLOLPOLNNGAPLIEHA
 HUTBf1 101 P--EKR--DMEK

 CATBf1 177 AASQSLSDANLIRFEELQOKITLEDROQIDQETFRVWQFNKSPQVUSRUNDATTFALT
 SCTBf1 164 KDDSEKSEKMLNKKQOSLAKGNVIAKMEQTMVAGDESESESRTEKAKFALS
 HUTBf1 116 KLAFCIFETL--ETGC-EEDM--EDVLFQTRD--LSQVDSLEHED-NELNADPDE

 CATBf1 237 LEOHKGVNV-----ASTIKVAVTSNDQWNVTRDINAEITIPLIKKAEDL/PNKN
 SCTBf1 224 TSGVTPHYNV-----ESTIKVAVTSNDQWNVTRDINAEITIPLIKKAEDL/PNKN
 HUTBf1 168 KSNKQDVGESAAFLSDVETQDCCGRTVYNTSDHESSEHATETP/LSIKTANRPHENMT

 CATBf1 293 GGEVNEFEFNSKIFERLARGKISLSNSAGDVNPTVLYNDQNKQKSKSSTLANSGGG
 SCTBf1 280 EPEVAREFESKIFERLARGKIQ--DREGDFTQVIRIDQEDQDOD--
 HUTBf1 228 EKEMINEFESVLEEDLNTGSK-----DFAKAKIDKGLKTMDS

 CATBf1 353 GSGAGGCGSNGSQGIQTESB-HMKKEHDLNEDQDASQKGNRPDFTVRYDEP-NVDD
 SCTBf1 328 -----MELHE--MKKEDHEDHEDDQVVRNRPDFTVRYDEP-NVDD
 HUTBf1 271 LE-----KME--LDDITRLEDEKLEDEGTCGESSVPS-SNSKSK

 CATBf1 412 NKKEFLNEFEMITMKAHNRLESSMNSSTNGCPKPS-----LIDGT-HA-E-NEVEE
 SCTBf1 364 -IN---ENSDGTDTKAGNRSEEMFALKNEYSRTLNKK--FNITNDEEDQDERN
 HUTBf1 307 -----ENSN--AAIKRATIRBAMTDAALRKQEAQEDTSEPEHNDGNHSDADGAP

 CATBf1 468 EDDQUNDSENLVYKATN-----DLAGKACDSEGSNTNKKISDELHYDS
 SCTBf1 418 ELKDDIANSMTMAIDAKGNHAKETPDADKSSASIKWDLKSNQPLQOLSMM
 HUTBf1 358 AKGRAKLESLEYEDSKNS-----VKETALNKKSEIRVHSPEDSGLVATSDQMAN

 CATBf1 521 OTFOGQETRETCTCKSETEKTSMEALIKQEDTEFLIKEDICTMTPNSLAE
 SCTBf1 478 DNLINKEDQGVVFN-NEVENINRRITATKIKRANIN-VISALSEPDVHDAHE
 HUTBf1 413 SEQSICQETEAYTECLQGVSSSAASSTPTALSPGALWQGG--TOOINDEAVPDEOSE

 CATBf1 581 ITYNFIVVPESEFENKIFMPCINSGQMKKETSLSKLDSGLEENKAIQFKSHDQ
 SCTBf1 536 EVKSTLPIDTESCR--MHTTCCEFLKBPNIHFQSGQRKSTKAYNIRKDCLES
 HUTBf1 471 KKHLYVAGCHLHEDS-CFPPVNTDFLEEKVKKNSLIRAFNKKCPQPMIR-----

 CATBf1 641 KKKQKQKPKDAS--KQMKIADKACVEYEVKAKPELHNGKRLPEE
 SCTBf1 593 NLEEDVAGDESNSSN--TAY--PVLNSTITATRAYDEYFMEYNNNSN---
 HUTBf1 525 --DNESTNEVSHIEHEOIAVINKETWOSRRREKKT-----

Spc98p (YNL126W)

CASPC98 1 -----TCTVITKTHANV
SCSPC98 1 -----NELEPTLGIITAPOLSO
HSSPC98 1 MATPDQSPENLLONCCAILGRSEADVAQEQVAVRVIGSNFATVRCHIVAEVANK

CASPC98 15 QATLISNTHKSIYVEFGAFOHSHIDLOTTLMIS -----EQRHII:INLAKH
SCSPC98 22 SHTATVSHANRSESTATORPETHFGOSDQ -----TTHIKHIDED
HSSPC98 61 ENHFORREADDANFSEKHLKNSQVIRKKSLSLYLLSEDPRAPEKHSYATTIAQ

CASPC98 69 OFLSNHLKKESEFONVHTKTKSLDLCVYD -----IDAIR--DEKVDI
SCSPC98 75 HFEZLADQAKLSEFELPSNVRKIMKS -----HNNEN--LANHRI
HSSPC98 121 NIPDAPSPHYARFOTLEPYODRASMS -----SSEVSGSGISSIICAIISCPAPKSI

CASPC98 117 -----TETNIS -----PKONVATVMI -----PATTSIIZIVYI
SCSPC98 123 HVPARPSIYHEIFENMDRESEKESPPR -----YVFTSTETHTROINAVYN
HSSPC98 181 FGGQNOAPFGVGDQIR--QOLSHLAWTILADOPSSOATTKGVFAVSENNHRSREGD

CASPC98 152 -----PESGTHITITVHTHNSUNPISSE--HYVHTHINKVMS--SMTASHPEE
SCSPC98 178 -----HPEEDITRSSTVTTTQHPID--HEOQTHSHSPFEGCHIDHIA
HSSPC98 239 TGGTHEHSAVMDQILVFOHHCENIOONITETCYKKGONLSRLRBTAVRUSGL

CASPC98 205 -----HNSQVTVVYVGTULAN--TATVITETATVYVNDHNPAM--
SCSPC98 229 HPLSISYHVEFEELNLSM--XELLTDESELSMTATVIMV--EG--
HSSPC98 299 HNKIKARYTIOREIDRSTFELVGOERCAHOREIREHTRLSVLFEQLDDQOQVNLGL

CASPC98 251 -KPEPLVANSFETVLSLITHTSNGHILGIMETIFVSYMIGDMITICVTA
SCSPC98 276 -TVHSTNREYVNTIRHYCFHEHDEISDUEFENIKSGILATEKATNG
HSSPC98 359 ESSLHDLAWTILPKHILITLADTVOLCEGRKEICQVAPAKITANTFETSVQHL

CASPC98 310 HEPHYVNIHETETKREH--HANNKEFELICEO-----EENSILKLPKIRAEI
SCSPC98 335 EHSSELSAERHAPVATHEHREHLCGHTCTOOFVTELEFNOERLPAET
HSSPC98 419 LSLSHVLSHETVETVREHEDVHEHETHSIPVYAT--IR--ELMDKTHPKSVTHH

CASPC98 364 KSED-----VTAQITPHIINVTIKVQVANSAILNKA--HOMAPYTHBMIRKUI
SCSPC98 395 FVGLATVHTIGKSYGIEVH--EACOMKESKMDVYOSYSEISN-----HFEHII
HSSPC98 476 THQSRSTHURKIRHIOVLEUTHHGHAVTSAESFGDADAFIDDEAKOGKIL

CASPC98 421 LAMVHTHETLHIGGKMLIIVANIKRYEETNDEIDATVUNIPENESVMSST
SCSPC98 451 CASHNTHVLLAQVAVANVHNNHMKSPHODALHESKILATINCAIPY
HSSPC98 536 AATFETSKELLQALKLSHMLKQAEVAMHOCMEIRHMLLAPVLETHHFAH

CASPC98 481 YHRTVIAHNSH-----VIANETVDD-----GISVINQOHTHETSTHETKQDLD
SCSPC98 511 KHTVTHFAVALL--EHLANSR--SSVINGLAAVITIGHSQMDVETLIDY--HFFP
HSSPC98 596 NALGHETVADVJNAQFDSHILRL-----HAPHLASST--DTHMVHILAN--HLLIC

CASPC98 532 TTYHEGHOHL-----OITVITETVIA:QOIHULSSEHFEHETKNNVATLSSP--RBP
SCSPC98 568 HLLLVANRPFGRKEILHINENETAFPAWTFYFKOKLAKSDHIE--SPANNGT--PLID
HSSPC98 648 EETVITRECHS-----HLLHNFETLAPAKI-----FETHTDIRKGHCHVILNHP--E--

CASPC98 587 PAKSIAHESMPTITVETNEJATSESVIETENI--CSHIVKLFKSNKO--O--ILNKEH
SCSPC98 627 HINKPESITDHCOCJNSKWSHFLNCTEENI--ET--TR--HUTENKS--NOET--HUN
HSSPC98 697 FSGVHOCNHPABENYHETMOCQYHETETVETCSGCHWNS--KOKADIRI--JANMEZFI

CASPC98 646 NLEHID-----INADPKETEN-----LIDHETVETG--K--DSHNSH--LAN--
SCSPC98 687 GTEHNGET--KAEHTYKSSSPKQNAIENTH--HETES--N--ETV--SHKFAVTS
HSSPC98 756 DIIISRCILDSDSRAILKQIR-----AVFDTHEIONADALTRV--DELORLATE

CASPC98 688 FVLSNENHLSIDOFETFOHOLENITLOMERHILNMYH--HMSIDE--AKI--DS--DOED
SCSPC98 747 KISVODJGOFHETEVITLPAVAKVYKCE--EN--D--HET--K--L--D--S--C--TG
HSSPC98 808 EAMGORTGCGVGVPA--EETEN--K--ICE--SEH----KCS--H--L--H--FT--OG--E--H--L

CASPC98 748 DEF-OLHILKIRKTI--DITONICAROLNLRNDNRINYNKOUSLI--
SCSPC98 804 KFN--HNLKELVSOHNFKOGULIEA--DINKIG--DEELFLKESIR
HSSPC98 865 ITTSDESSEHFLSEZLDESEHVAKAPRILSVS--GTRGRSSM--

Comparison		Density
Sac-Can		30.0%
Sac-Hum		21.5%
Can-Hum		19.9%

Figure 13

Bfr2p (YDR299W)

Comparison	Identity
Sac-Can	42.1%
Sac-Hum	22.5%
Can-Hum	20.7%

scBFR2 1 -EKSIAIQTSDPAIKGVNKDEQIEDEEN---ASFOHNEK-----NG
ca_BFR2 1 MAKSLSEIQTSSVTP-KNDYDIQDHLGVSKDNGIFQHHGA-----CS
human_CHE1 1 -GSPATLQFQLNRPSEADPADPEATLAARVDRFDGDEGDEGLVVGSIKRLAS

scBFR2 40 ESTLSYGNSTEEKAAHYVEVEKSKIR-EKKEEINDEQVGVKGSR---QALVEEVS
ca_BFR2 44 ENESEDE---DTGIRNEINJESSKSKIRQONEKNG-EKIVAVNISR---SKVHDEE
human_CHE1 60 ASLITQKRCYCGKTSKAKNEDHWEQITPSSDEEISDEGSGDSDGGLGLEEYDEDO

scBFR2 96 -----ENEDEDEDEDE-----EEKEDASERTDSEDEE-VETD-EESDAD
ca_BFR2 96 DKQPTGASSDEELDGE-----SAGEEDESEEDVADDEDOESDRSSSDAE
human_CHE1 120 LGAAEECECHRSKKTTRSHSAKTPGFSVSSISDFEKETNGVDDLGSSDEDEESGME

scBFR2 137 GEETEEAQT---KRAHLSKGFQOCTKOAHNLSOSVQDASKGYSILQTKLFDMILDR
ca_BFR2 144 NDEDENTISH---KRELKQKMSKERSHLLKLSOSAPDALGYSIQONKTEKILIDAR
human_CHE1 180 EGEDADESSESEERAGORNSEDDGVNTFTSVKVEEVEZKGRVKKQIAVDDDMTEGR

scBFR2 194 IKLOKAVIAANKLPITTESNEEAKDDSEETKRLKENEKLENNETNLENFRIKTQLGD
ca_BFR2 201 KKEOMSVTESMPLINTSVSETISEDSIE---LTKAKKQKSLIDELFTNEIDEET
human_CHE1 240 IKLOKALHTVNLQLPD-PDVPEVPEKDGGEPEFASAKNSHKAUKALERSLGLGOEHLFQY

scBFR2 254 -HITONEEVAKHKESKRSKLKELYETNSIDSEIK-----EYQAVLNKSTKVSASGNAA
ca_BFR2 258 SKKTP-----KRSFAKYSEVTSAPDQFPG--NSRNOVLTAKSAKVANSNGRNA
human_CHE1 299 PDTRY-----VVDGKPNAGSEBESSDDDEIVEEKQOORRVPARKLEDEDYPSFYA

scBFR2 310 FSSNKKKAINLPALVAVENKLSDSRLVKRT-KINRRNTPPEQKQANGRLPELISPV
ca_BFR2 307 ANANKKMINSEEDQVNNILSDMDRLKRT-KINRRNTPPEQKQANGRLPELISPV
human_CHE1 352 KALFTLOSTGTFLQKHDKTKLASQNLGEGGAFERSTFLOPHILNSKERLERRIQKR

scBFR2 369 VKDSVDNENSDDSLDIPKNYDPRRKNNAIDI-----TENPWFDDDEYRVLLNDLID
ca_BFR2 362 KKKSTDEO---DD--DIPEDTSVRKN--TQS-----LENNYFDDDEDFYRVLLNDIYD
human_CHE1 412 SVYRVLGKPEEAPQPPESIPGEPEILLQAPANAHLKDLCEDEDDDDDFYHLLRELIE

scBFR2 424 KRRSNHNSG---SALITITSTNARENKKAKNQOTKASKGRKLNVSQDPIANFEADITS
ca_BFR2 408 KKLQTSOP-----LSGITISLRAAQKSNKKNVDTKASKGRKRYHVQEPANFEISRG
human_CHE1 471 ERTSSLDENDQVAHKAQACNPEVPAKSTKKVDRKASKGRKLRHVLKSLSEFMAPIDH

scBFR2 482 GKKSSDDOIDEFFACILGQKYNENENEDDEQHARIENDPELEAKNDQ-IQHFEG
ca_BFR2 464 -GRANDDOIDEFFASILGQKYNENETDE-DEEDQENDI-NDIPEPNGIQHFEG
human_CHE1 531 -TTMNDDEPTE-----

Figure 14

Comparison	Density
Sac-Can	51.5%
Sac-Hum	32.1%
Can-Hum	33.7%

Figure 15

[illegible]

Gcd7p (YLR291C)

Comparison	Identity
Sac-Can	52.2%
Sac-Hum	34.5%
Can-Hum	35.6%

CAGCD7	1	-----MSKLLTPETLALIDPVVSELKRHQ-IVDDKEIALTIAQLIMKVISAAARWSN
SCGCD7	1	MSSQAFTSVHPNATSEVNVITIDIFVAKLRKO-VQGSYALALELLOLMREISAARNNH
HSGCD7	1	-----MPCSAKGSERIEFVEILKRGGRSSEVARETIGLIROHIDHRWSN
CAGCD7	51	TYDLIELIROVGVIFTEAYPRKVI PGNHVRRVLAIRDETETETETETETETETDNI--PMVS
SCGCD7	60	VNDLIEQIRDIGNSIEKAHPHAFSCGNVIRRLAVIRDEVEEDIMSTVTSTSVAEPLIS
HSGCD7	54	AGELVELIRREGRRTAAQPSSETIVGNVRRVLKIRREYGRHLGRSDESDQOE-----
CAGCD7	109	SMFSLIAIHNK-NETIKEQTQLQKKQTSMDRAHIOGIRDLVDEISNVNDGLETMAVDL
SCGCD7	120	SMENLLQKPEQPHNRKNSSGSSSMKPKTDYRQVALOGIKDLIDEIKNHIDEGIQQAFDL
HSGCD7	108	SHKLLITSGGL-NEDFSFHYAQLQ--SN-----LIEAINELIVLEEGTMENIAAQADEH
CAGCD7	168	IHDDEILLTPTPNSETVQHILIKARLK--RKFTVVVTENYPNDIKAAHKEVKTAEHNIE
SCGCD7	180	IHDHEILLTPTPDSKIVLKELITARESRNRTETVLVTEGEPPNNTKVAHEFAKKLAOHNIE
HSGCD7	159	IHSNEVAVTIG-FSRTVEAEIKEAARK--RKEHVIVVAECAP--FCQGHMAVNLKAGILE
CAGCD7	226	TEETPDITLMAVMSRVGKVIIGTNAVFPANGGCHS-NSGVANVVECAKEHRRPVPFAVAGLF
SCGCD7	240	TVVMPDSAVPAEMSVRGKVIIGTKAVFVNGGTHSSNSGVSSVCECAKEERTPPVFAVAGLY
HSGCD7	214	TVVITDAIIPAVMSRVNKKVIIGTKTILANGALRA-VIGTHPEALAAKHHSPLIVCAPMI
CAGCD7	285	KLSPLYPPTFRNDLIEVNSCKVINDDFELQONVDVVTNPEDYTPPQHIDIEFTNIGGF
SCGCD7	300	KLSPLYPEVKEVEFGCSQRLBRMD---PRKADTVNQTDXVPEPENIDITVITVGGF
HSGCD7	273	KLSPQEPNEDESEHKVAPEEVLPETEG-DILEKVSVHCEPFDXVPEPELITIEFISNIGGN
CAGCD7	345	SPSFIYRIVLDNYKAEDNKLK-----
SCGCD7	357	NPSFIYRIAMDNYKQIDVLELAKNKA
HSGCD7	332	APSFIYREMSSELHPEDHVL-----

Figure 16

Nip1p (YMR309C)

Lcp5p (YER127W)

Comparison	Density
Sac-Can	34.7%
Sac-Hum	18.0%
Can-Hum	18.6%

CALCP5_SER	1	MSKVDTMLKHEIISSTKSTSPASVYKELHAFVKOSSQHP-----ELVRNLDKSNSSLEGVSL
SCICP5	1	MSLGNALLKDDINGSITATSESIERLSGHSYNSANDEIPESNQHHEHFFYDAKKPAEKVSL
HS_CAB43232	1	WALGVLESDDPSATVLLKNLOEQWMAVTAJVS-----LTQKVOAGAYPEKGCSE
CALCP5_SER	57	LGLKNESATSVYNNNEVAVVLSHLERLESSEIGSAVERSIIQRTVLEKGVKPLEKKLSY
SCICP5	61	LSLKNGSTLGYINSCULMIGNLDECKD-PSANDABERSIOHRVVLGKGVKPLEKKLAY
HS_CAB43232	53	LEKKDQLMAYMDLTHLIDKASGSLQ----GHDAVLELVEIRTVLEKLEPLDOKIKY
CALCP5_SER	117	QLDKMIRAVGNEQDEIKRQCNLDRCGENDENDENSEEDSEDESEDDDEAYRP
SCICP5	120	QLDKLTRAVVKEKEYKDEKKALEKSHVNNISG--ND--DSE-D--DESEDEAYRP
HS_CAB43232	109	QDOKLIKRTVTCGSLSENDFLEKPHPSNUSKLS--SE--DEE-E--DEDEDD-----QS
CALCP5_SER	177	DASSEAKTSAKTKSKPTSSAVSTSNEK-----YPPKISAMAPPTAVVSED-LDAN
SCICP5	172	NTSGIINTNKKSSAYRVEEAKKOENGENDDNETGVYPPKTHAVLPQOTFEEDRFDAR
HS_CAB43232	157	EASG-----K-KSVKGVSKK-----YVPRHVPVHYDEAEAE--KKR
CALCP5_SER	228	TTSSK-NR-KUCSMEEYLOQSDMENVASVGSTIVEHGRGGVKTQDPRKEREIOTVEE
SCICP5	232	EHKDPSNKSEWCAMEEYHRESDDPDWSSHIGADIVANHGRGGUKSLDTEKERRVTSSEE
HS_CAB43232	193	LERAKRRALSSVIRELKQVSDAP-----EETDRHHPHVTRQSQDQHRIN-YEE
CALCP5_SER	286	DNFVRLPTSPTKK-SFKEKORD-----ERNQFAGEDNSVFNKNDVTRQGS-KERATUM
SCICP5	292	DNETRLNLTWKA-E-KRKQKORERNARMMVIGEGDEGEHSSKRKLEDDSTSRGAKKTRSAN
HS_CAB43232	244	SMNVRLSVSRKREKGRKRANVMSSQHSSEHFSDISALAGCTVHLDQDNP-IKKRKKIP
CALCP5_SER	341	DKVKKKKNT
SCICP5	351	ORQQRRL--
HS_CAB43232	303	QKSKKKKGQ

Figure 19

Figure 19

Nce103p (YNL036w)



CANCE103	1	MGRENILKYOLEDHESDLVTEKDQSLLDNNNNGMNTIKTHPVRVSSGNHNFPET
SCNCE103	1	-----MSATESSIEFT
CANCE103	61	LSSESTLQDFLNNNKFFVDSIKHNHGNQIFDLNGQGQSPHTLWIGCSDSRAGDQCLATLP
SCNCE103	12	LSHNSNLQDILAAANAKWASQNNNIQPTLFPDHNKAGQSPHTLEIGCSDSRYNENCLGVLP
CANCE103	121	GEHFWHRNANIIVNANDISSQGVHQAIDVLKVKKHIICGHTDCGGIWASLSKKRIGGVL
SCNCE103	72	GEVETWKNVANIICHSEDLTLKATLEFAIICLKVNKVIICGHTDCGGIKTCLINQREALPK
CANCE103	181	DLWLNVPVRRHRAANLKLLEEYNQDPKAKK-----LAEINVISSVTAKRRHPSASVALK
SCNCE103	132	VNCSHLYKYLDDIDTMYHEESONLIELKTQKEKSHYLSHCNVKQRQFNRIENPIVQTAMQ
CANCE103	236	KNEFEVWGVLYDVATGYLSQVEIQDEFEDDLFEHVHDEHDEEYNPH
SCNCE103	192	NGELQVYGLYNVEDGLLQTVSTYTKVTPK-----

Figure 20

Eco1p (YFR027w)



CAECO1	1	MGSINSQ-----KAQKIQSIIAAPSNFKK---ITCSTCDMTYNPHISQDKLLENKYHTNF
SCECO1	1	WKARKSQRKAGSKPNLLQSKLQVNNNGSKSNKIYKCDKCEMSYSSTSIEDRAHEKYHTLQ
CAECO1	53	INGIPMN-----YKTDNDVHIIENFTLVEPTKLNSTGKSLKLTQTRQTFKGSITCI
SCECO1	61	LHGRKMSPNMGSIIVYTERNHRSRTVHHSRSTGTITPLNSSPLKKSSPSITHQEEKIVYVRP
CAECO1	104	NKSNKRHHQKVELHENNVNDELNASQDS-GQMKKPEFDRSKAFVIIIDSKATGCTTDTT
SCECO1	121	DKSNG-EVRAHTEFMTLVNNELNAPHDENVIWNSTTEKSKAFVYIRNDRAVGI I I I E N E
CAECO1	163	QP-----DQGRWMIHKIQOSTVPPNCHNKNVVGIGLSRIWISRKWRQYGGGKKLNNVVLKNS
SCECO1	180	YGGNGKTSRGRWVYDSRRPVQN-VYPDFKIGISRIMVCR TARKLGIA TKLIDVARENI
CAECO1	217	IYSVQLLKNQVAIESQPSFSGGMLAKSENGVKHKSGEMLLPVYIE
SCECO1	239	VYGEVLPRIYQVAMSOPTDSGGKLASKYNGIMHKSGKILLPVYI-

Figure 21

ORC2p (YBR060C)

Comparison	Identity
Sac-Can	26.7%
Sac-Hum	22.0%
Cap-Hum	21.0%

Figure 22

[illegible]

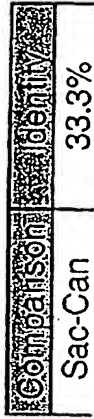
Cns1p (YBR155W)

Comparison	Identity
Sac-Can	51.8%
Sac-Hum	25.6%
Can-Hum	26.8%

SCCNS1	1	VSSVNAVANGG---YTKPQ---YVVGPGPPPELPOLSEFKDKTSDEHKENNRMPFVWK
CACNS1	1	MSKHEPVTEKEEYVSEWDRRYVVPKAGPPPELPOLSEFSNKHDEVAIEELNRQPPFVWT
HSTTC4	1	---MEOPGQ---DPTSDVMDSDSEKFKFSQ---PYRGGFH---EDGWEKEFEKMFLEMS-
SCCNS1	54	LDETDGAGGENVLEALKKALAYEGE---PHEIAENFKKOGNELYKAKREKDKAREIMSKGLA
CACNS1	60	LDETDGCGGENVNLEALKSLAYEGE---PHEIASNEKNQGNOCYKFKYKDAHIEYTKGLE
HSTTC4	48	RAPSEIDPRENPDLACLQSHIIEEERSPEEQAKTKDEGNYEKEKDYKKNMISYTEGLK
SCCNS1	112	VEQEDKSNESLYANRAACELELKNVRRCIEDCSKALTINPNVVKCYRHSKAFEOINL
CACNS1	118	VNCQVDALNSALYLNRAACNLELKNVRRCIEDCKAVLMDEKNKACERSGKAFFAEK
HSTTC4	108	KKCADPDENAVLYTNRAACYYLGNERSALNDVTAARKIKPCHKAIIRGALCHLEIIEH
SCCNS1	172	HEAKSAATEANORIDPENKSIILNMLSVIUD-RKEQELKAKEEKGQNEAQERENKKTMLPSA
CACNS1	178	HEAKKVLGYG-LNIEPENKDLOKILQQVQKRQETLAQIKAKKAOEEEOER-IKNIMLENS
HSTTC4	168	AEANVNWCEEG-LQIDAKEKKLLEMRKADKLRIEQEDVRKANLKEKKER-NONEALDQA
SCCNS1	231	MTLRNITNKKTHSPVE-----HINECKIRLEDPM-----DEESOLITPALLIMYPTQ
CACNS1	236	IKLRHEFKKSSSPPE-----MLKTAKIRLEDPK-----DQOSOLIEPAMILYPTT
HSTTC4	226	IKARNIRISEAACEDDSASEGLGELFLDGLSTENPAGARLSLDCQGRLSMPVLEFLYEX
SCCNS1	277	DEFDVGEVSELTTVQELVDHVLGEPQERFKKEGKENFTPKVILVFVETK--AGGLIKAG
CACNS1	282	DEFDPIAGEHSELTPTEELLENVILNRPREMEDDPKHKDENVKKECFMETE--SGGLIKYGC
HSTTC4	286	AQSDPISAFHEDSRFEDHLMVWFGETPSPMDLEQKYCLIIWRSTLRMRTGQNYHGGLEFRAP
SCCNS1	335	KKQHEFDILKKESPDVPLFDNALKIYIVPKVESEGWISKWDKQKALERRSV
CACNS1	340	KIESK-----
HSTTC4	346	CYRFSTRGTL-----

Figure 23

Ypd1p (YDL235c)



CAYPD1	1	NKTFIMSEDK	LQKLQD	SGVDM	AVFSEI	VIMDEDE	EGFSKSL	VEVY	SQVEET	FEET	TDKY
SCYPD1	1	-----	MSTIPSE	LINMT	ILNEL	ISMDE	DSDESKGL	IQE	DQAQT	TEAQ	MQRQ
CAYPD1	61	LK-EKNLEK	LSSGH	FLKGS	AAALGL	TKISNQ	CERION	YCHKN	-EDNFQ	LED	EKT
SCYPD1	50	LDGEKNL	TELDNL	GHFLKGS	SAALGL	QRIAW	CERION	LCPKME	HEFFPN	KTE	ELN
CAYPD1	119	AVSAENV	AVNDGE	INPEN	GSNG	NETS	NNKTNT	SNIP	DESSD	DFW	FAL
SCYPD1	109	-----	KS-IING	INID	ED--	DEEIK	IQVD	DKDEN	SI	ILIAK	ALN
CAYPD1	179	QSRRA	LDEYYE	---							
SCYPD1	154	LARIEL	SKYYNT	NL							

Figure 24

Figure 25

Srb4p (YER022W)

```

SRB SPICED 1 -----
SCSRB4 1 -----
HSELS_SRB 1 MYCSAASVGVKVFSSQFGRSPRLPRSLGRRRTNSGCGSGSGGCGTSLSMIO
-----
SRB SPICED 1 -----
SCSRB4 1 -----
HSELS_SRB 61 SAAUAVATSGHTLSDIEMHSEIITHTLGRGCPYGVVTAWSPIAAGVAVS
-----
SRB SPICED 1 -----
SCSRB4 38 -----
HSELS_SRB 121 OTIATGEHPPYASSTWILACGRONTIICLOTOLAEVTLIURLDQDQVMS
-----
SRB SPICED 1 -----
SCSRB4 88 HPHHETGSHPLGDIETIRGCGPQFQOLNENEVTLKQDGSISRAVSGKDDP
HSELS_SRB 181 PMSQNTTNSPILAKERADIDDSKKITIMEQTRVMEHNGHOPQIOIIGDNIOR
-----
SRB SPICED 17 HEPPIA -----
SCSRB4 148 GATENI -----
HSELS_SRB 241 DDKOLFQSSSRGTCPCVAELITETIIFORJAHHERVAVGELFLAKNTLEPHELAIETVO
-----
SRB SPICED 34 -----
SCSRB4 193 -----
HSELS_SRB 301 -----
SRB SPICED 90 -----
SCSRB4 253 -----
HSELS_SRB 361 -----
SRB SPICED 145 -----
SCSRB4 308 -----
HSELS_SRB 421 -----
SRB SPICED 197 N-----
SCSRB4 361 -----
HSELS_SRB 491 -----
SRB SPICED 251 -----
SCSRB4 420 -----
HSELS_SRB 541 -----
SRB SPICED 302 -----
SCSRB4 474 -----
HSELS_SRB 601 -----
SRB SPICED 353 -----
SCSRB4 519 -----
HSELS_SRB 661 -----
SRB SPICED 413 -----
SCSRB4 578 -----
HSELS_SRB 721 -----

```

```

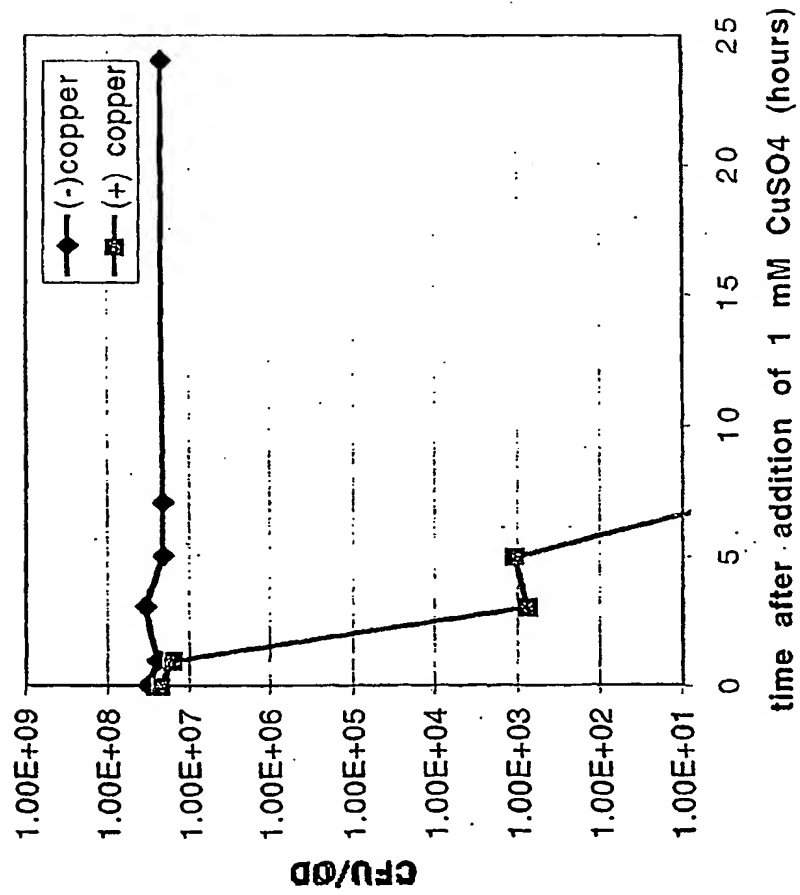
SRB SPICED 471 -----
SCSRB4 635 -----
HSELS_SRB 781 -----
SRB SPICED -----
SCSRB4 841 -----
HSELS_SRB -----
SCSRB4 -----
HSELS_SRB 901 -----

```

Comparison	Identity
Sac-Can	28.4%
Sac-Hum	18.0%
Can-Hum	18.0%

Figure 26

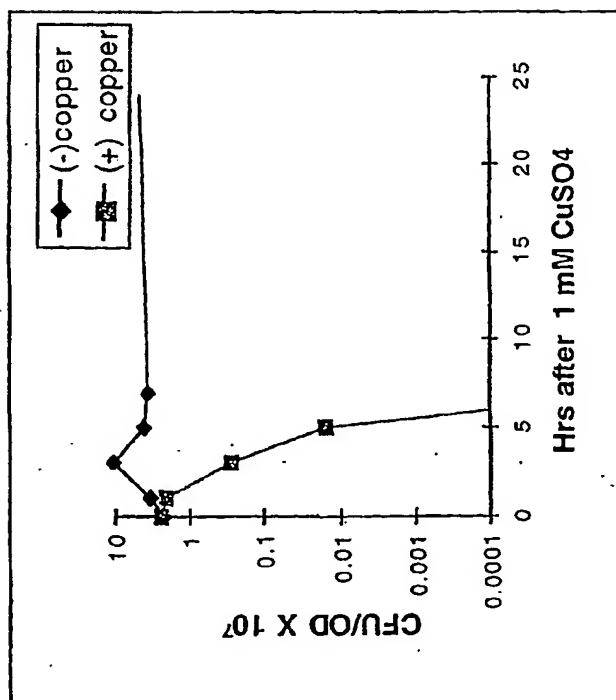
S. cerevisiae RPC34 (YNR003C) inactivation



$t_{1/2} = 0.11$ hours

Figure 27

S. cerevisiae POP3 (YNL282W) inactivation



$t_{1/2} = 0.34$ hours

Figure 28

S. cerevisiae TFA2 (YKR062W) inactivation

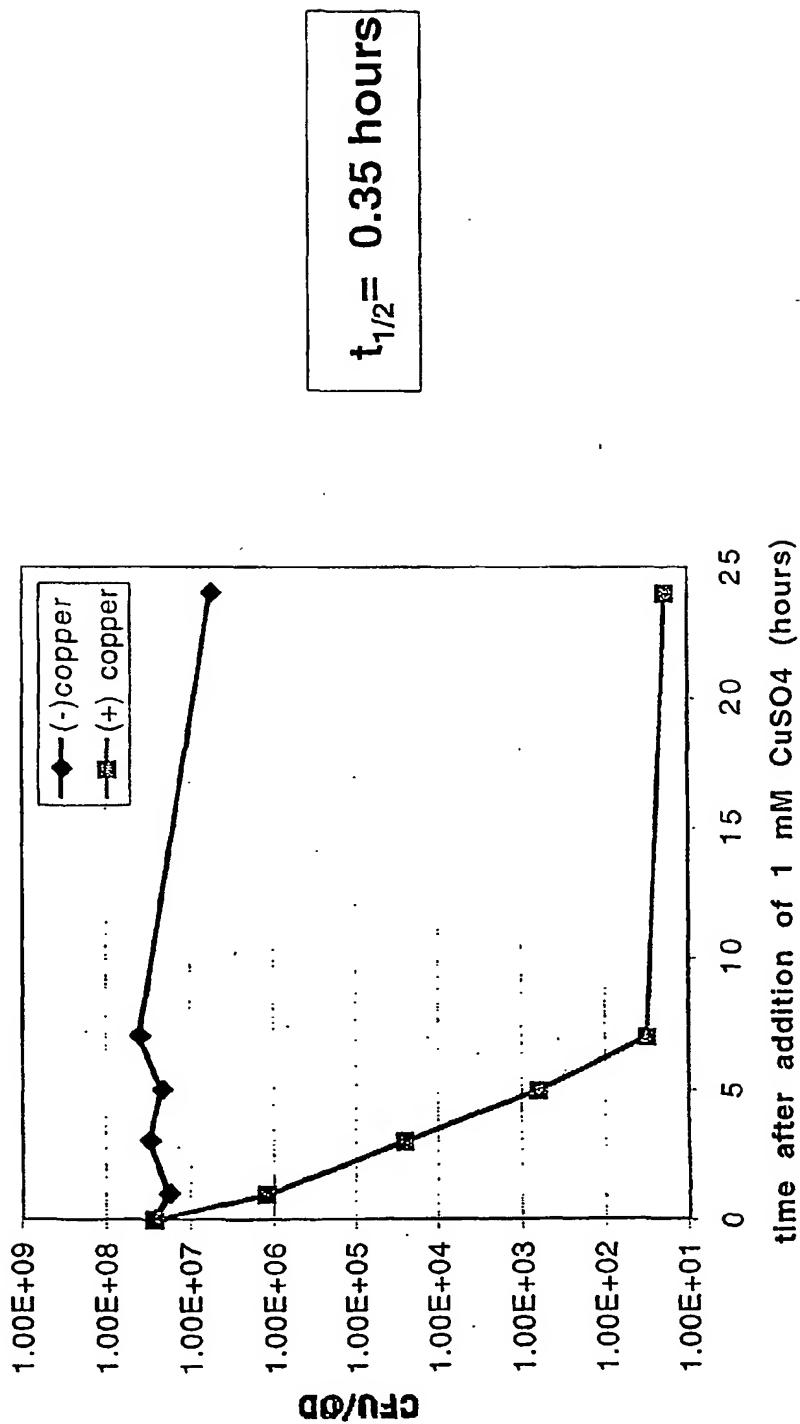
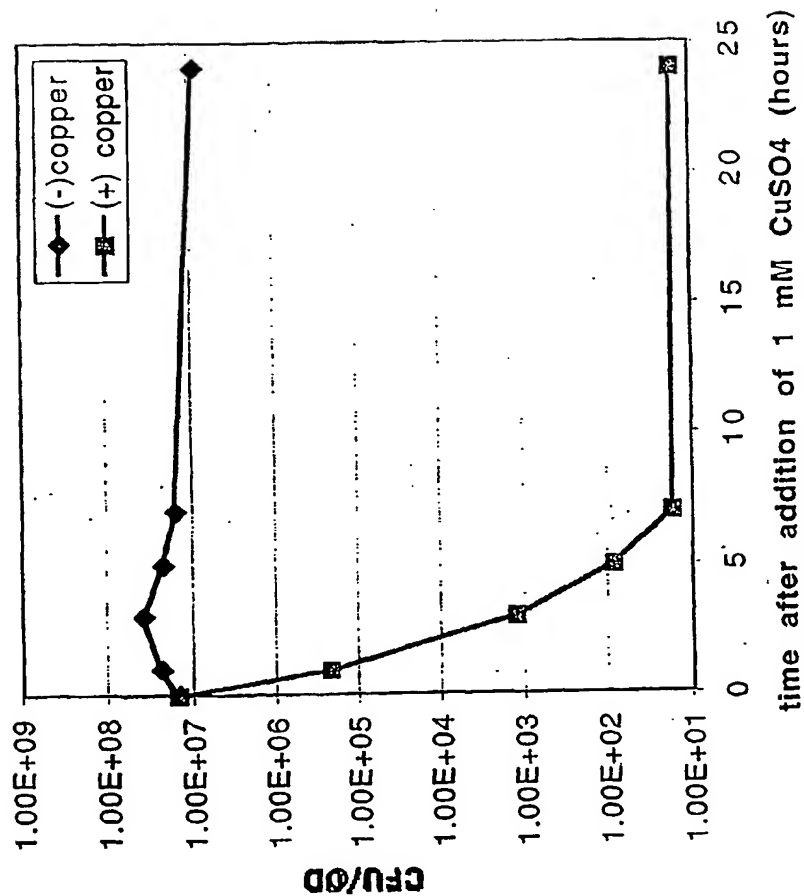


Figure 29

S. cerevisiae NAB2 (YGL122C) inactivation



$t_{1/2} = 0.36$ hours

Figure 30

S. cerevisiae MPT1 (YMR005W) inactivation

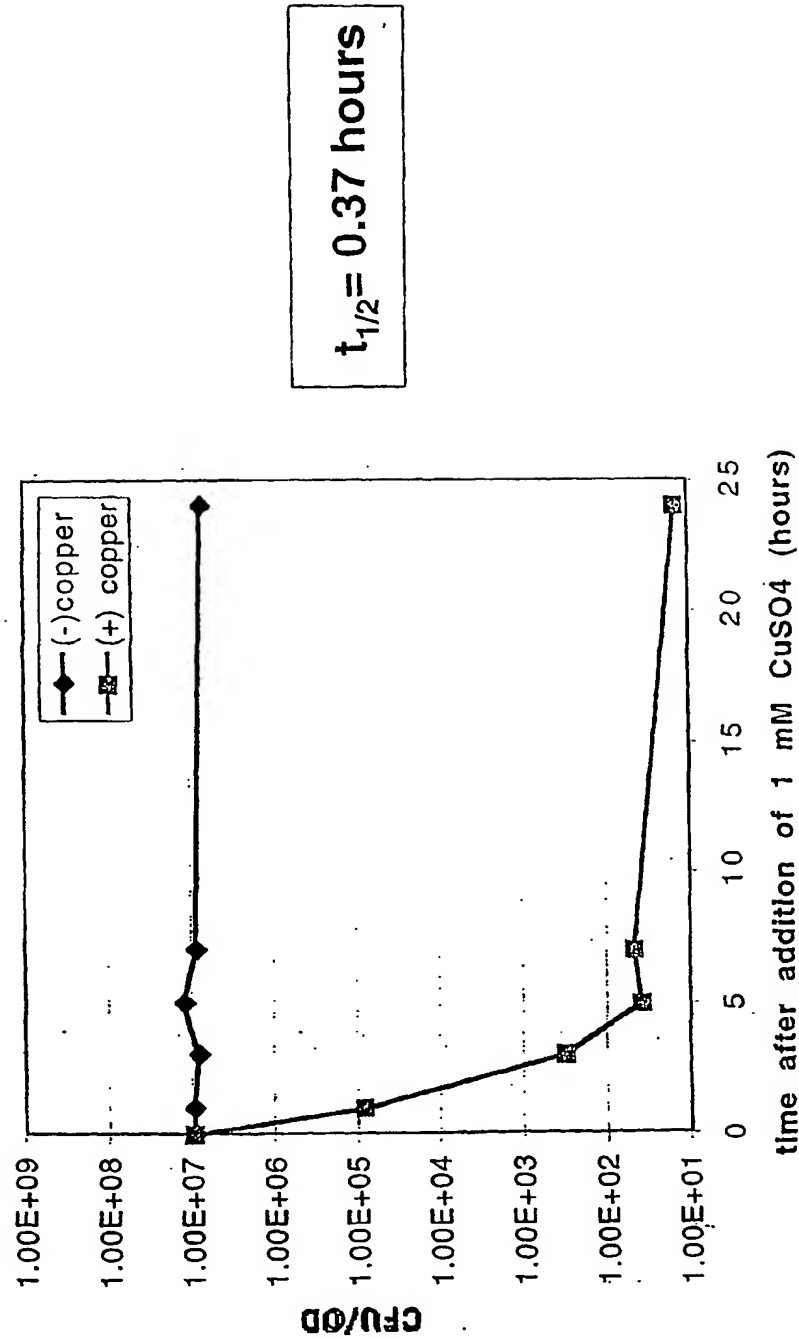


Figure 31

S. cerevisiae MTR2 (YKL186C) inactivation

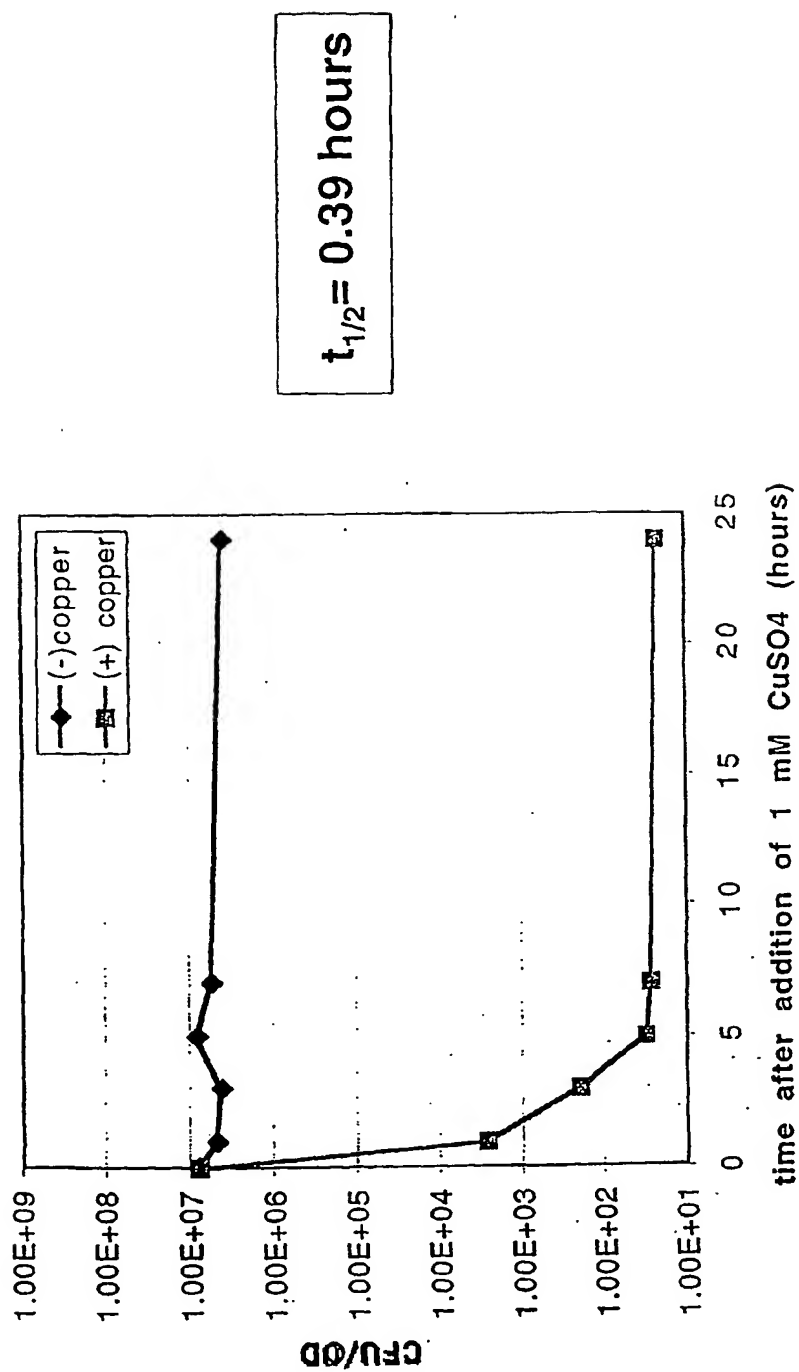
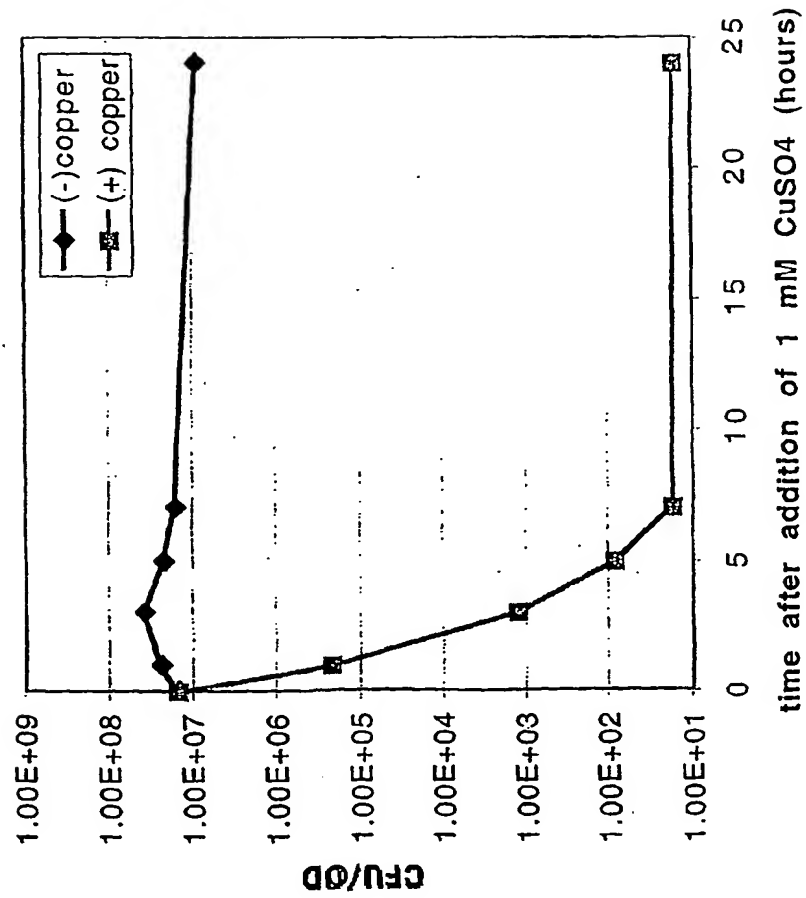


Figure 32

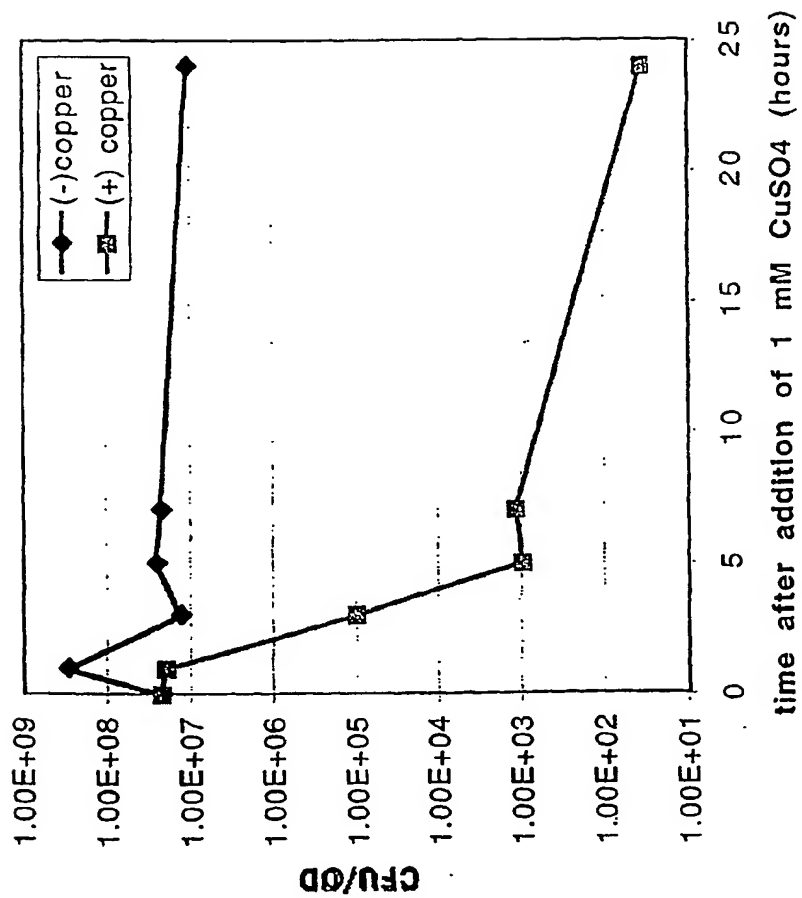
S. cerevisiae BOS1 (YLR078C) inactivation



$t_{1/2} = 0.44$ hours

Figure 33

S. cerevisiae POL30 (YBR088C) inactivation



$t_{1/2} = 0.49$ hours

Figure 34

S. cerevisiae YMR131C inactivation

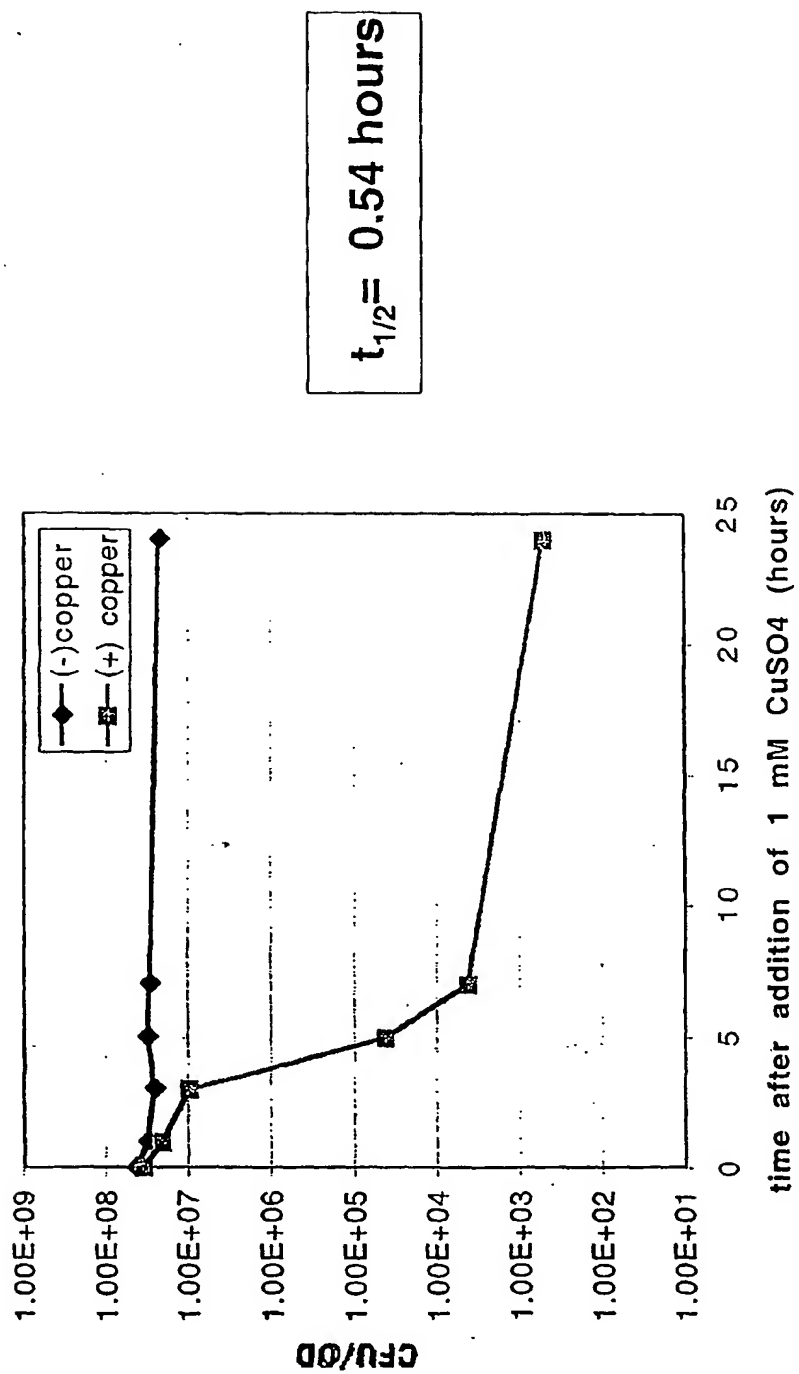


Figure 35

S. cerevisiae SQT1 (YIR012W) inactivation

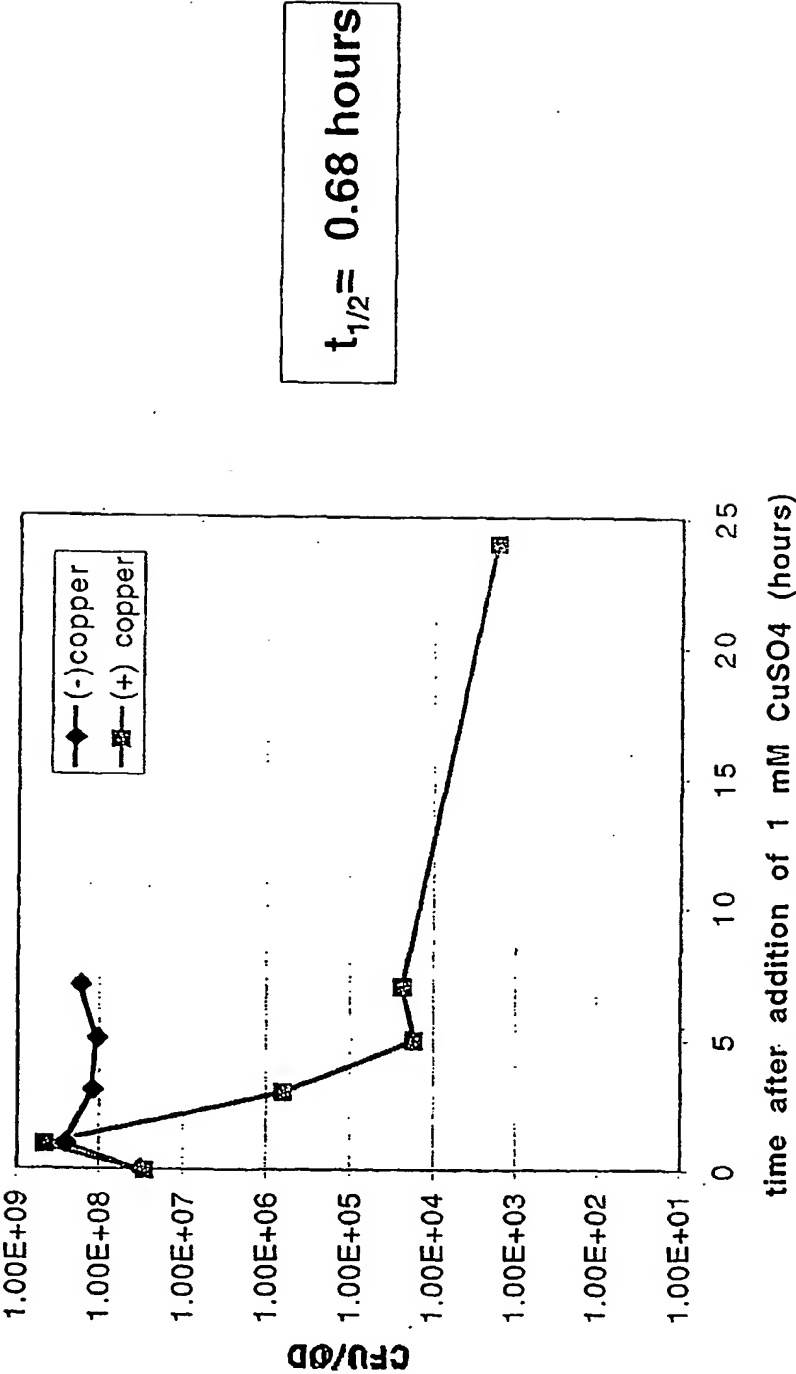


Figure 36

S. cerevisiae MTW1 (YAL034W-A) inactivation

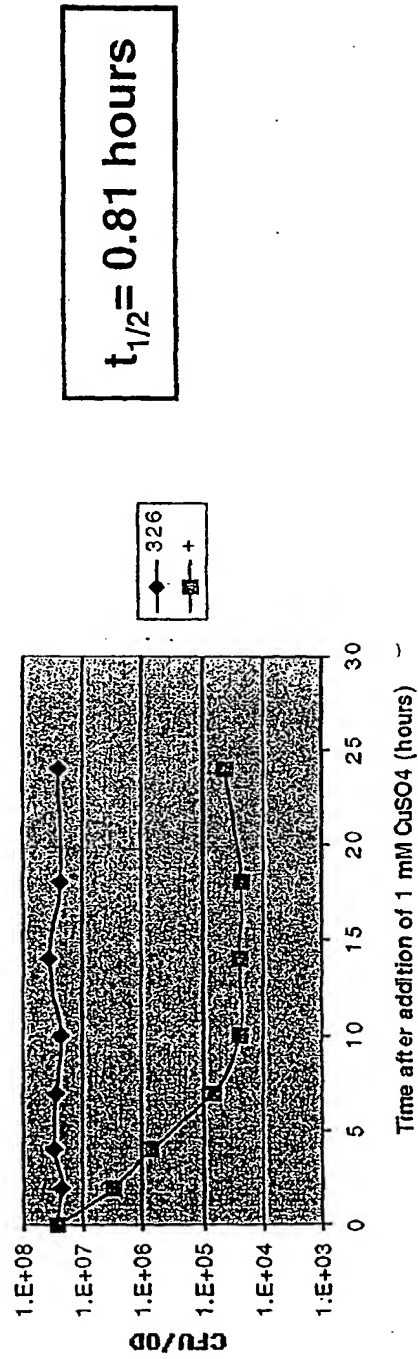


Figure 37

S. cerevisiae TFB1 (YDR311W) inactivation

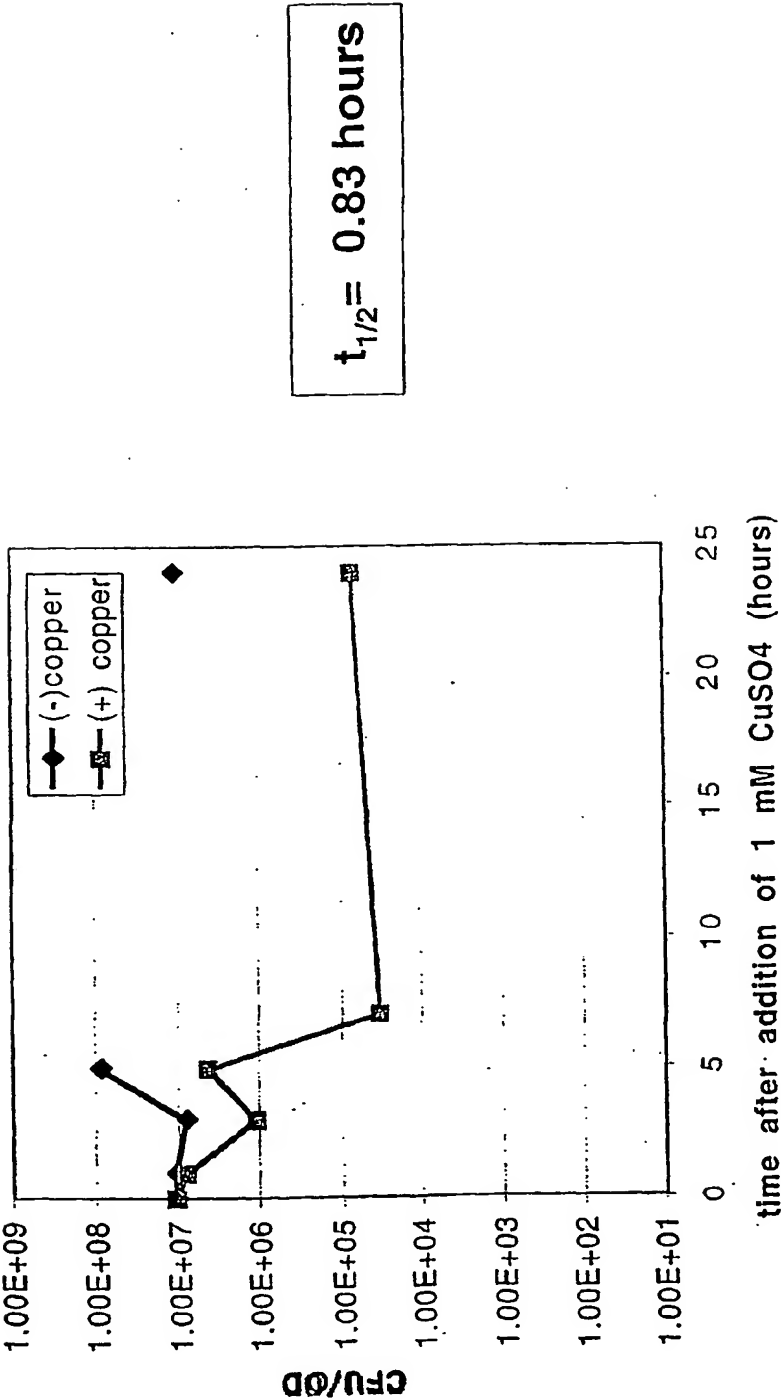
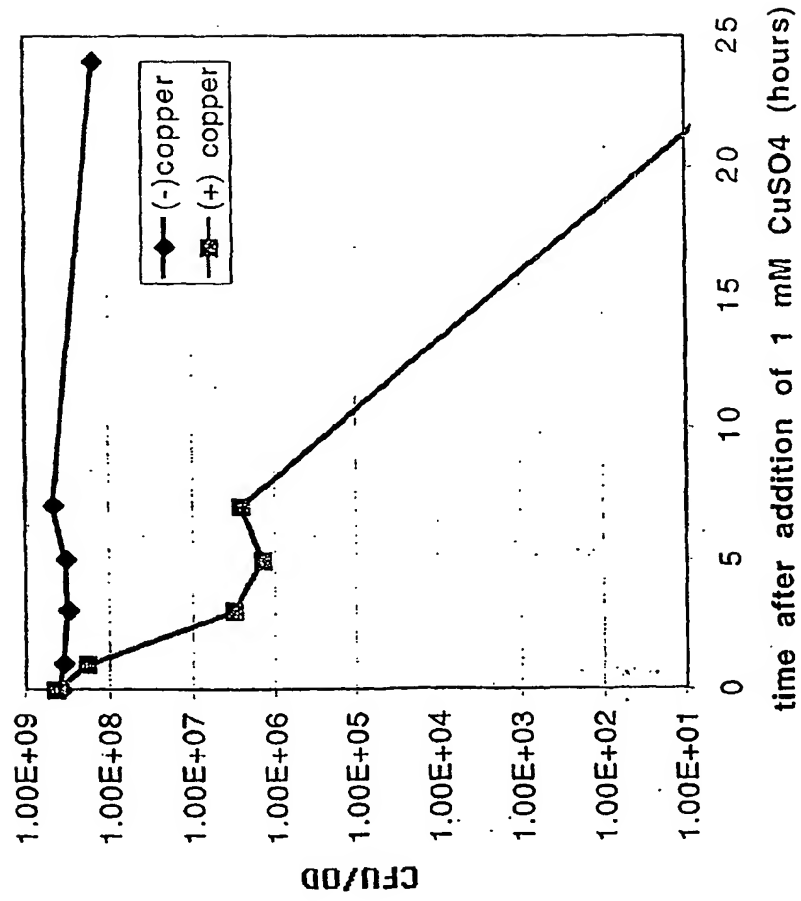


Figure 38

S. cerevisiae SPC98 (YNL126W) inactivation



$t_{1/2} = 0.84$ hours

Figure 39

S. cerevisiae BFR2 (YDR299W) inactivation

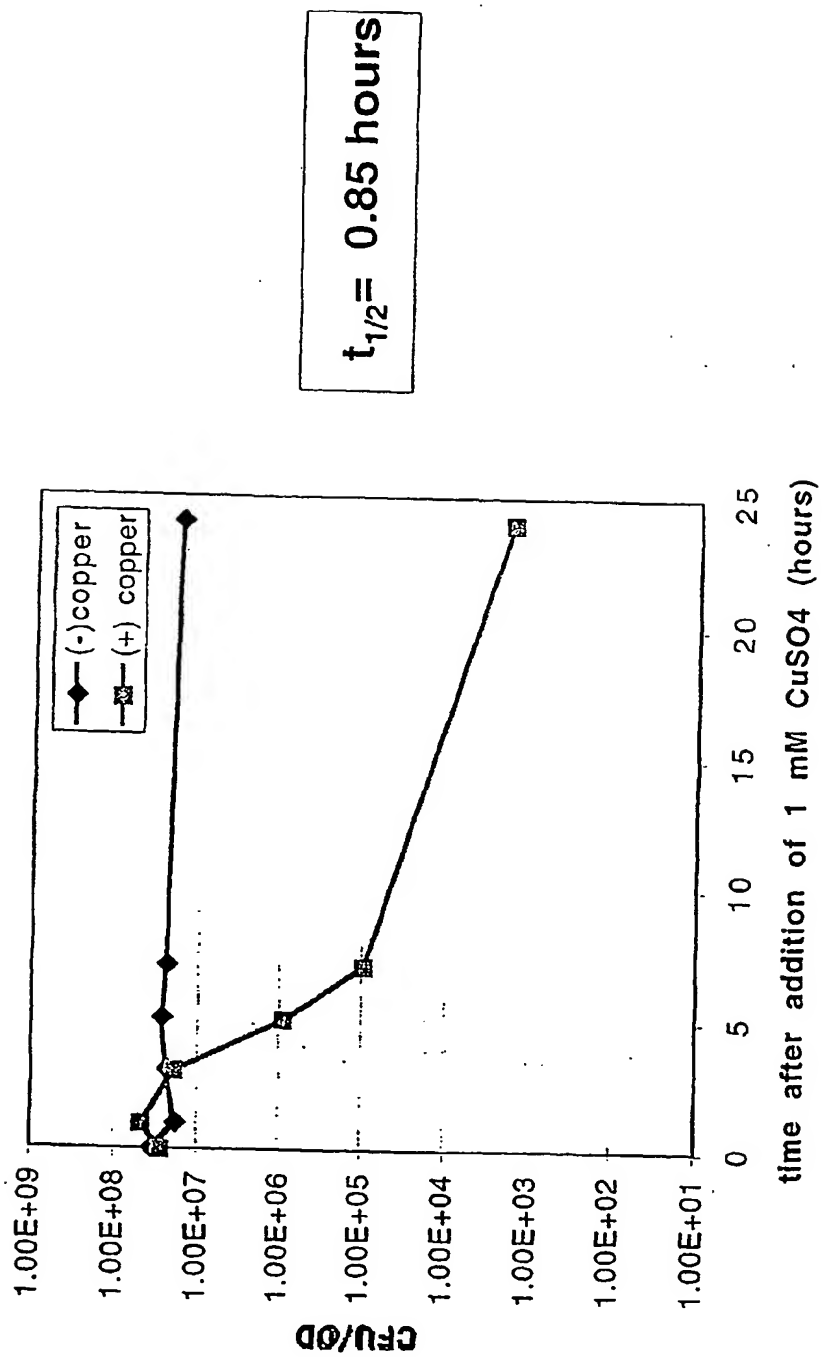


Figure 40

S. cerevisiae RNA1 (YMR235C) inactivation

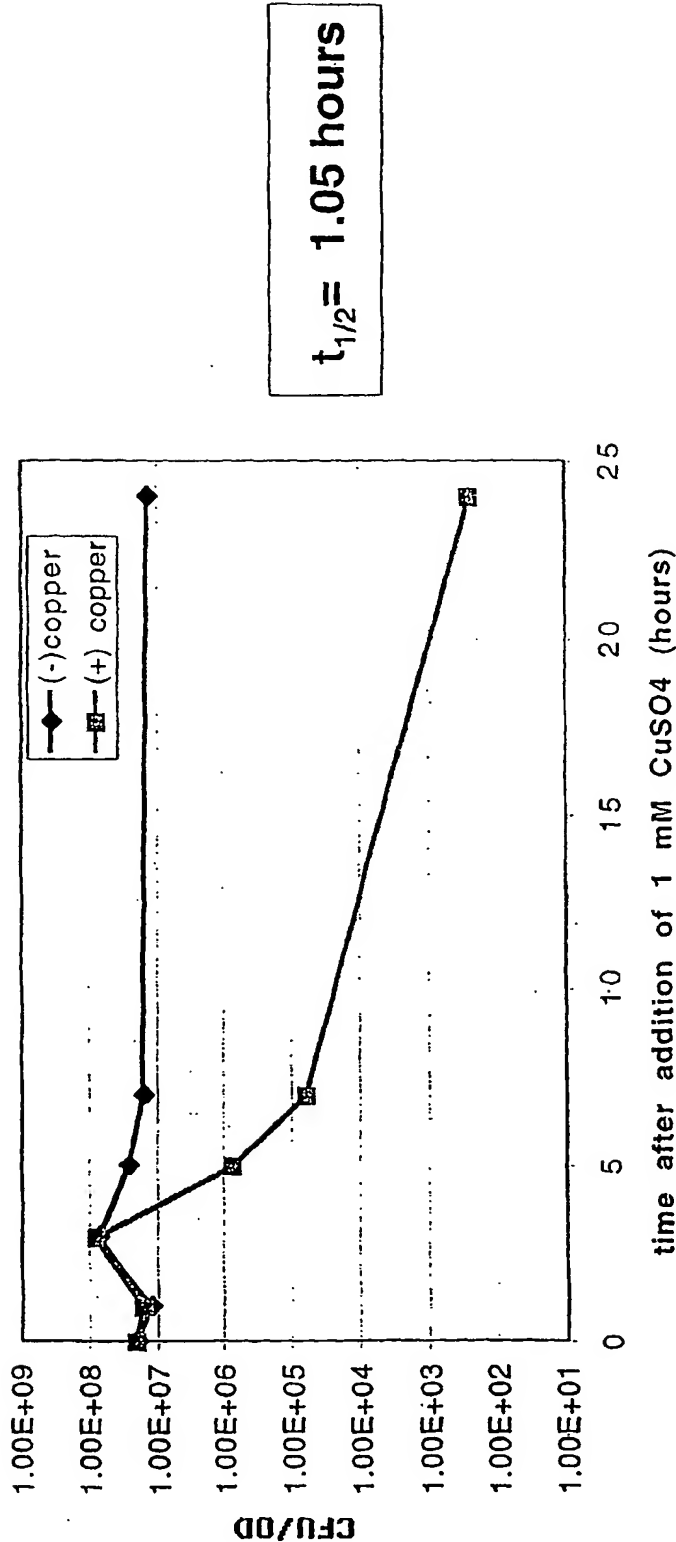
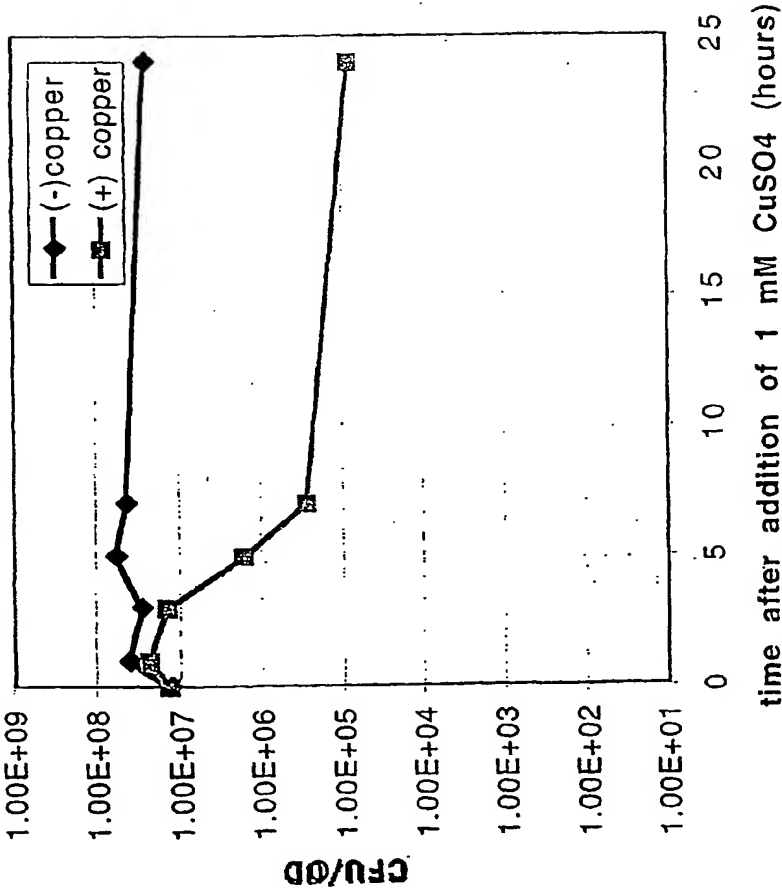


Figure 41

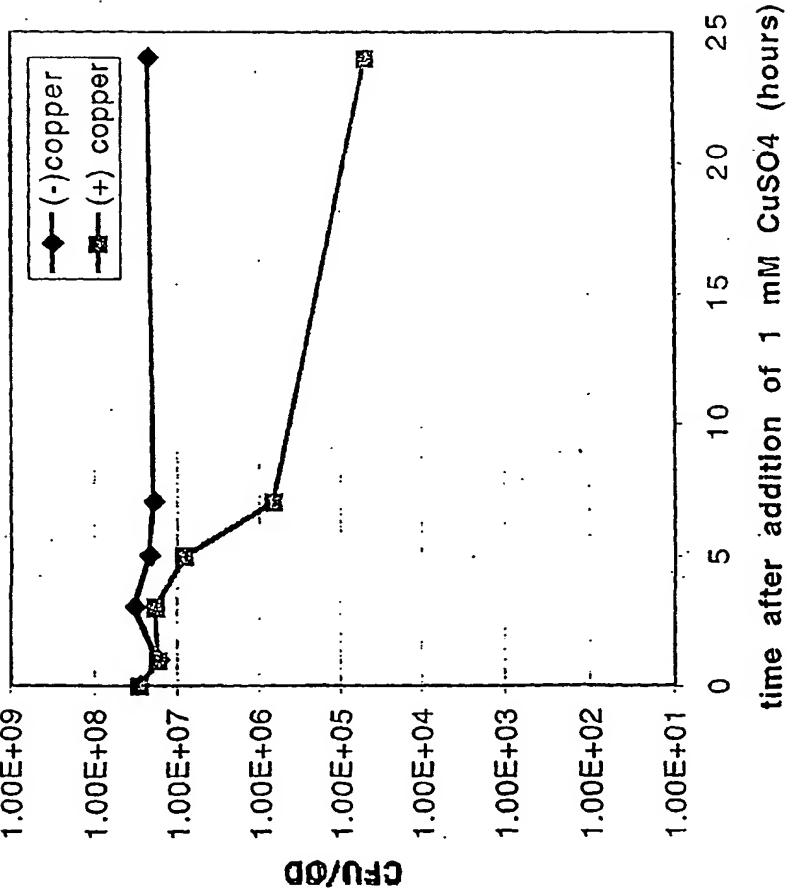
S. cerevisiae GCD7 (YLR291C) inactivation



$t_{1/2} = 1.06$ hours

Figure 42

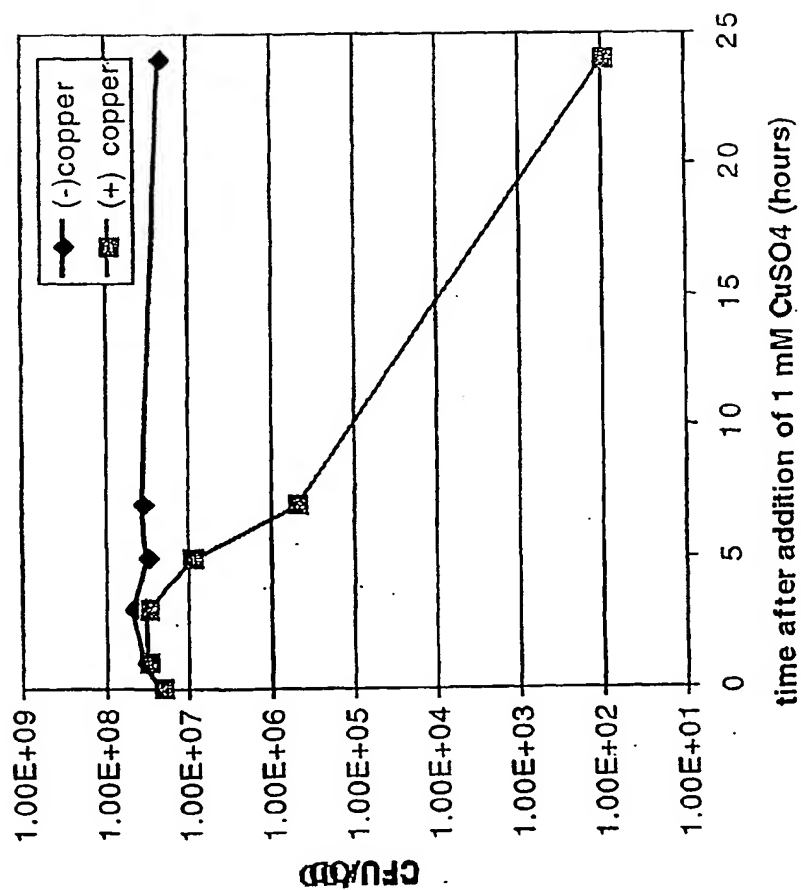
S. cerevisiae SKI6 (YGR195W) inactivation



$t_{1/2} = 1.27$ hours

Figure 43

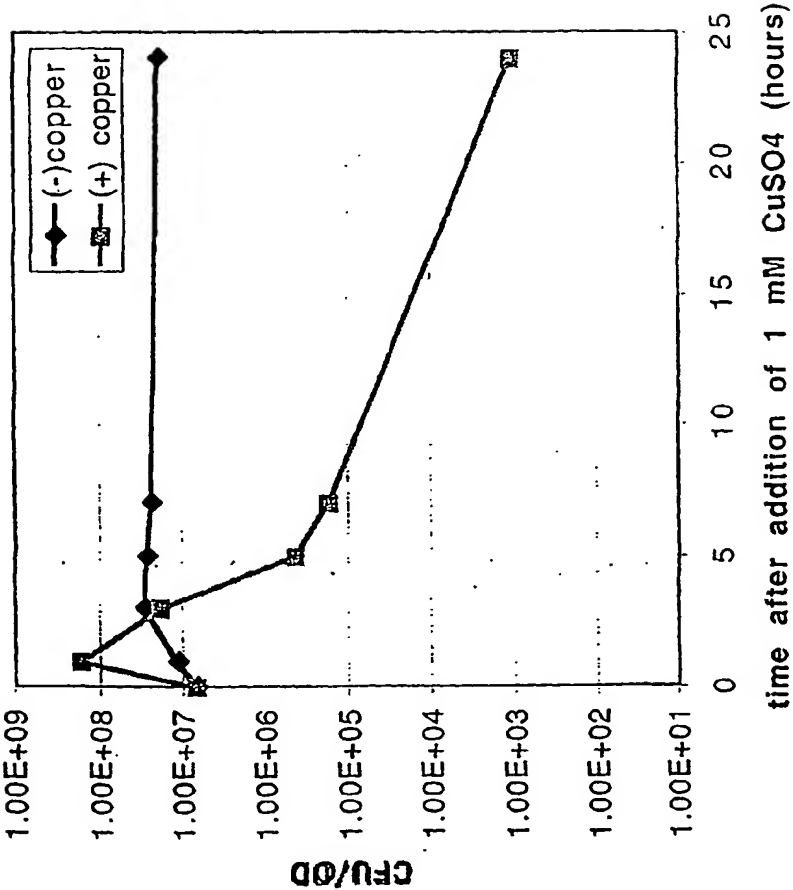
S. cerevisiae NIP1 (YMR309C) inactivation



$t_{1/2} = 1.28$ hours

Figure 44

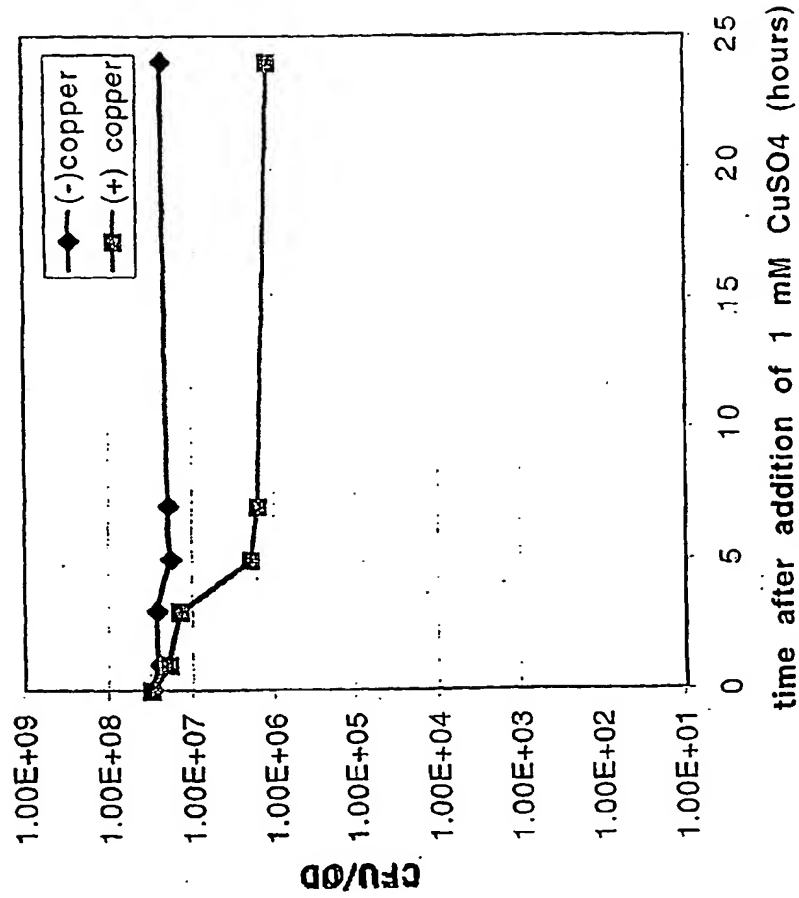
S. cerevisiae LCP5 (YER127W) inactivation



$t_{1/2} = 1.32$ hours

Figure 45

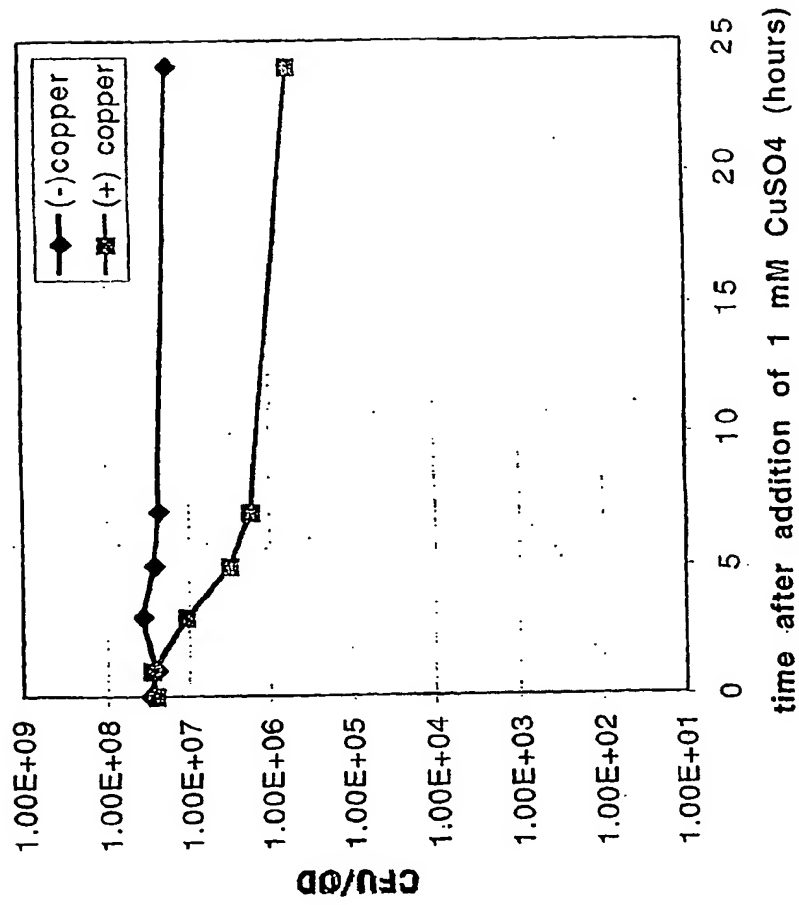
S. cerevisiae NCE103 (YNL036W) inactivation



$t_{1/2} = 1.63$ hours

Figure 46

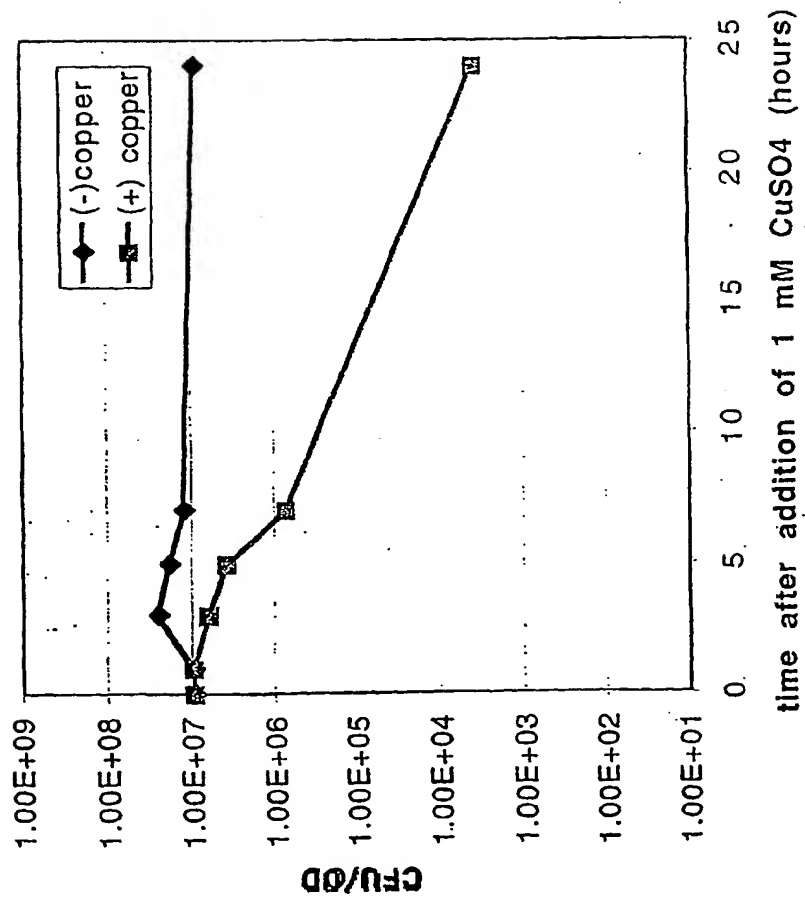
S. cerevisiae ECO1 (YFR027W) inactivation



$t_{1/2} = 1.67$ hours

Figure 47

S. cerevisiae ORC2 (YBR060C) inactivation



$t_{1/2} = 1.86$ hours

Figure 48

S. cerevisiae CNS1 (YBR155W) inactivation

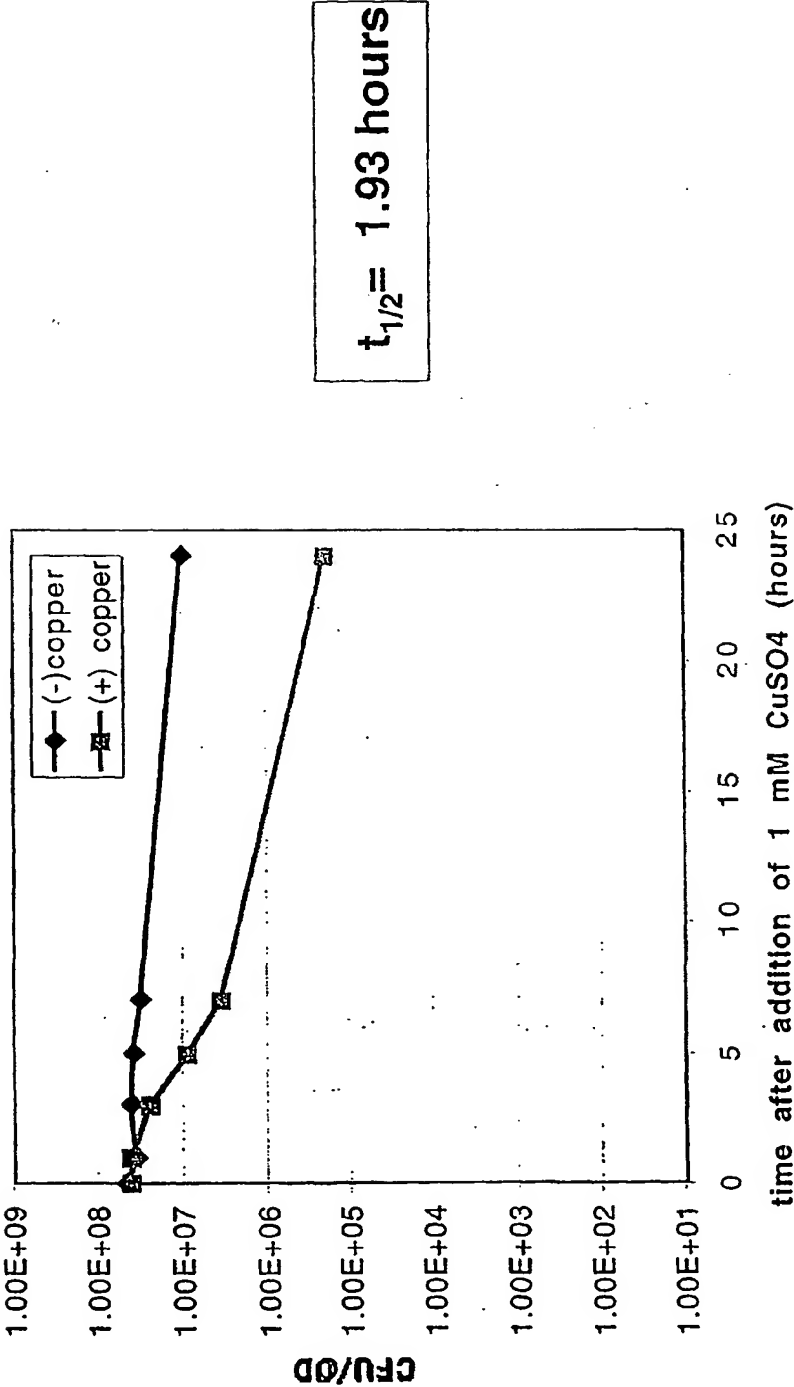


Figure 49

S. cerevisiae YPD1 (YDL235C) inactivation

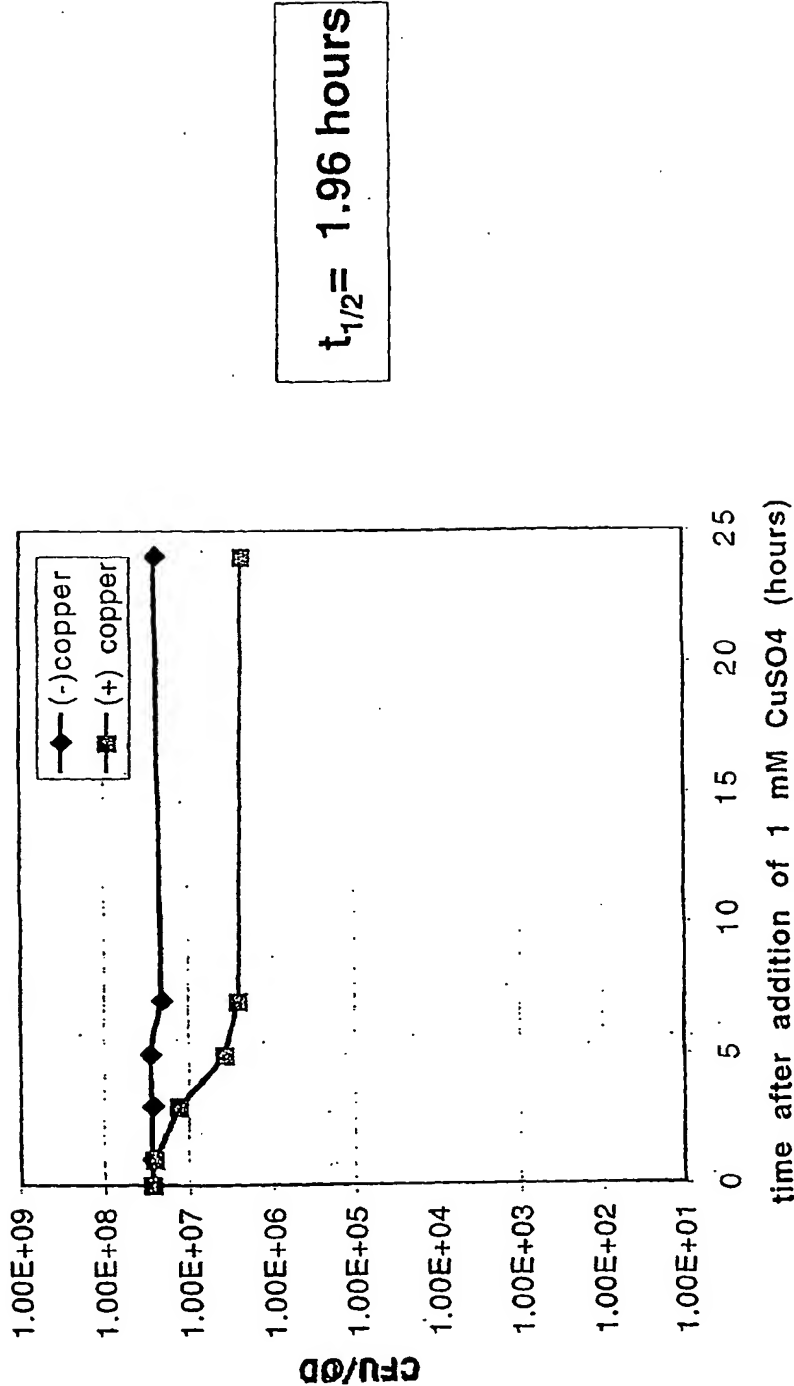


Figure 50

S. cerevisiae TIM10 (YHR005C-A) inactivation

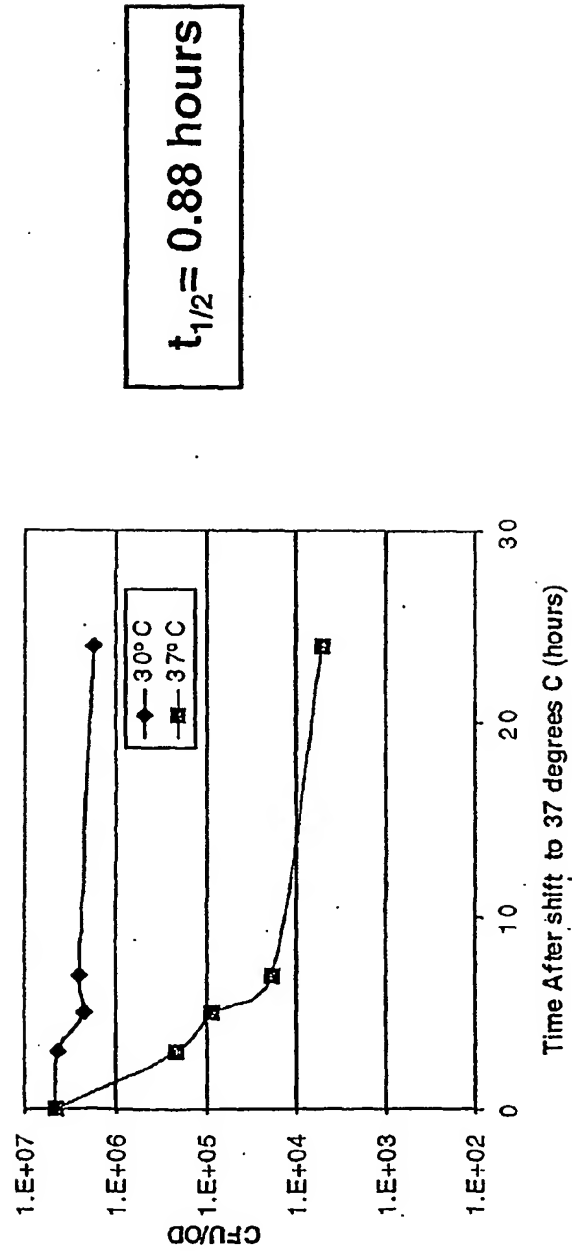
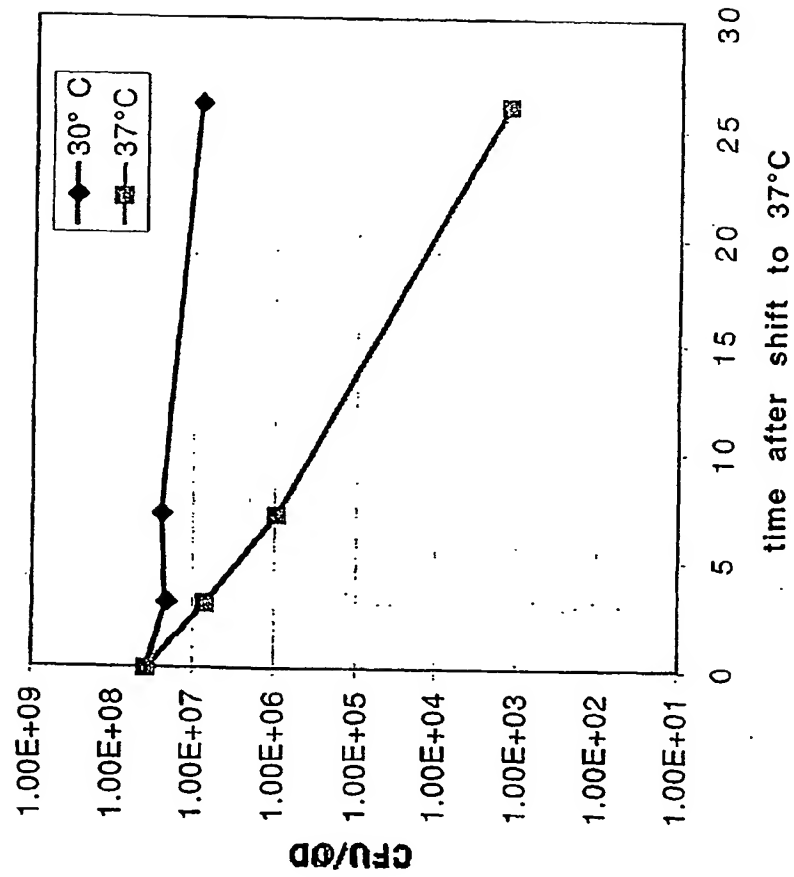


Figure 51

S. cerevisiae SRB4 (YER02W) inactivation



$t_{1/2} = 1.30$ hours

Figure 52

C. albicans RPC34 deletion analysis

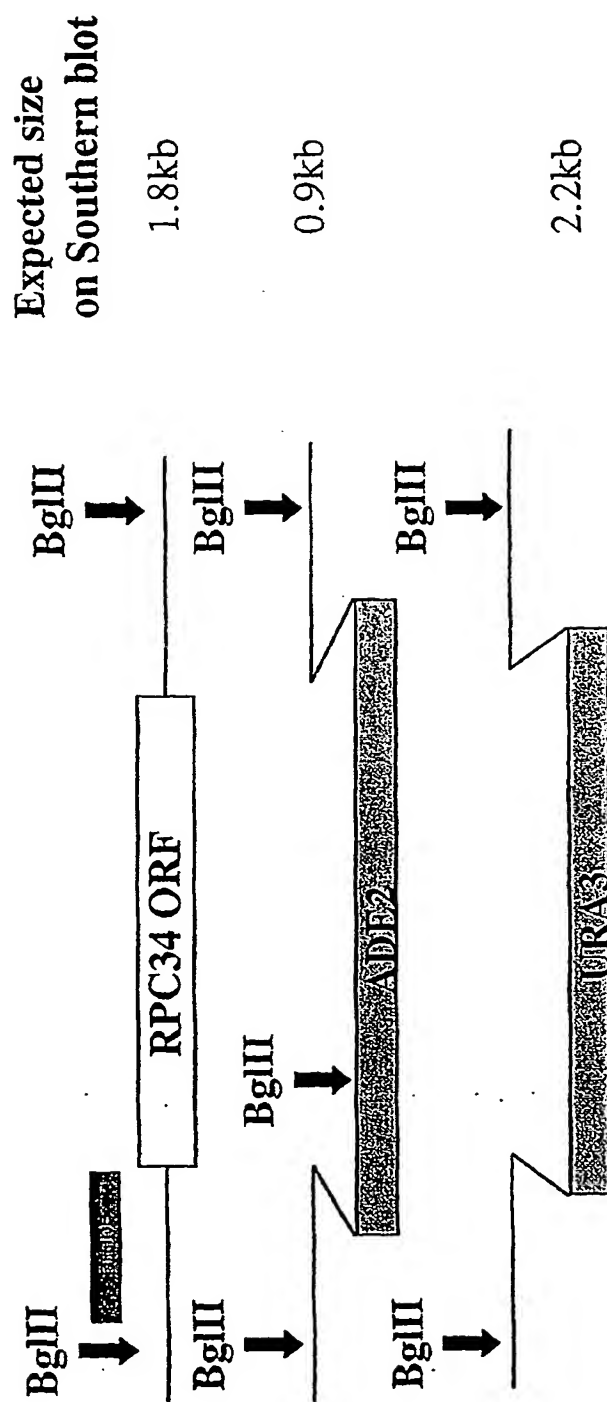
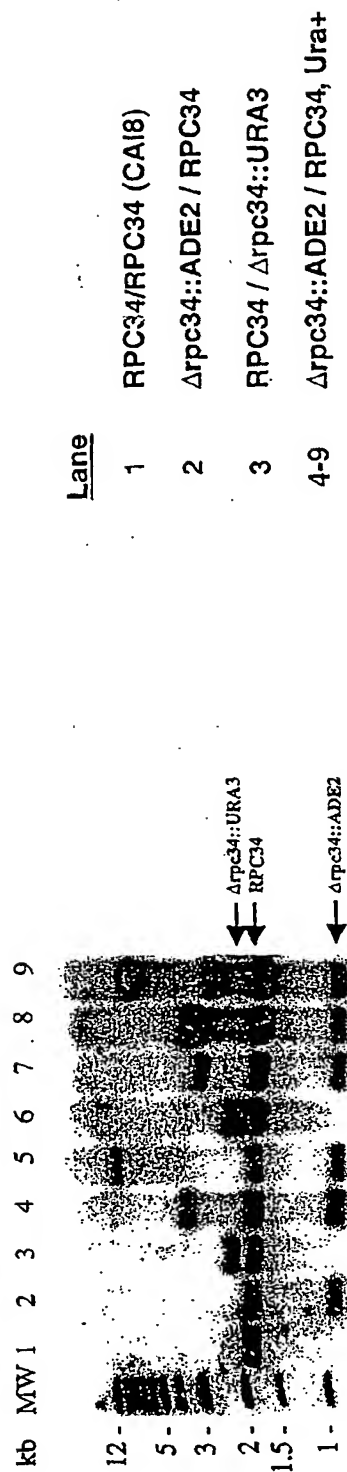
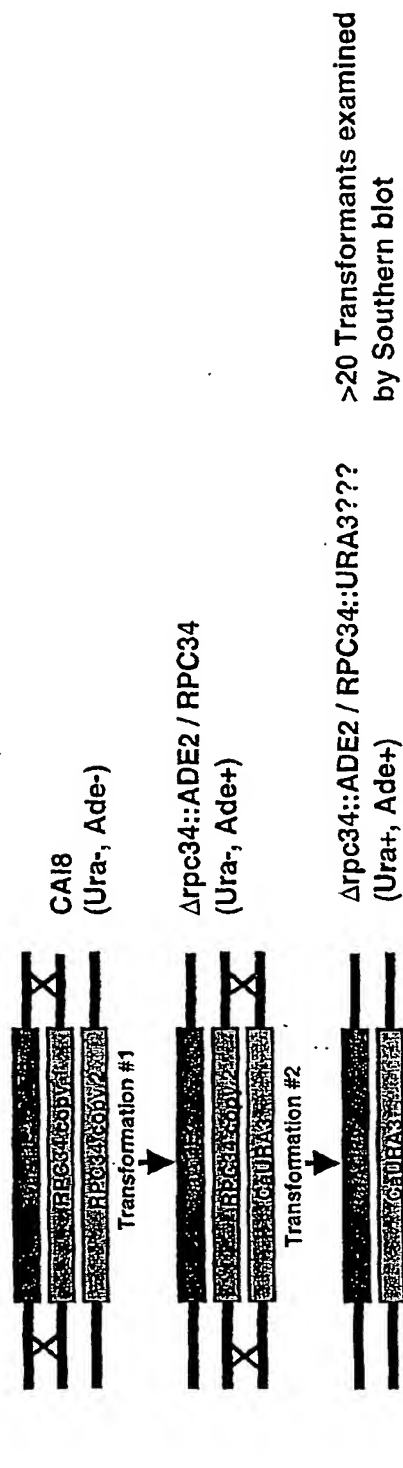


Figure 53A

C. albicans RPC34 deletion analysis



Unable to delete second copy of RPC34

Figure 53B

C. albicans POP3 deletion analysis

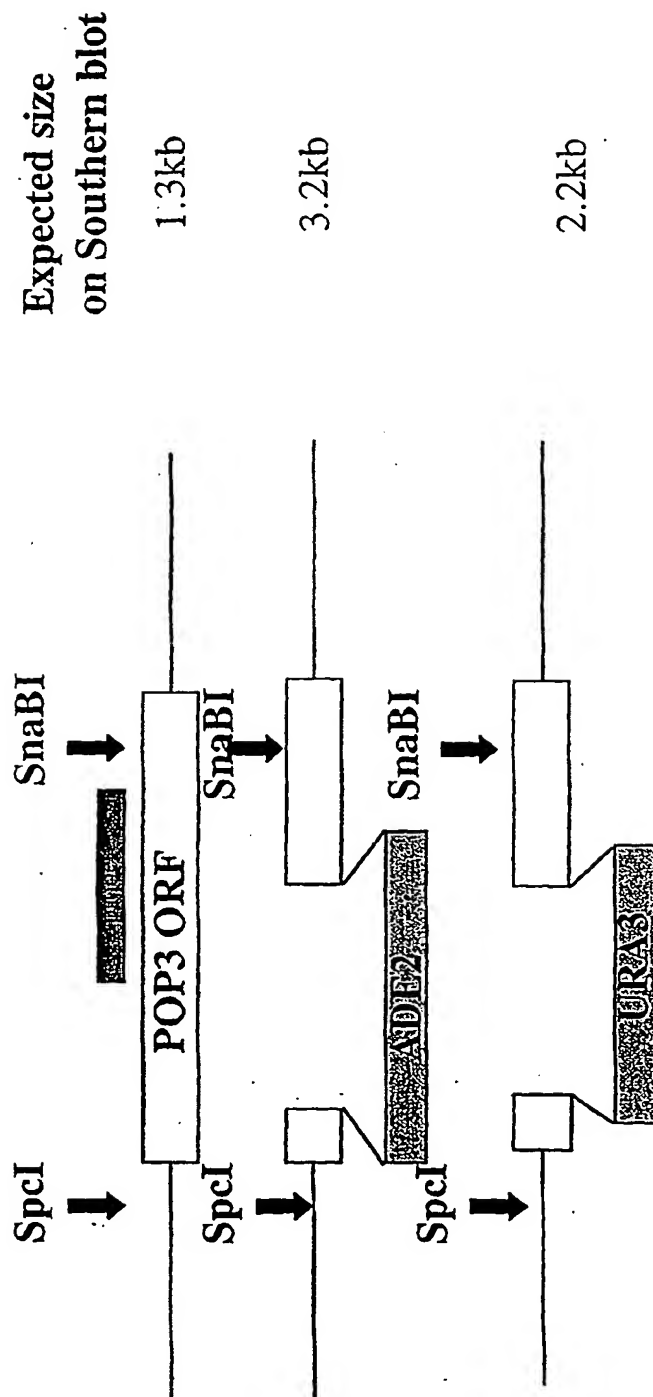


Figure 54A

C. albicans POP3 deletion analysis

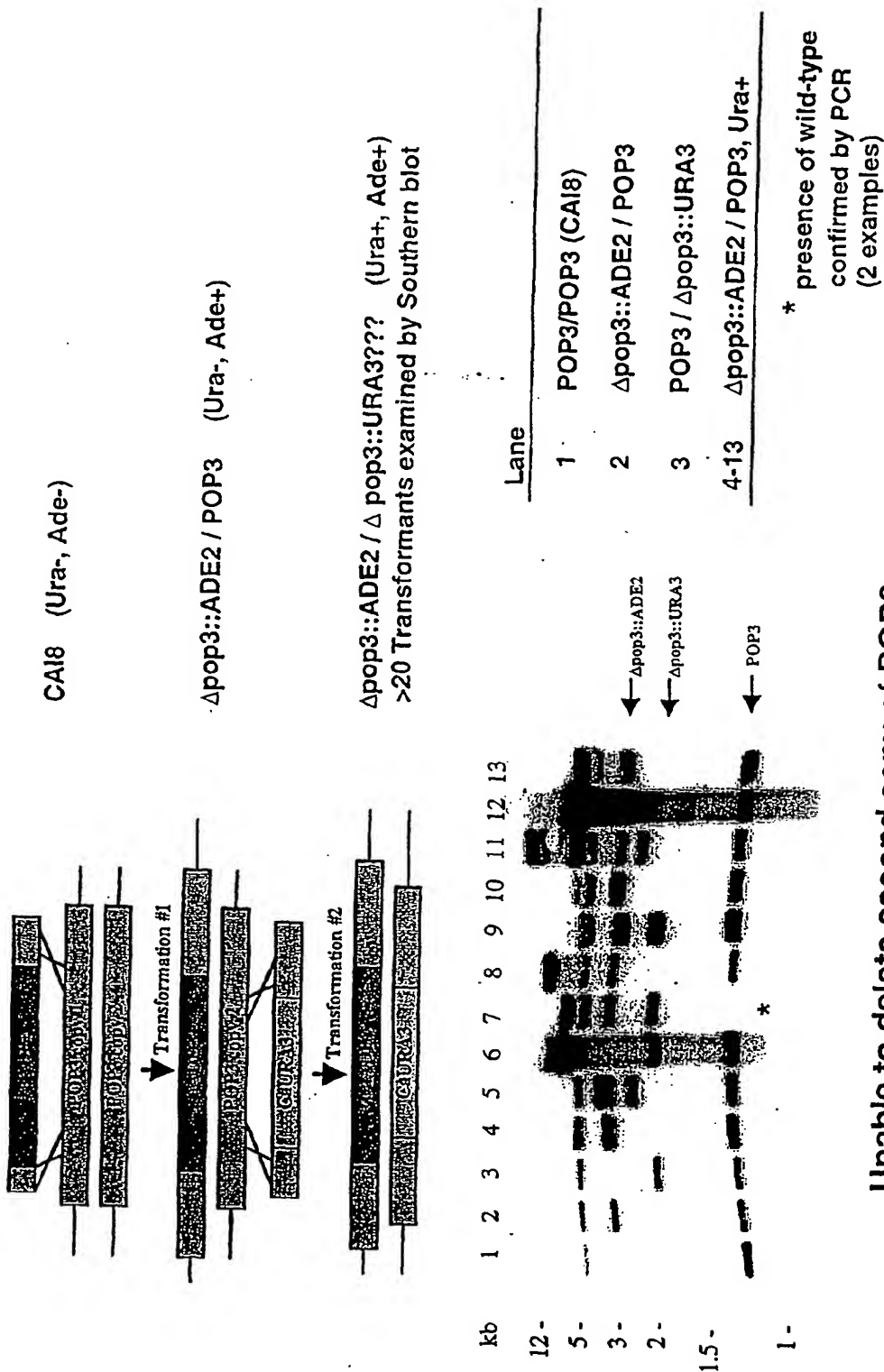


Figure 54B

C. albicans TFA2 deletion analysis

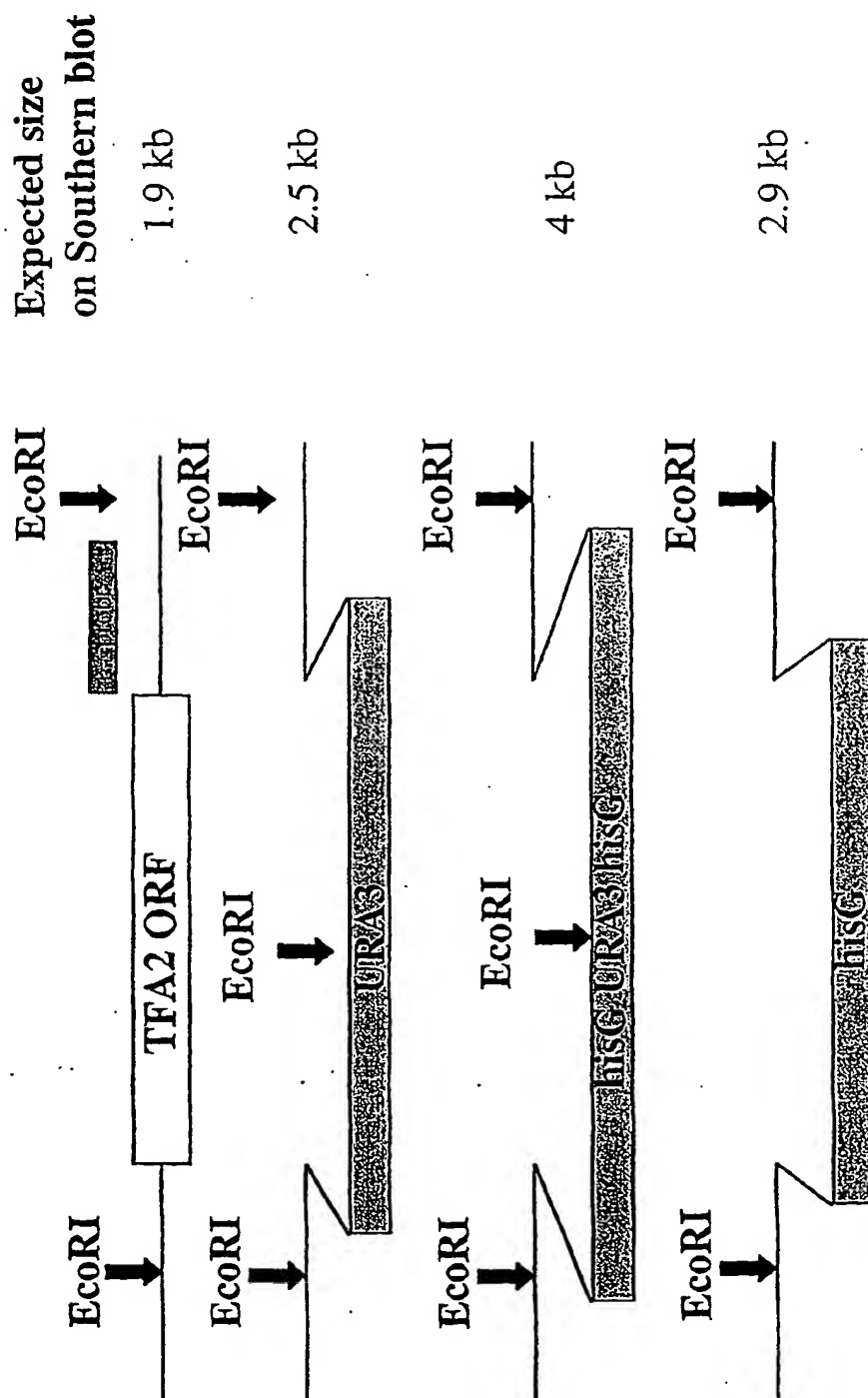
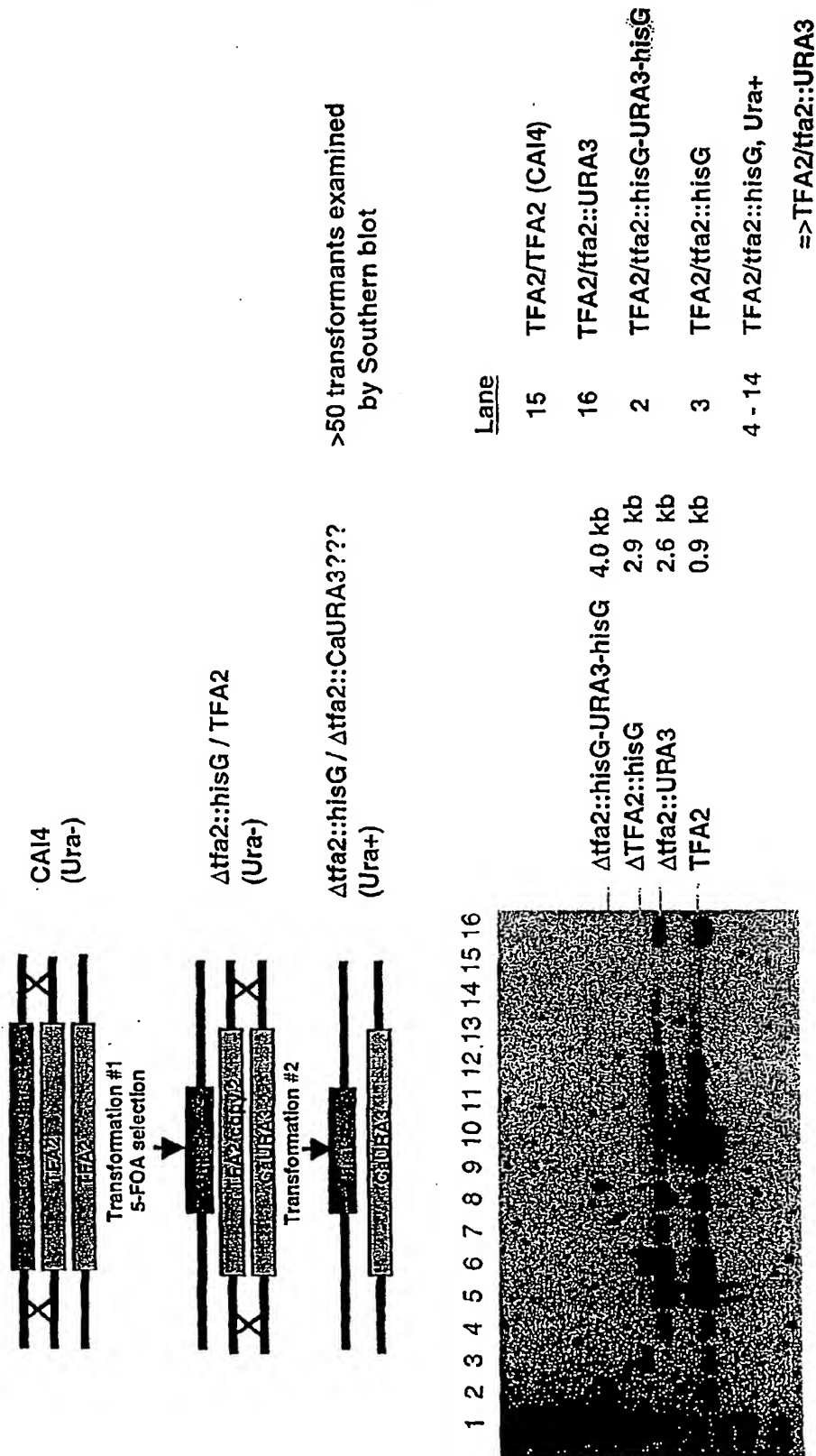


Figure 55A

C. albicans TFA2 deletion analysis



Unable to delete second copy of *CaTFA2*

Figure 55B

C. albicans NAB2 deletion analysis

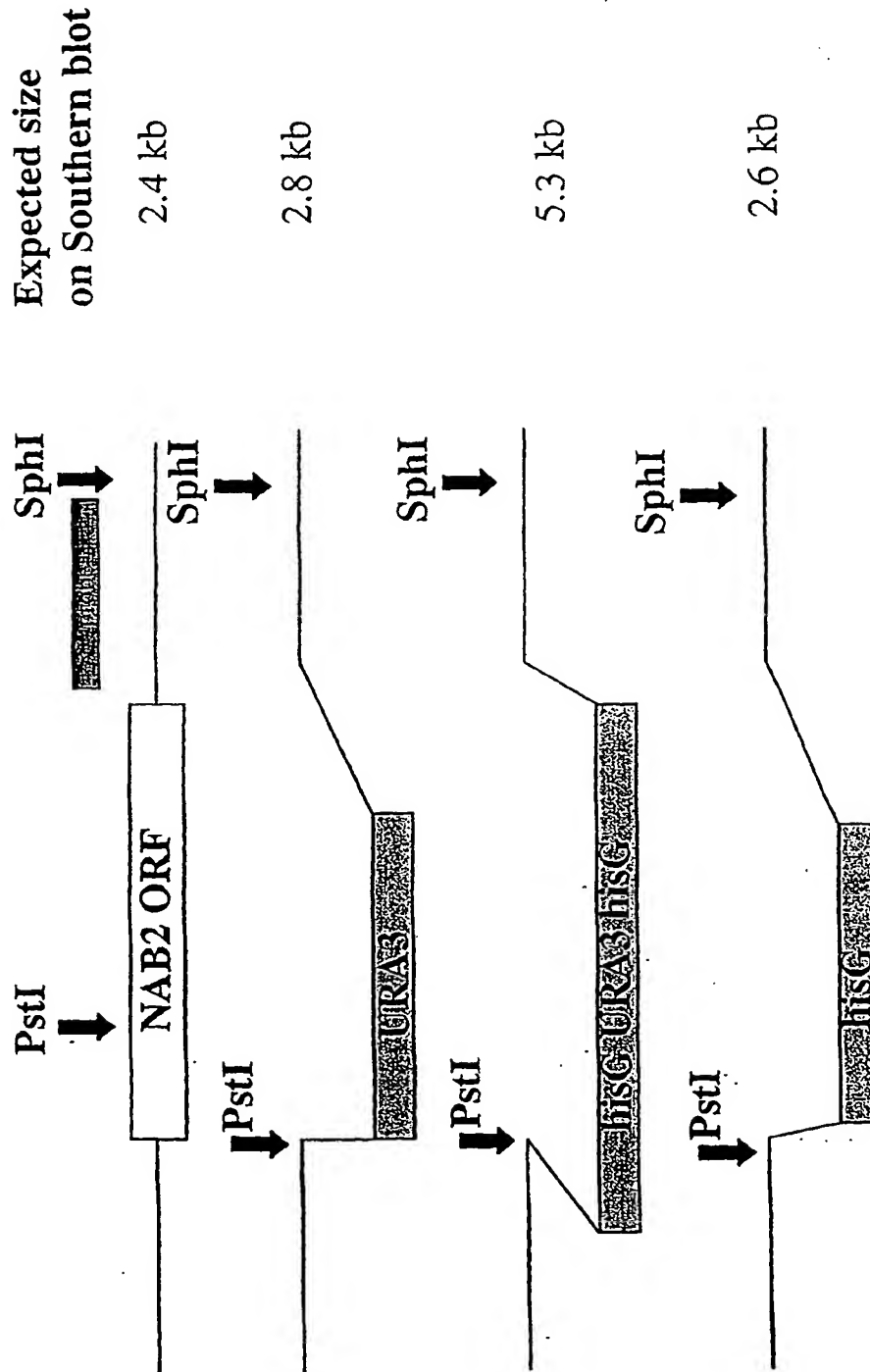
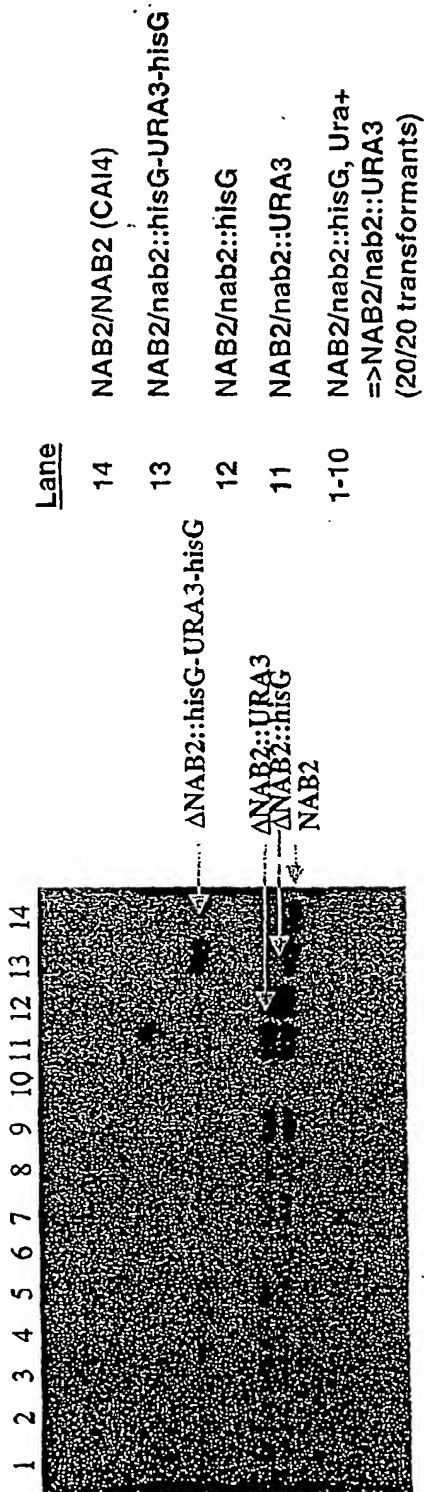
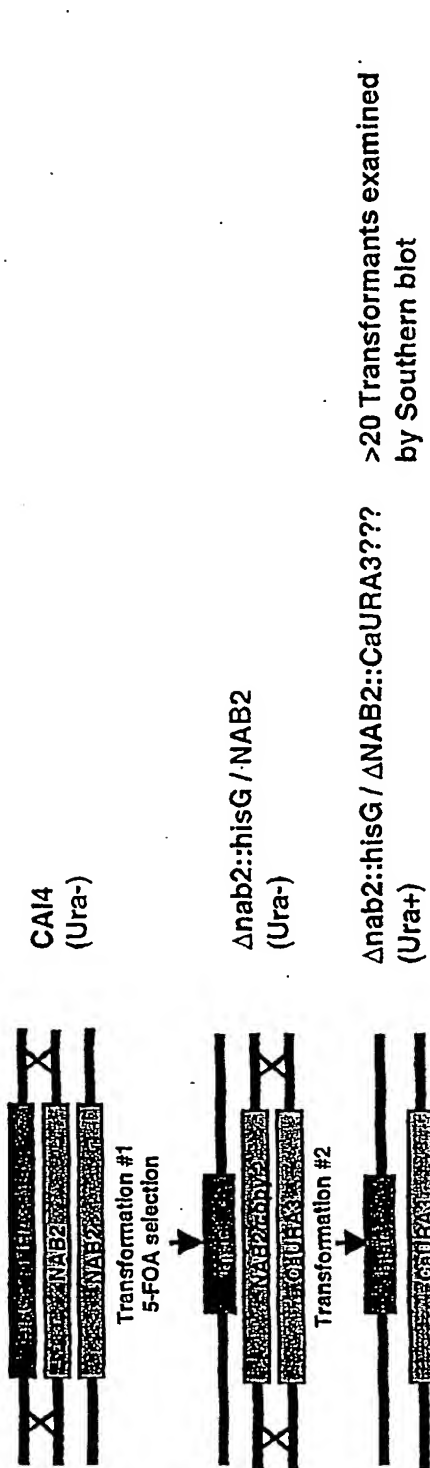


Figure 56A

C. albicans NAB2 deletion analysis



Unable to delete second copy of *CaNAB2*

Figure 56B

C. albicans MPT1 deletion analysis

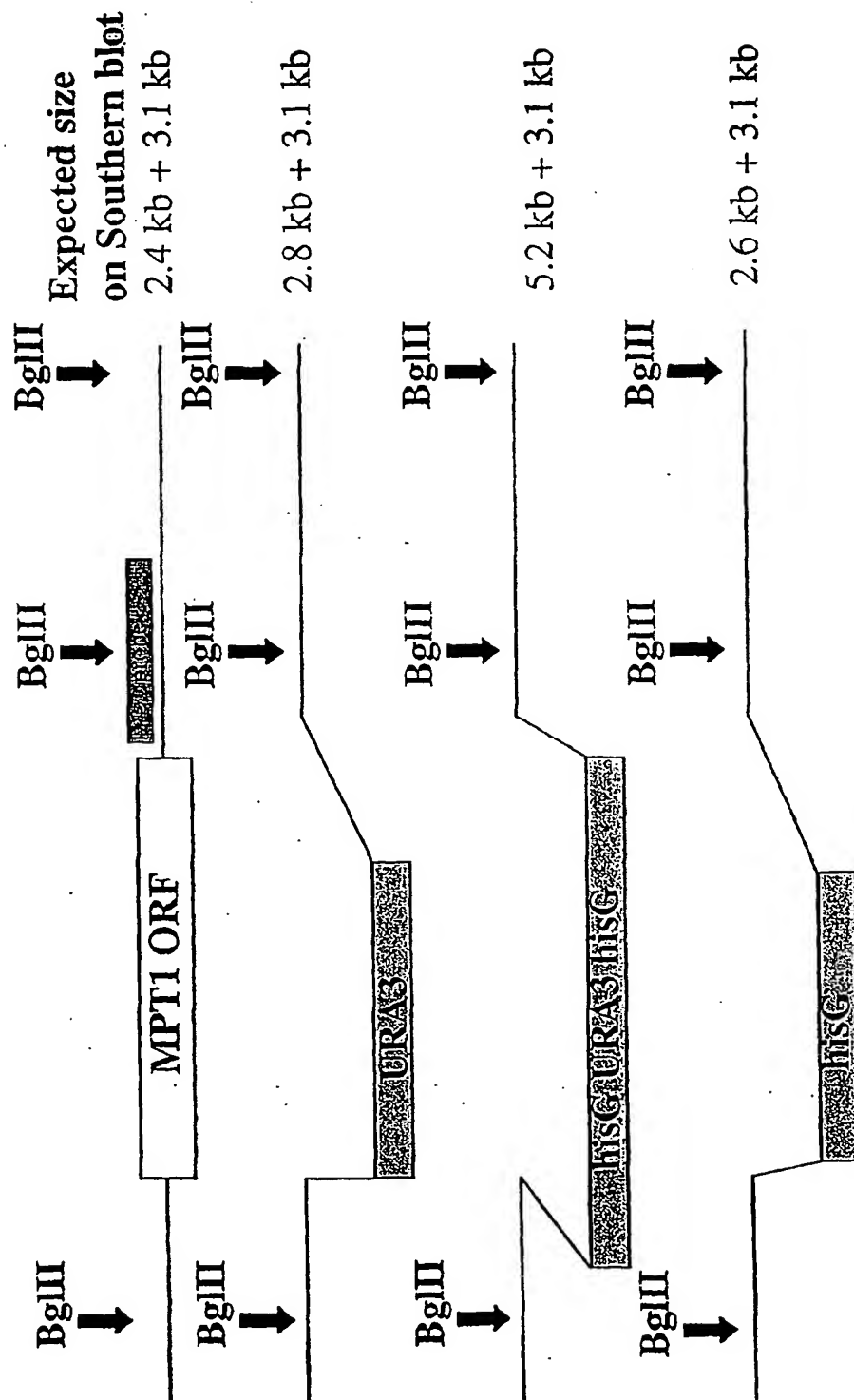
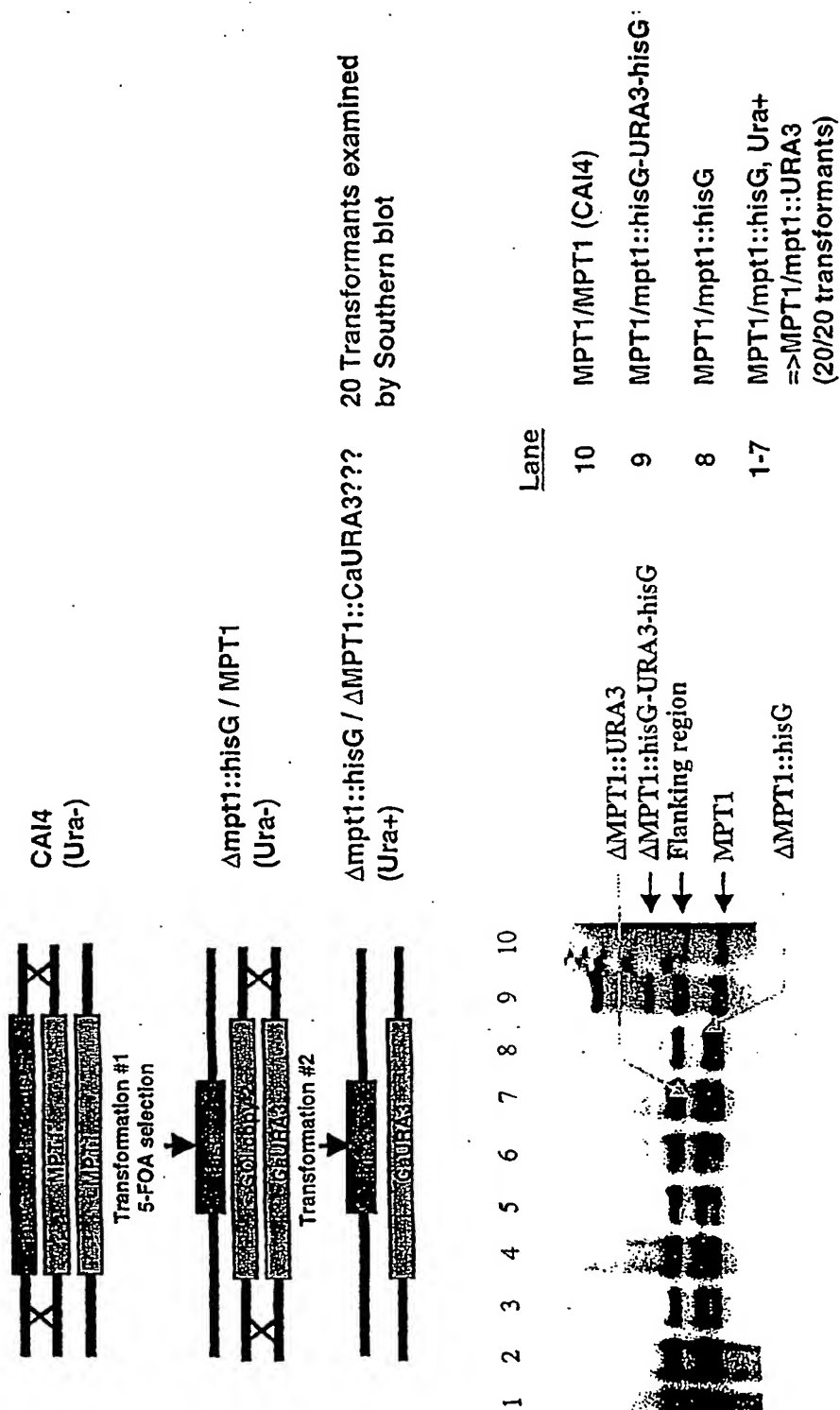


Figure 57A

C. albicans MPT1 deletion analysis



Unable to delete second copy of *CaMPT1*

Figure 57B

C. albicans MTR2 deletion analysis

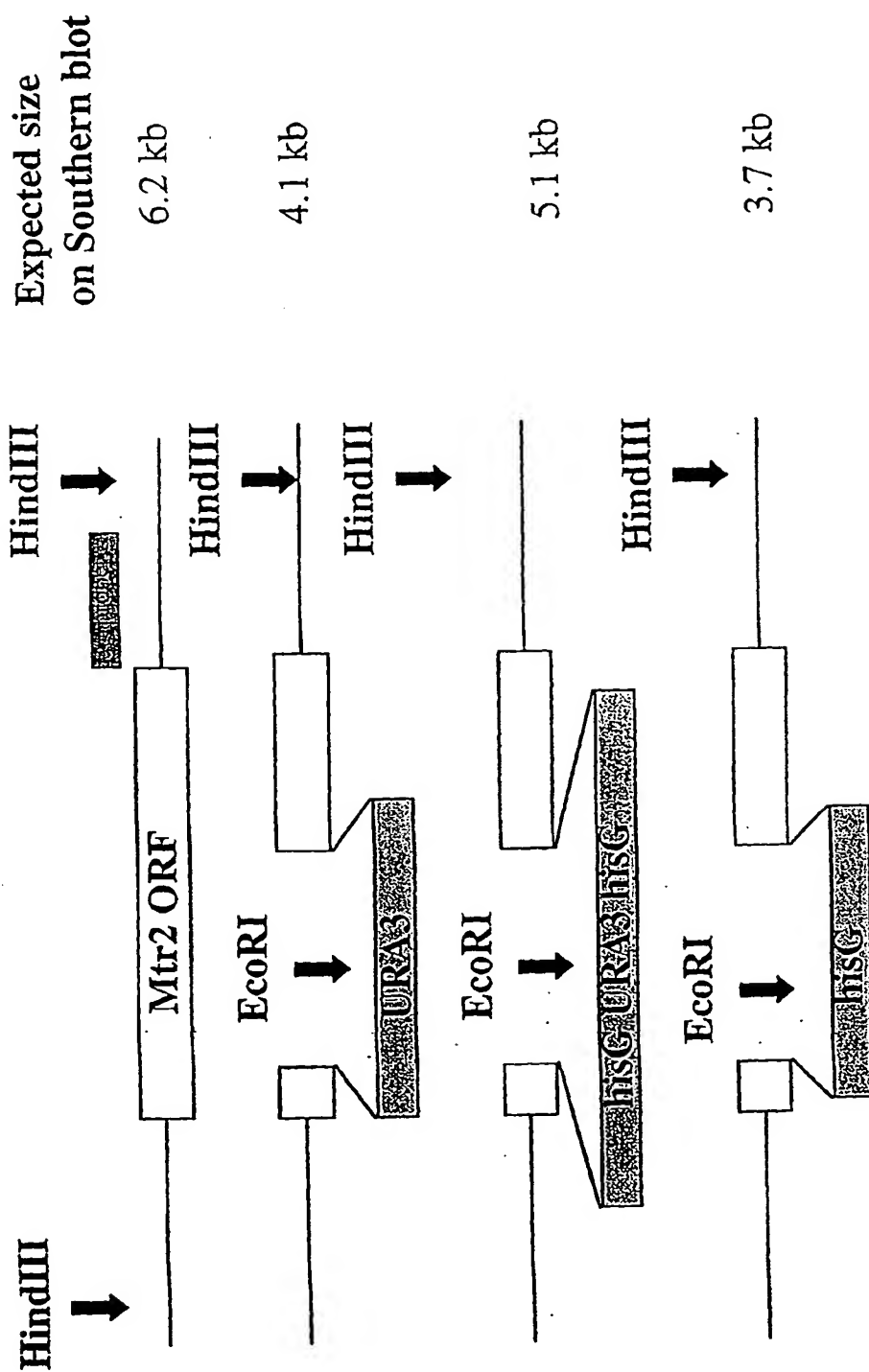
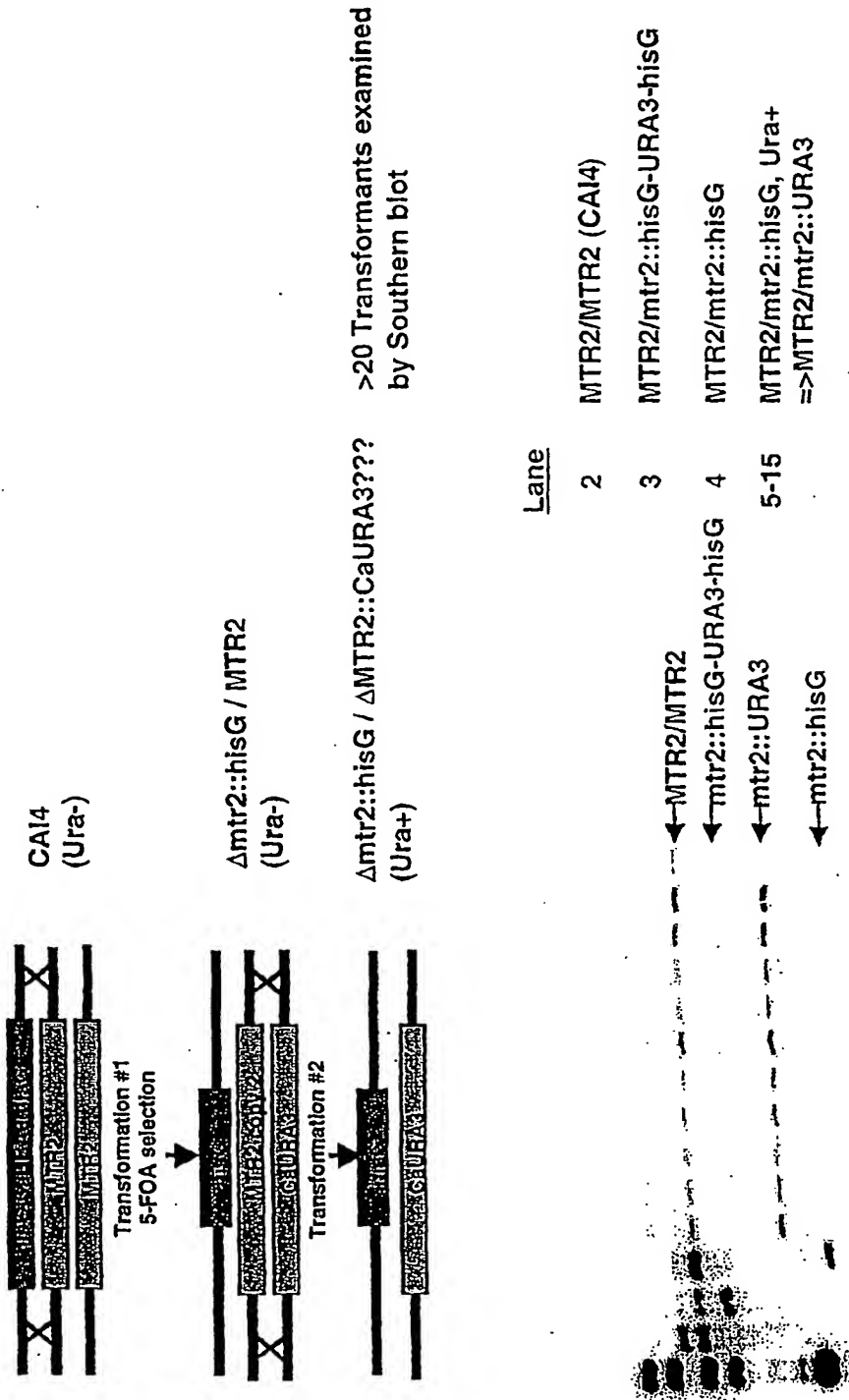


Figure 58A

C. albicans MTR2 deletion analysis



Unable to delete second copy of *CaMTR2*

Figure 58B

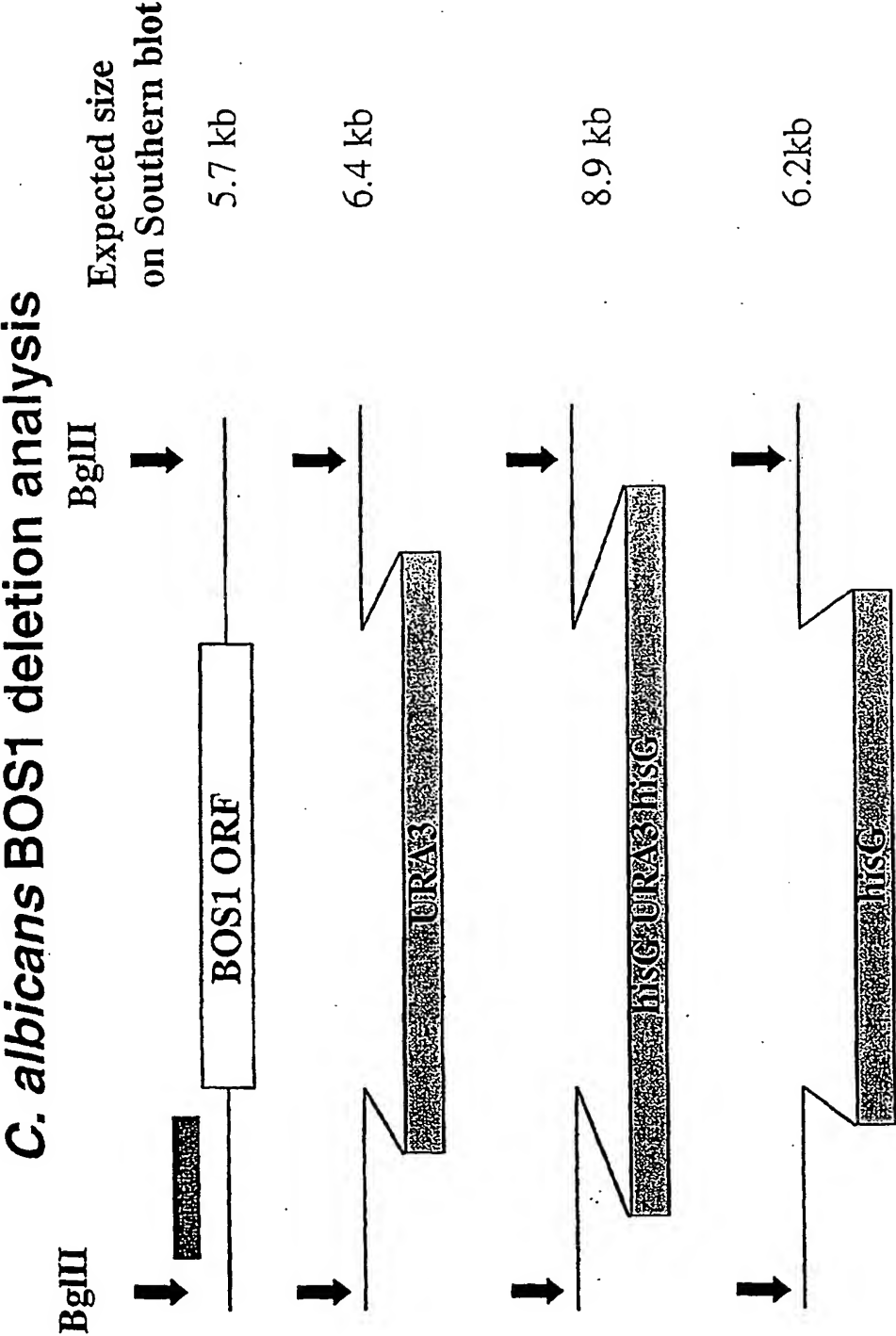
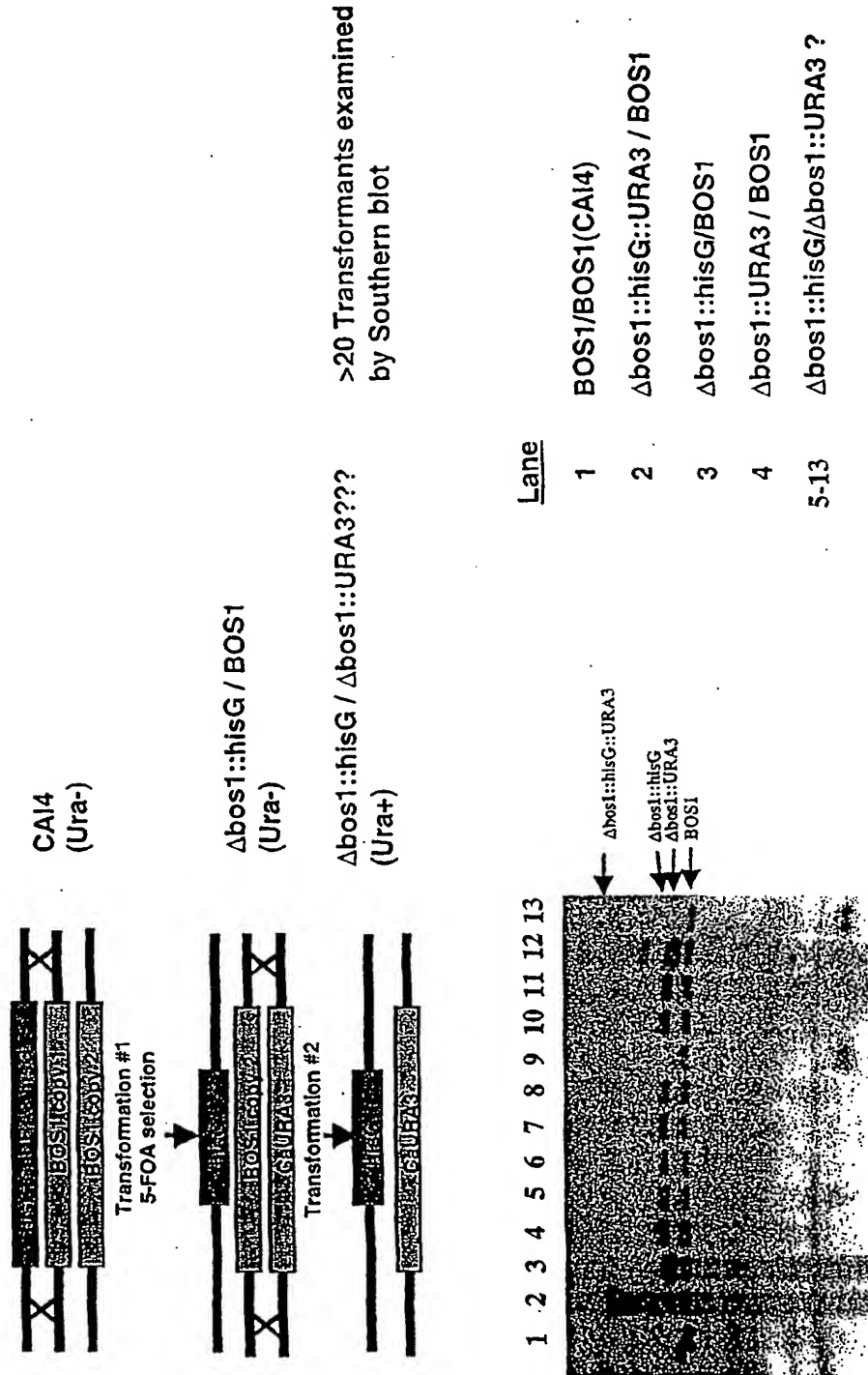


Figure 59A

C. albicans BOS1 deletion analysis



Unable to delete second copy of BOS1

Figure 59B

C. albicans POL30 deletion analysis

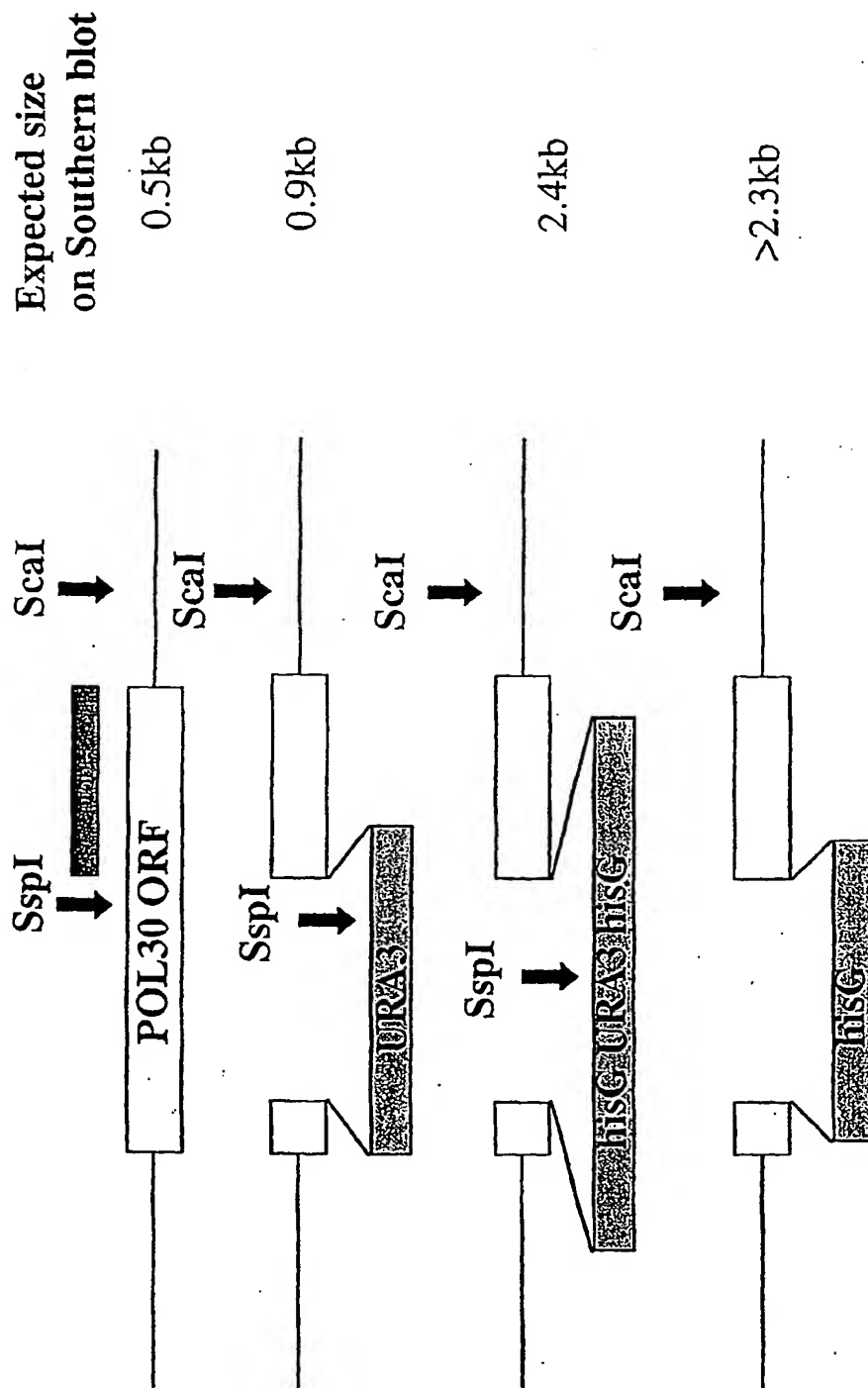
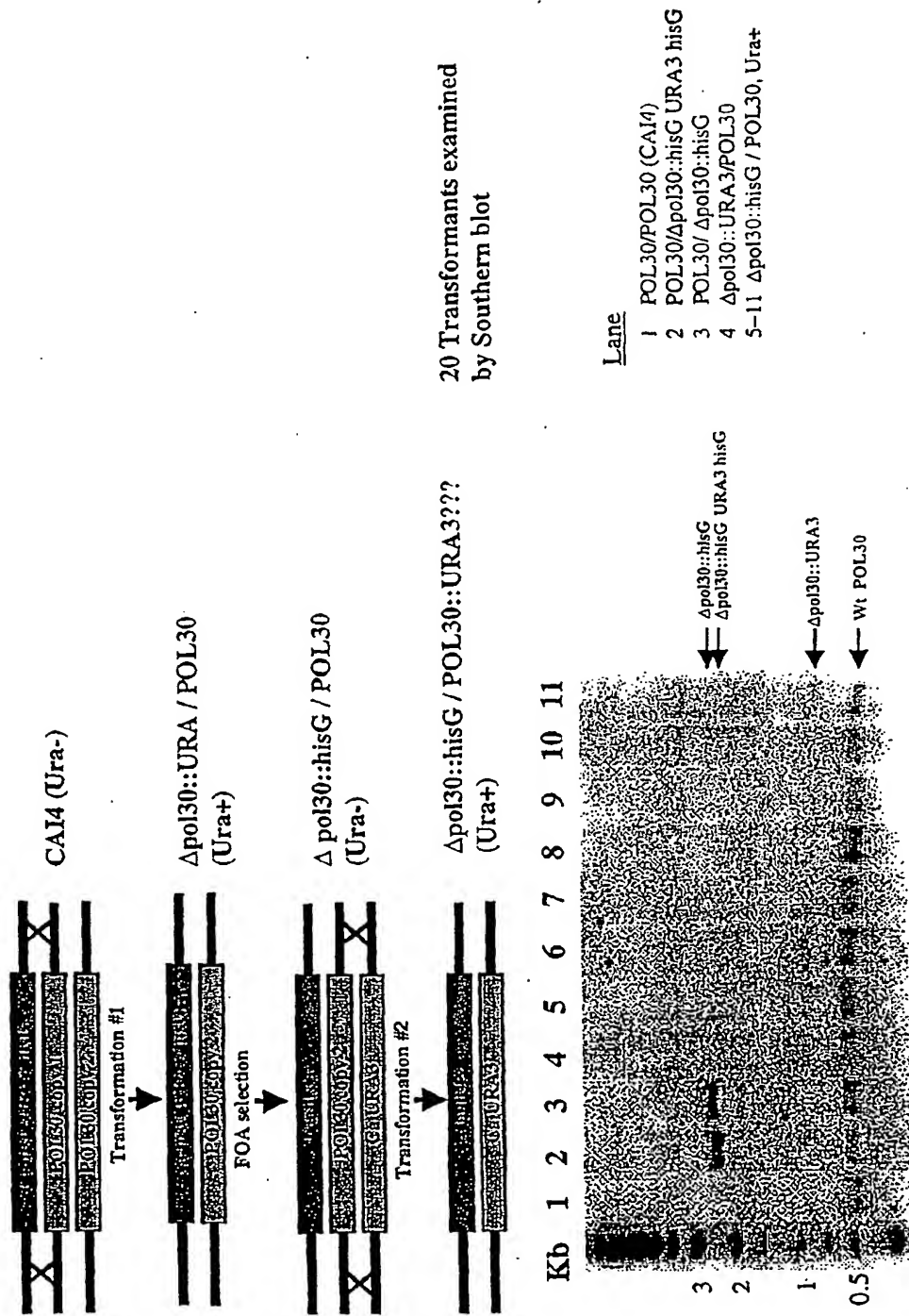


Figure 60A

C. albicans POL30 deletion analysis



Unable to delete second copy of POL30

Figure 60B

C. albicans YMR131C deletion analysis

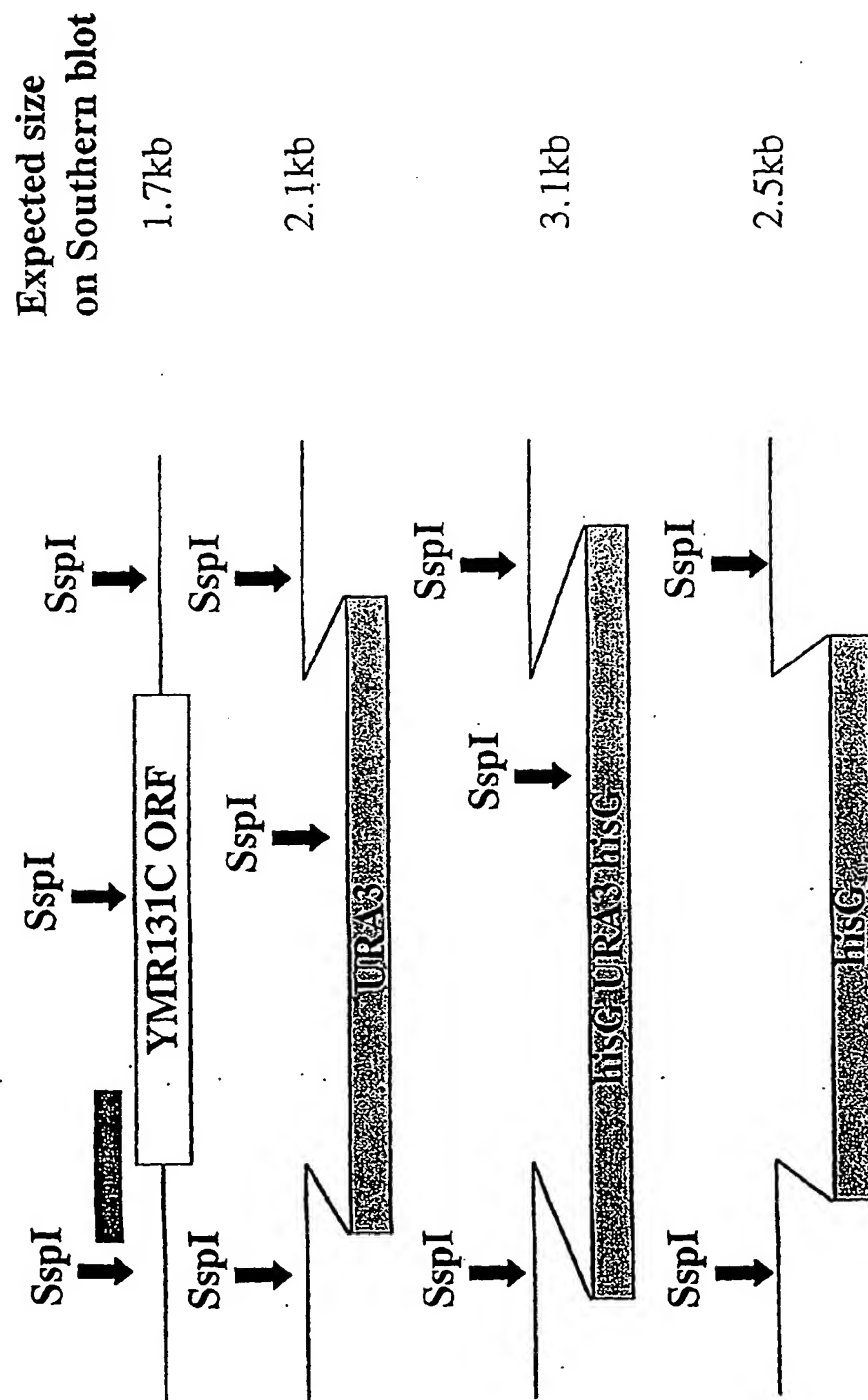
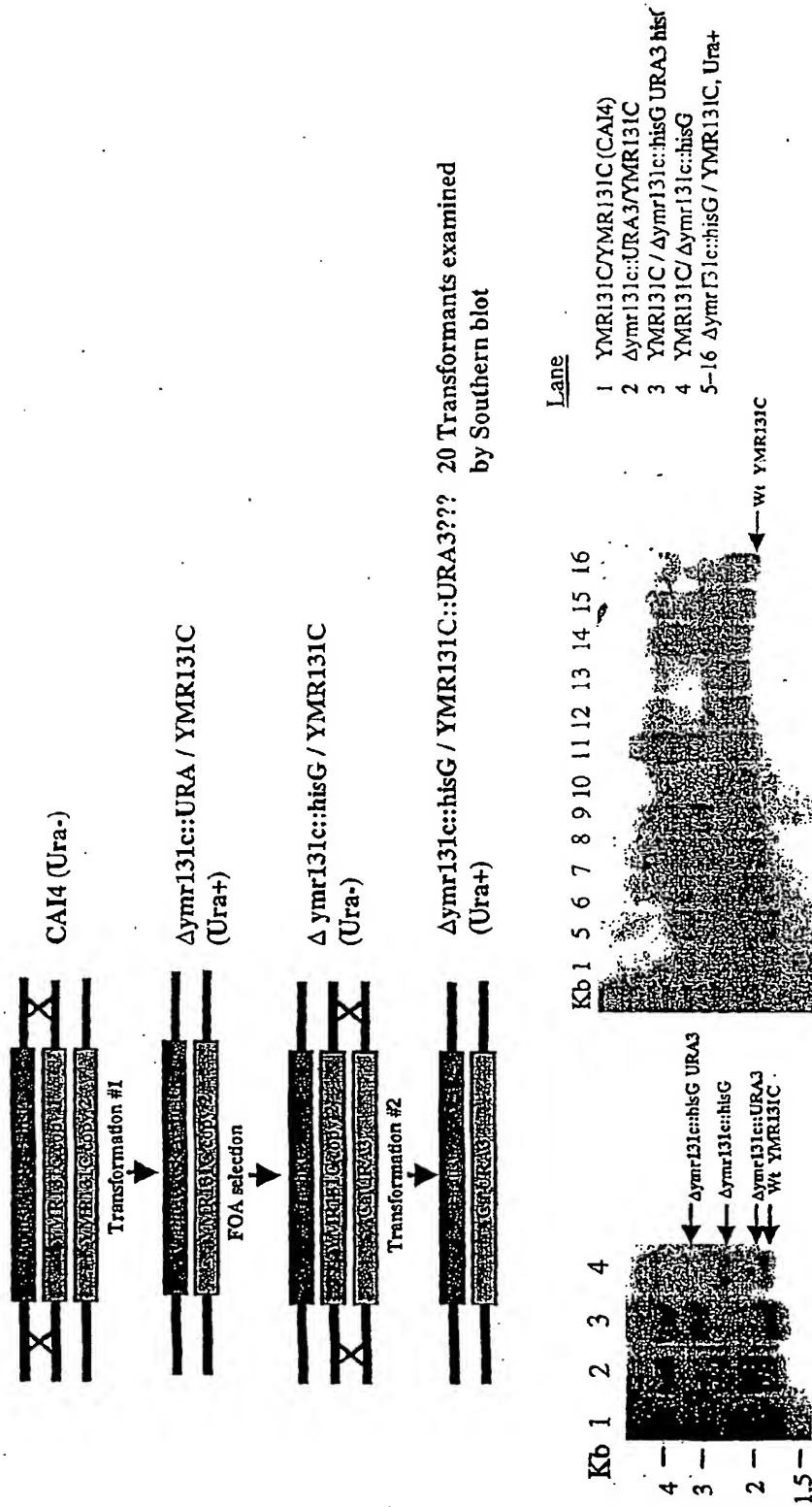


Figure 61A

C. albicans YMR131C deletion analysis



Unable to delete second copy of YMR131C

Figure 61B

C. albicans SQT1 deletion analysis

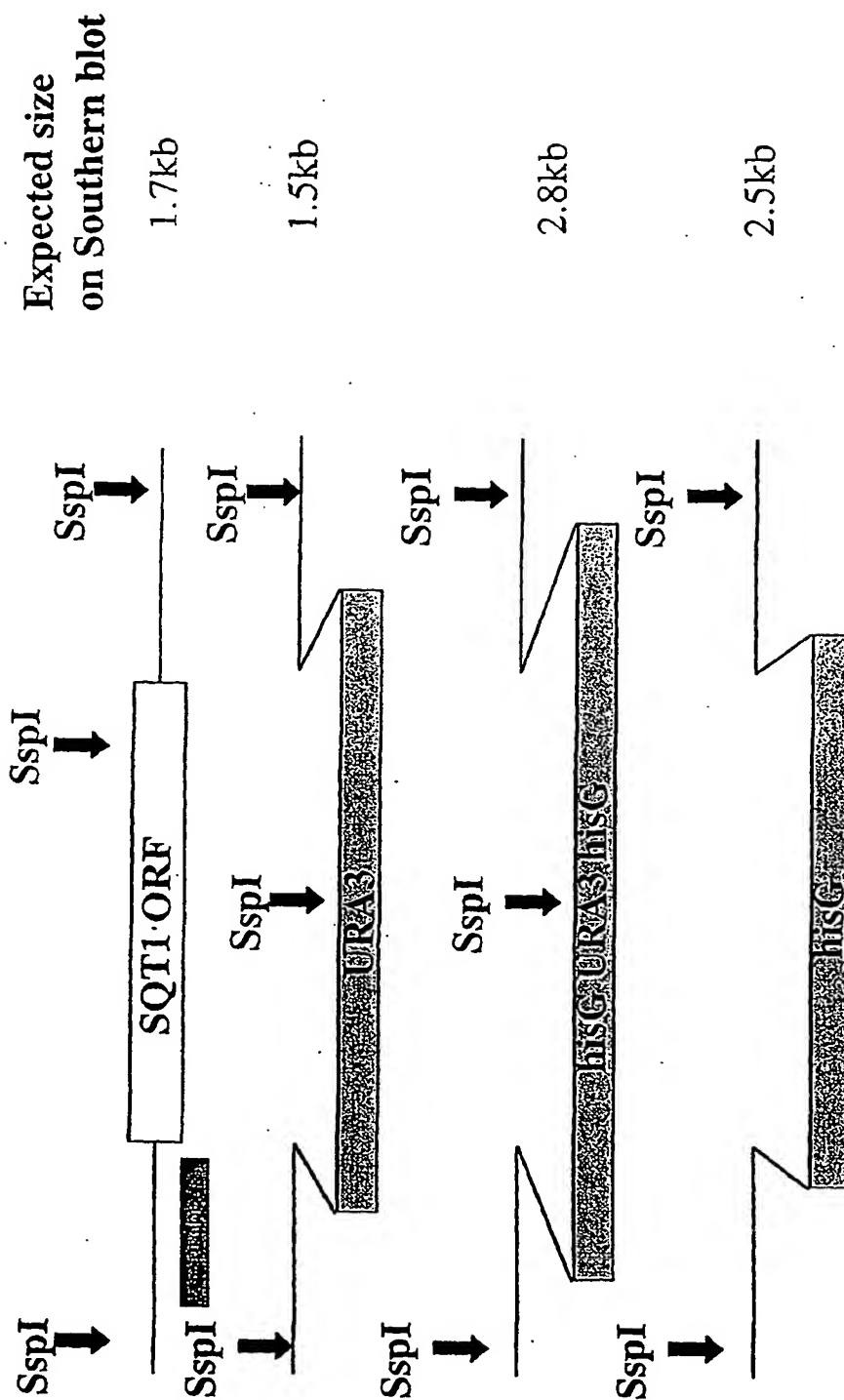


Figure 62A

C. albicans SQT1 deletion analysis



Unable to delete second copy of SQT1 in 20/20 transformants

Figure 62B

C. albicans MTW1 deletion analysis

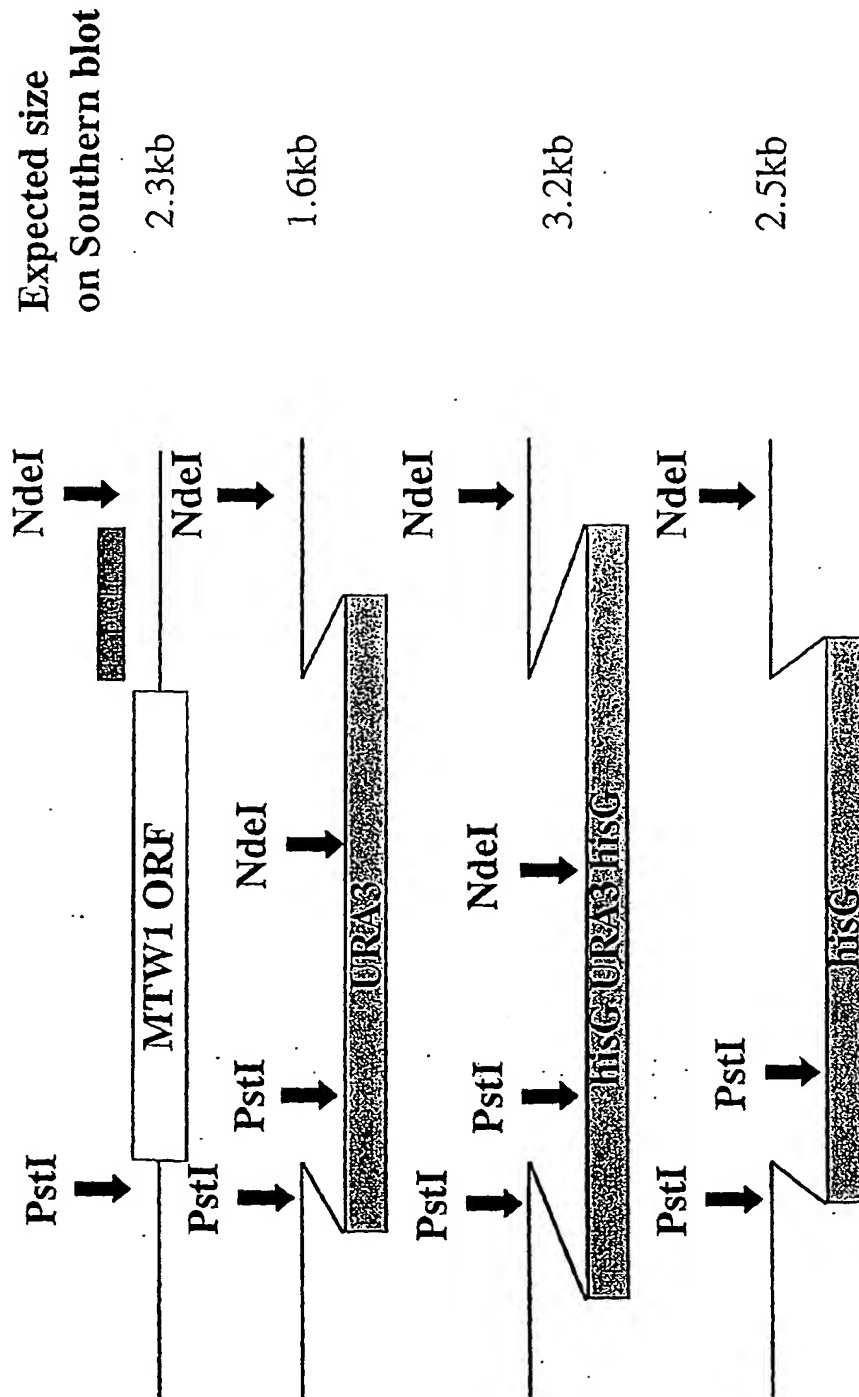
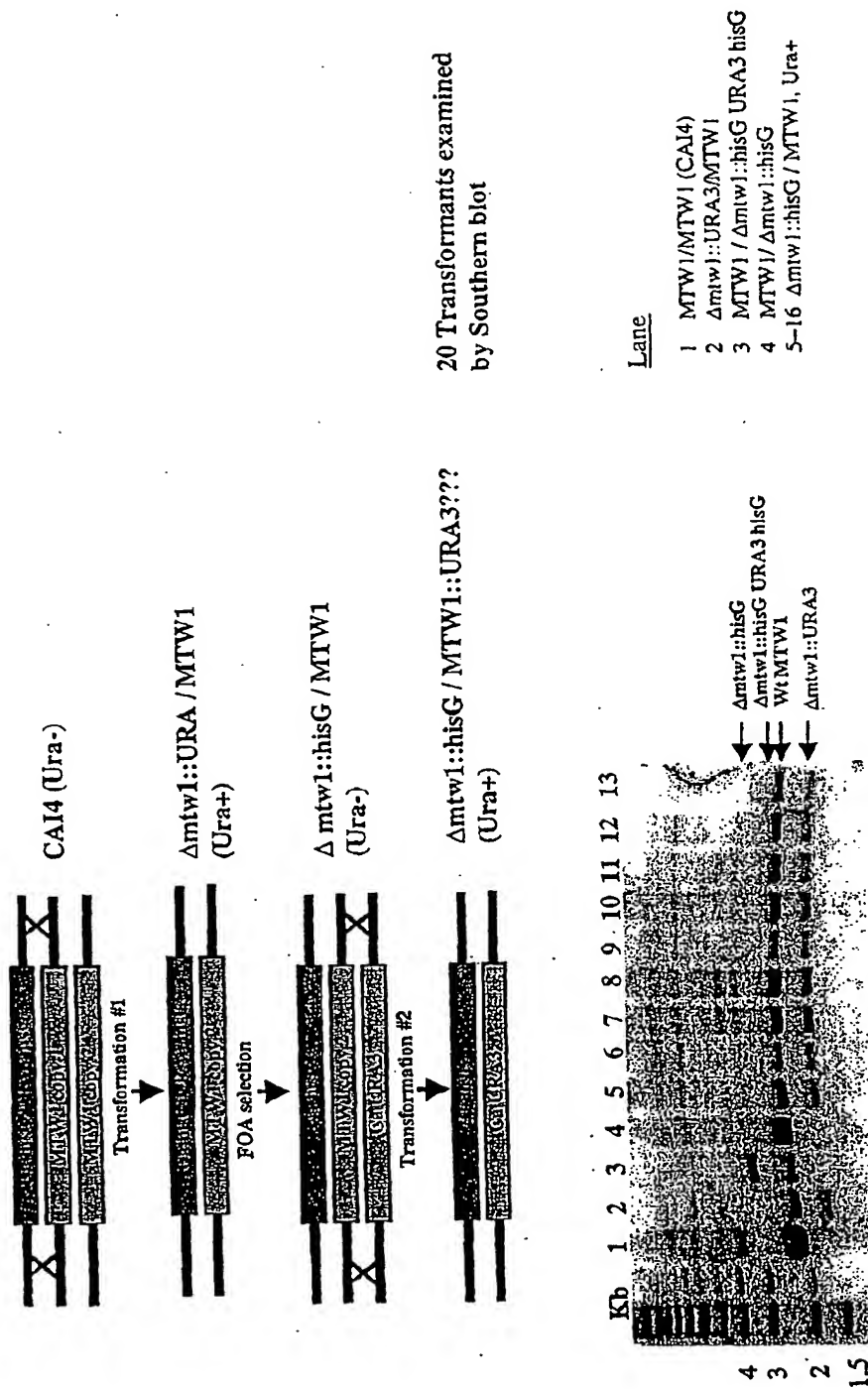


Figure 63A

C. albicans MTW1 deletion analysis



Unable to delete second copy of *MTW1*

Figure 63B

C. albicans TFB1 deletion analysis

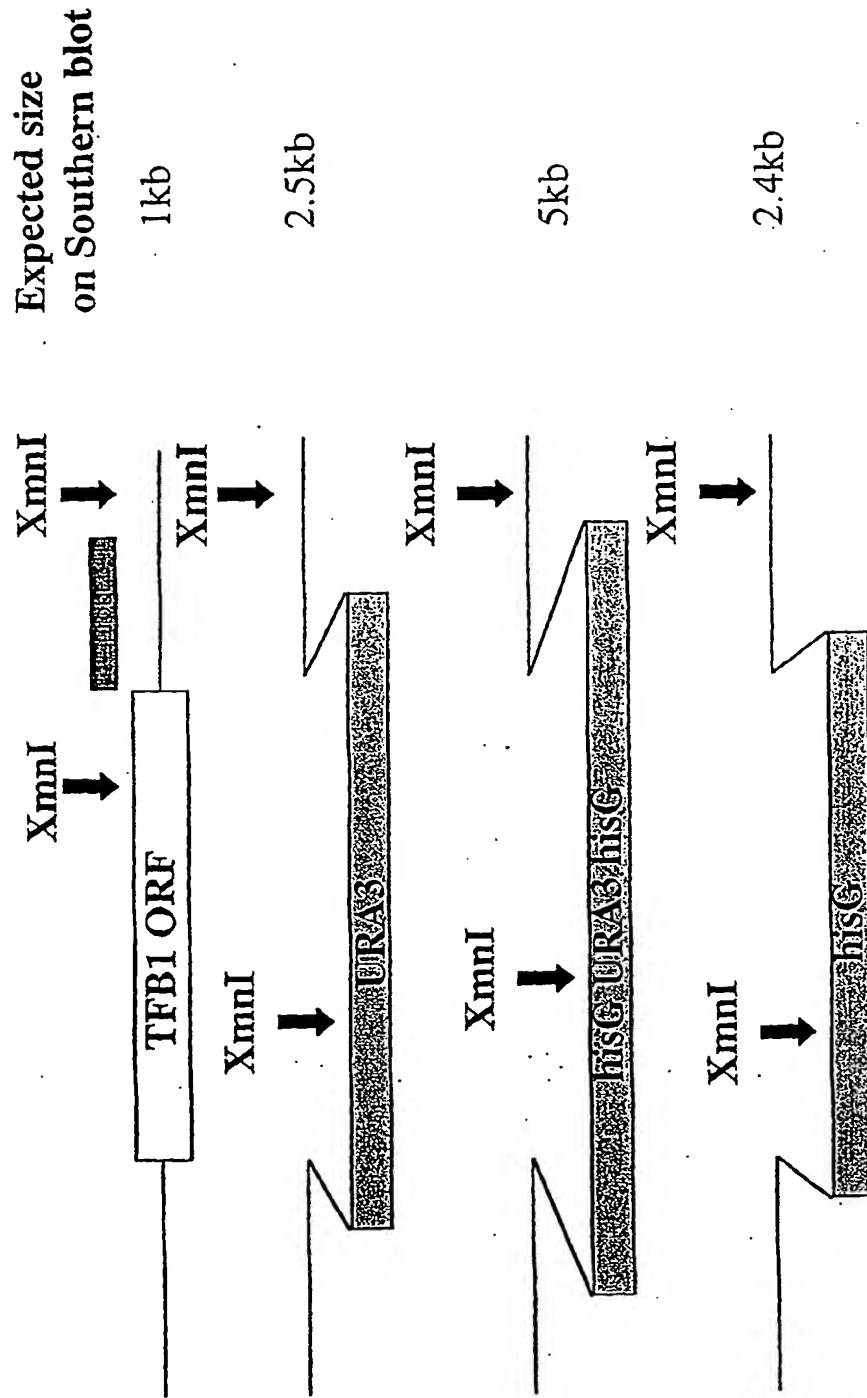
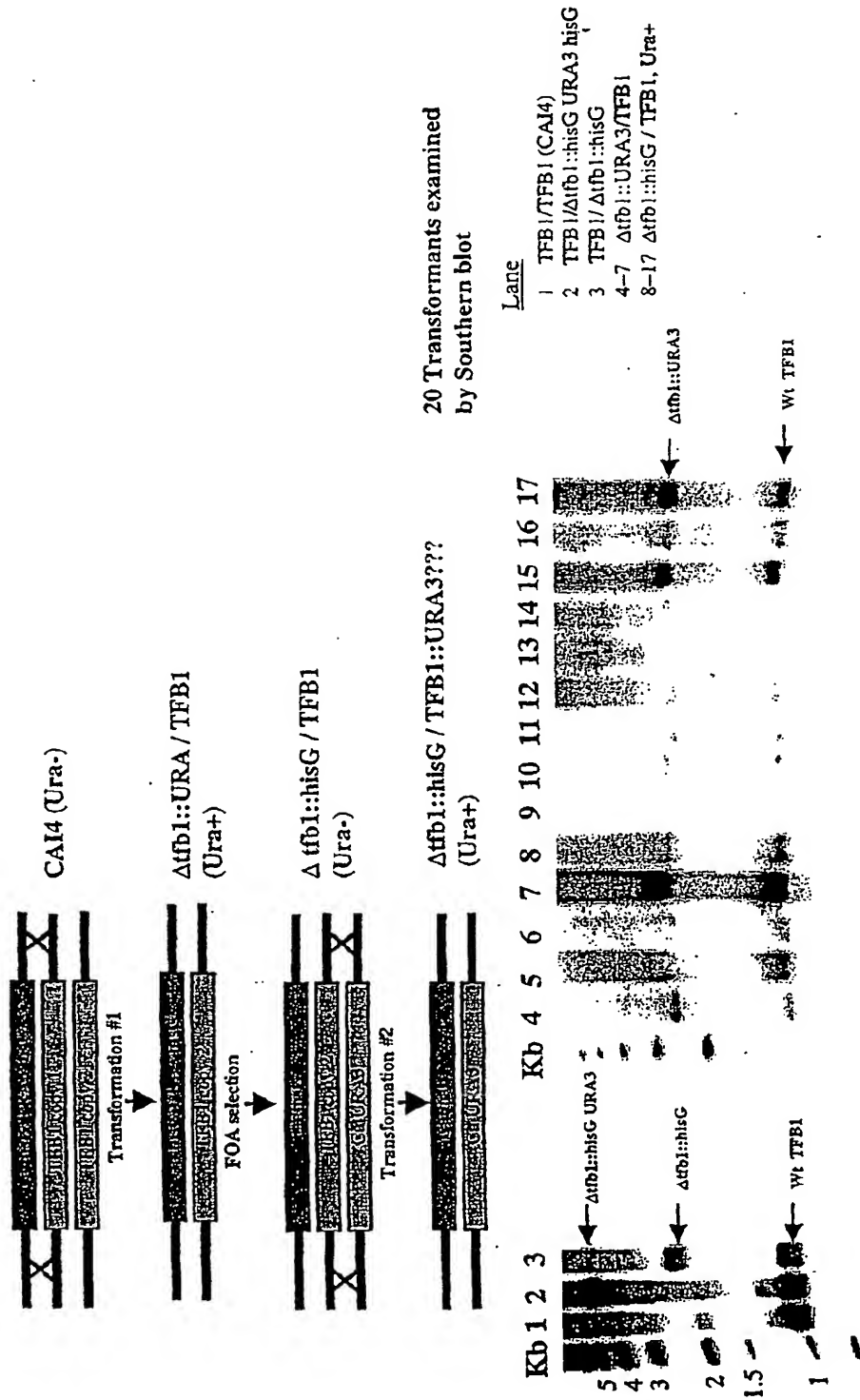


Figure 64A

C. albicans TFB1 deletion analysis



Unable to delete second copy of TFB1

Figure 64B

C. albicans SPC98 deletion analysis

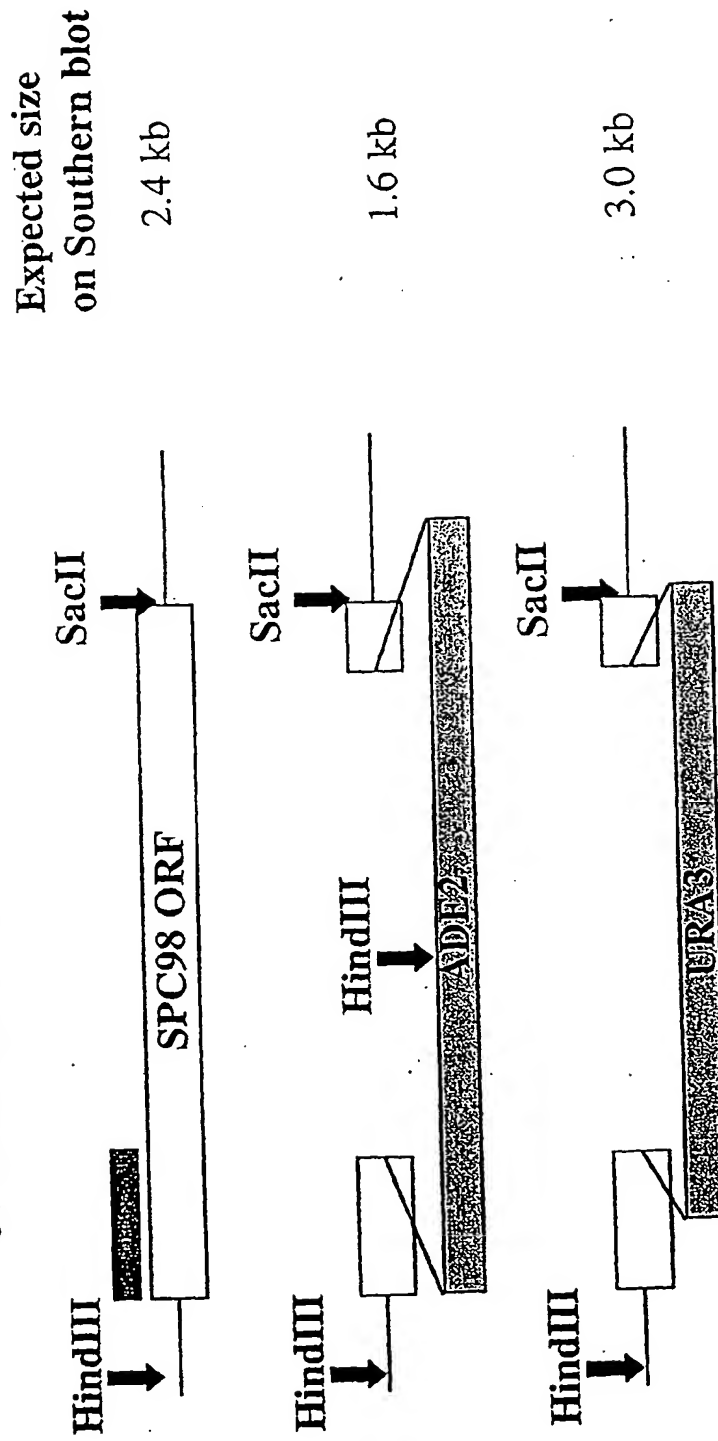


Figure 65A

**>20 Transformants examined
by Southern blot**

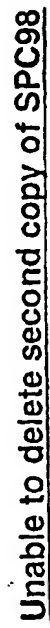


Figure 65B

C. albicans BFR2 deletion analysis

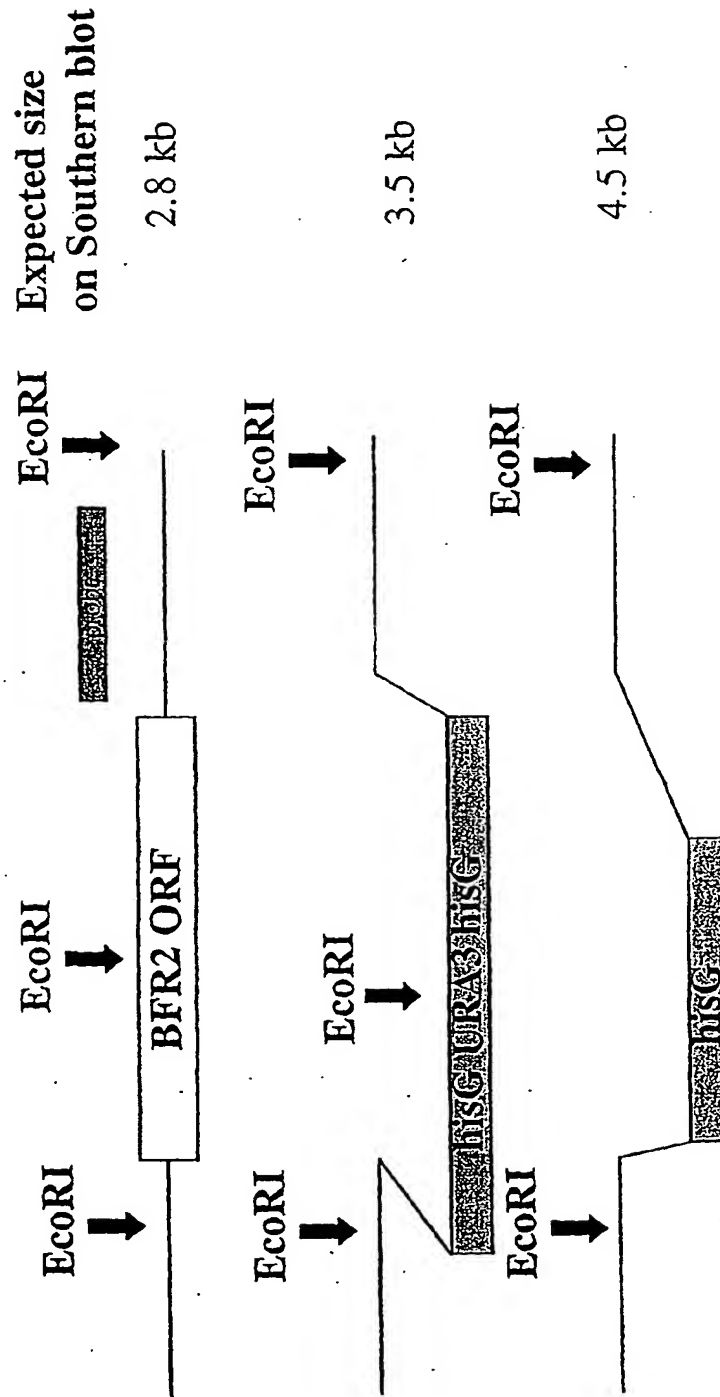
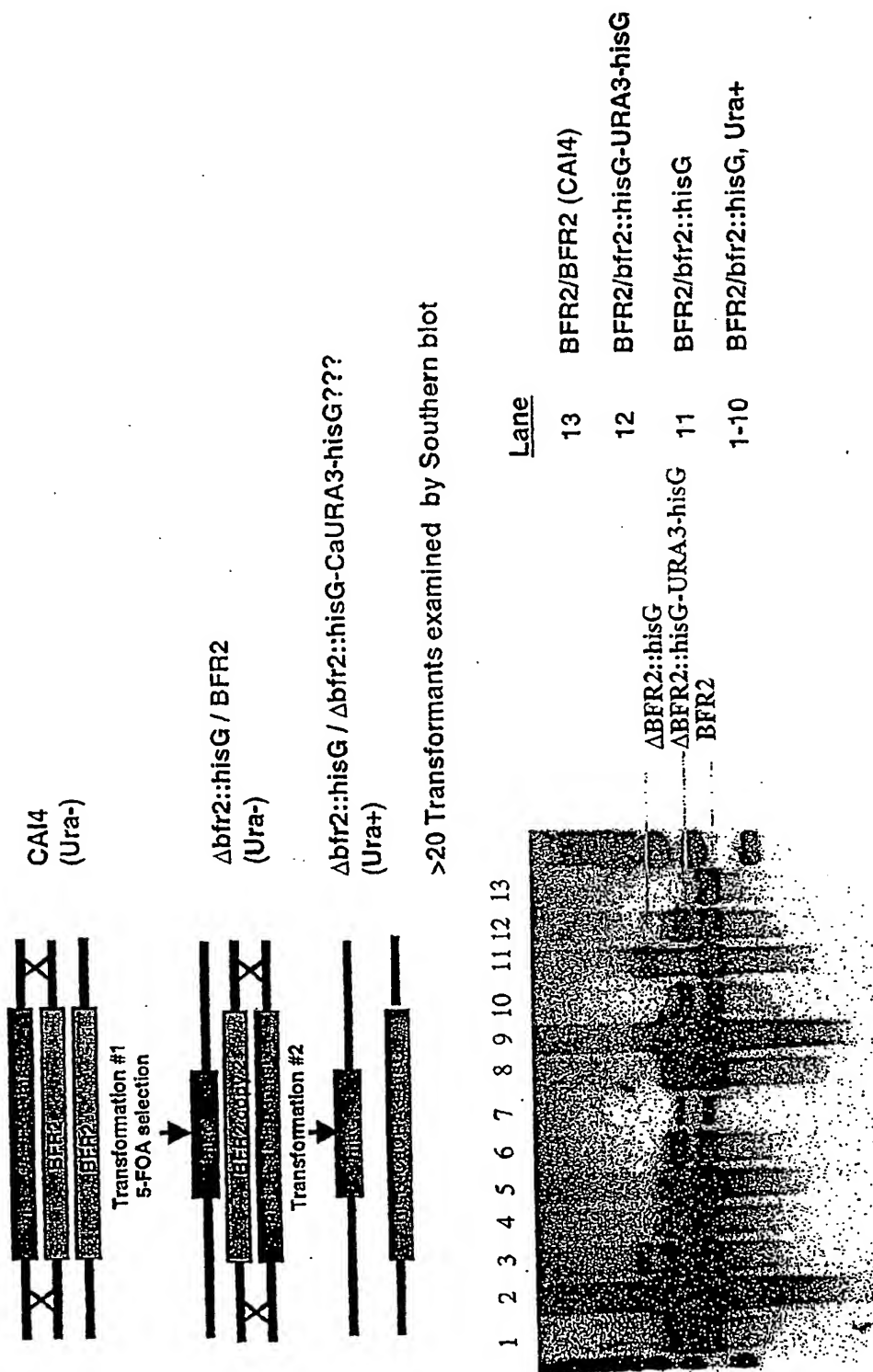


Figure 66A

C. albicans BFR2 deletion analysis



Unable to delete second copy of *CaBFR2*

Figure 66B

C. albicans RNA1 deletion analysis

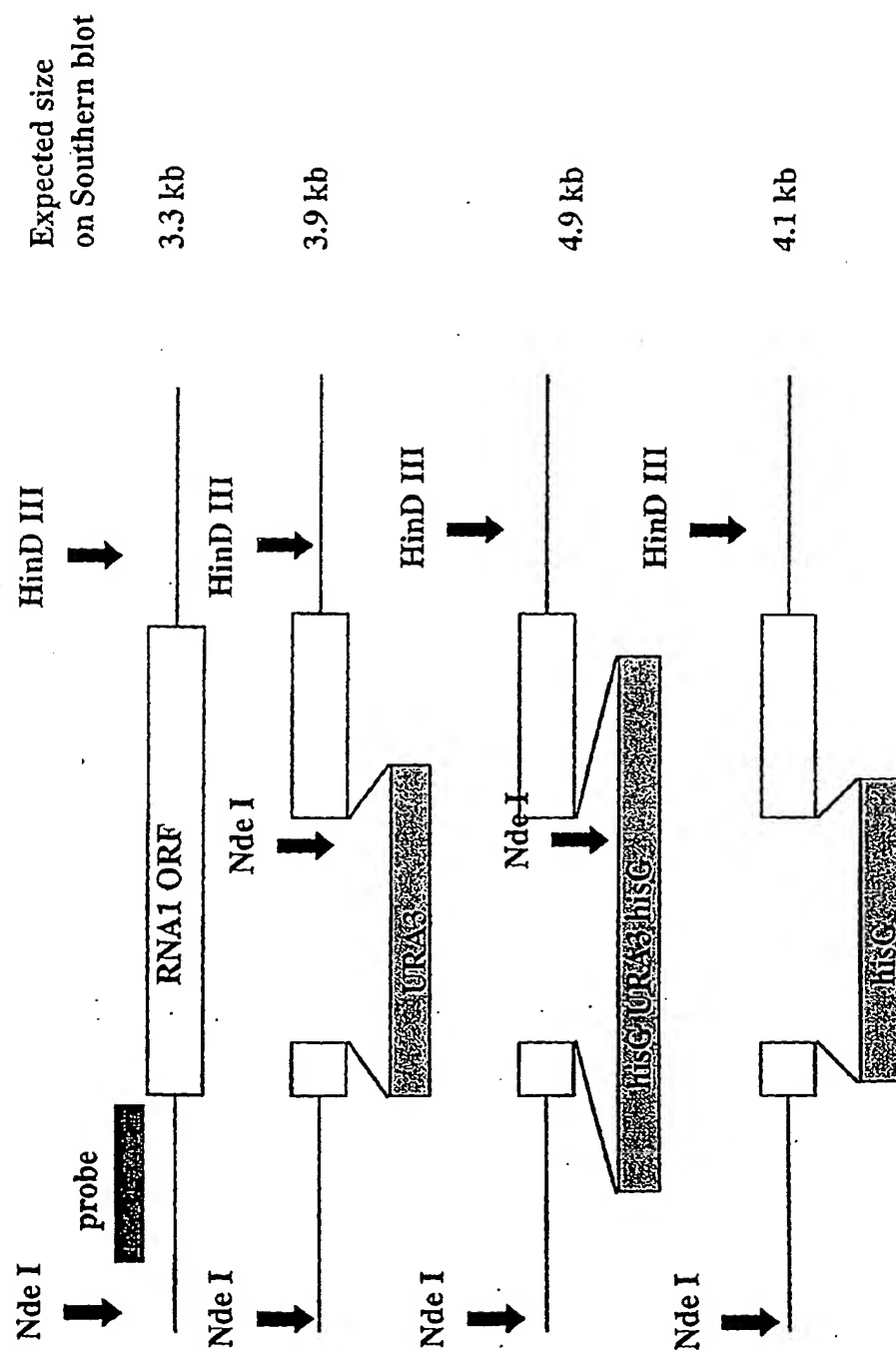
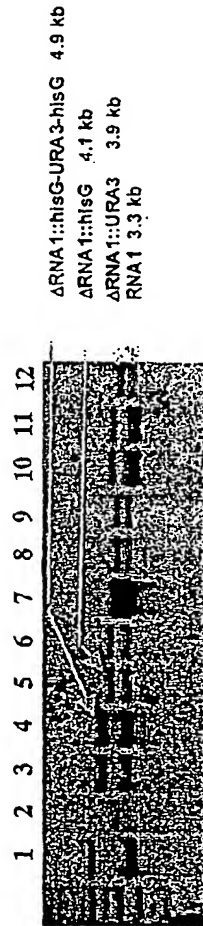
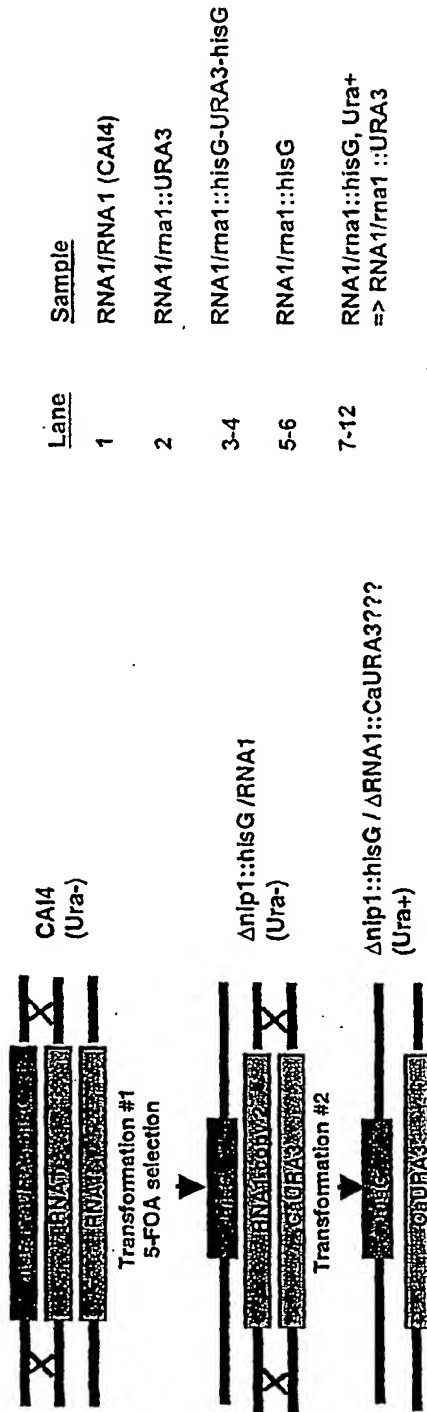


Figure 67A

C. albicans RNA1 deletion analysis



Unable to delete second copy of *CaRNA1*

Figure 67B

C. albicans GCD7 deletion analysis

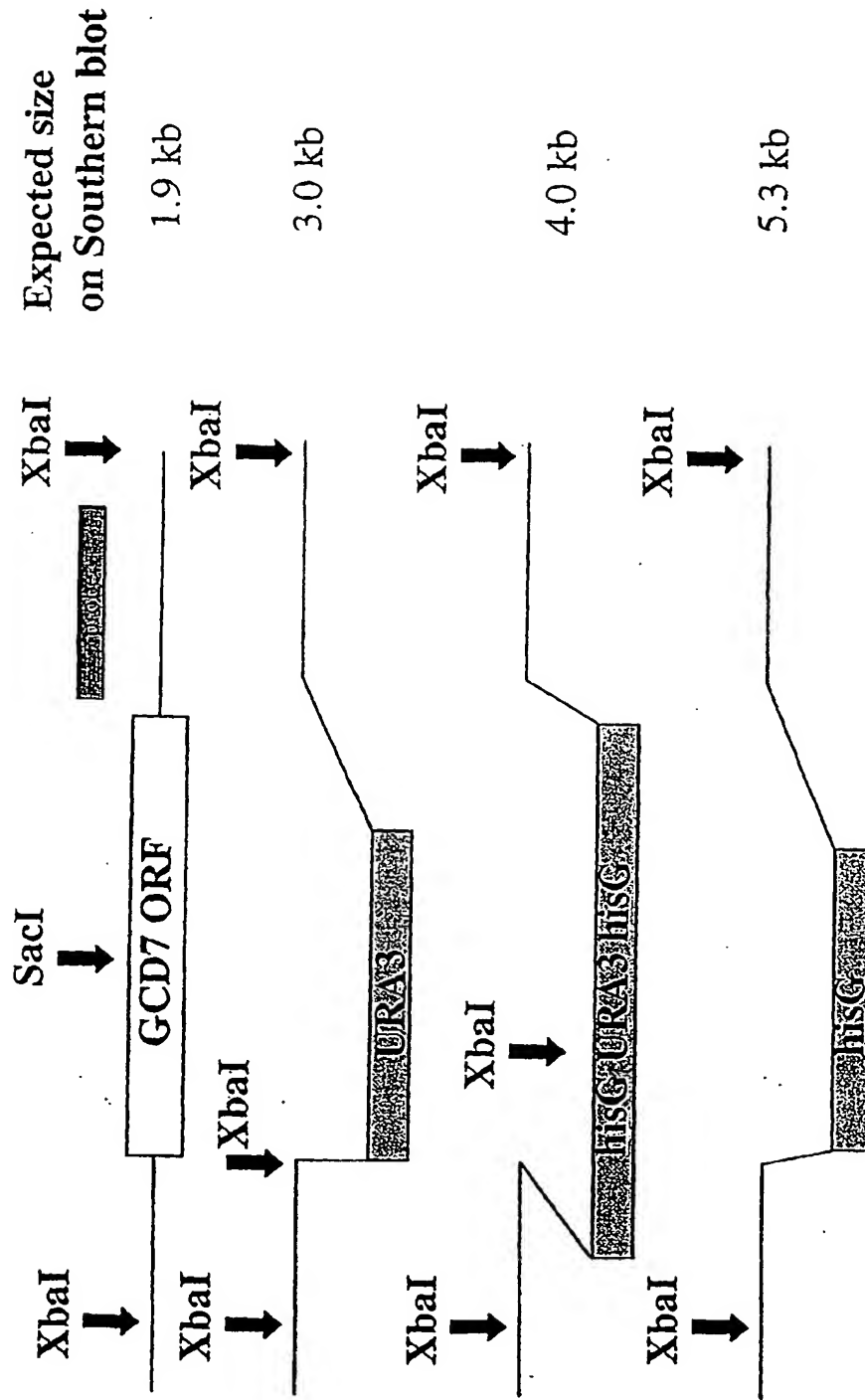


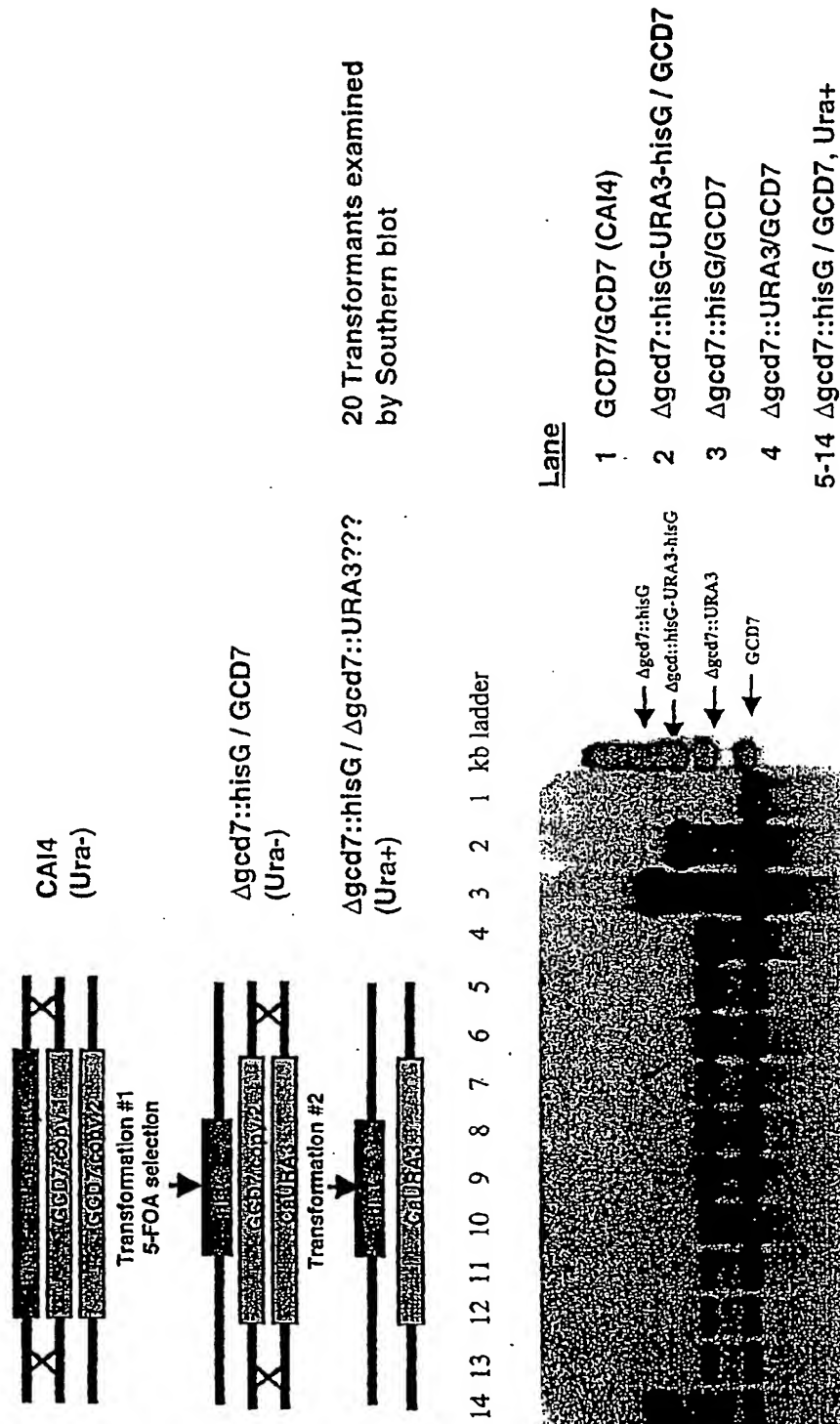
Figure 68A

C. albicans GCD7 deletion analysis

WO 02/02055

84/173

PCT/US01/20592



Unable to delete second copy of GCD7

Figure 68B

C. albicans SKI6 deletion analysis

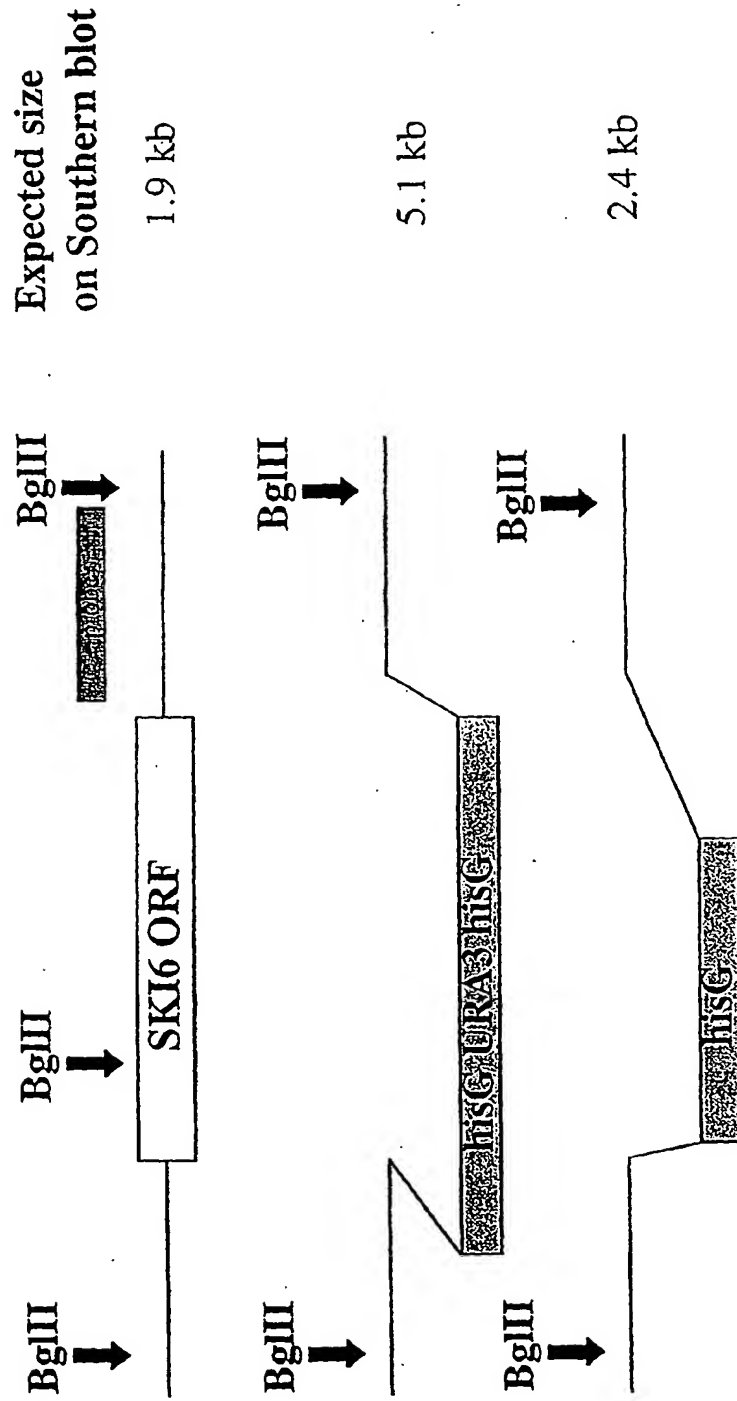
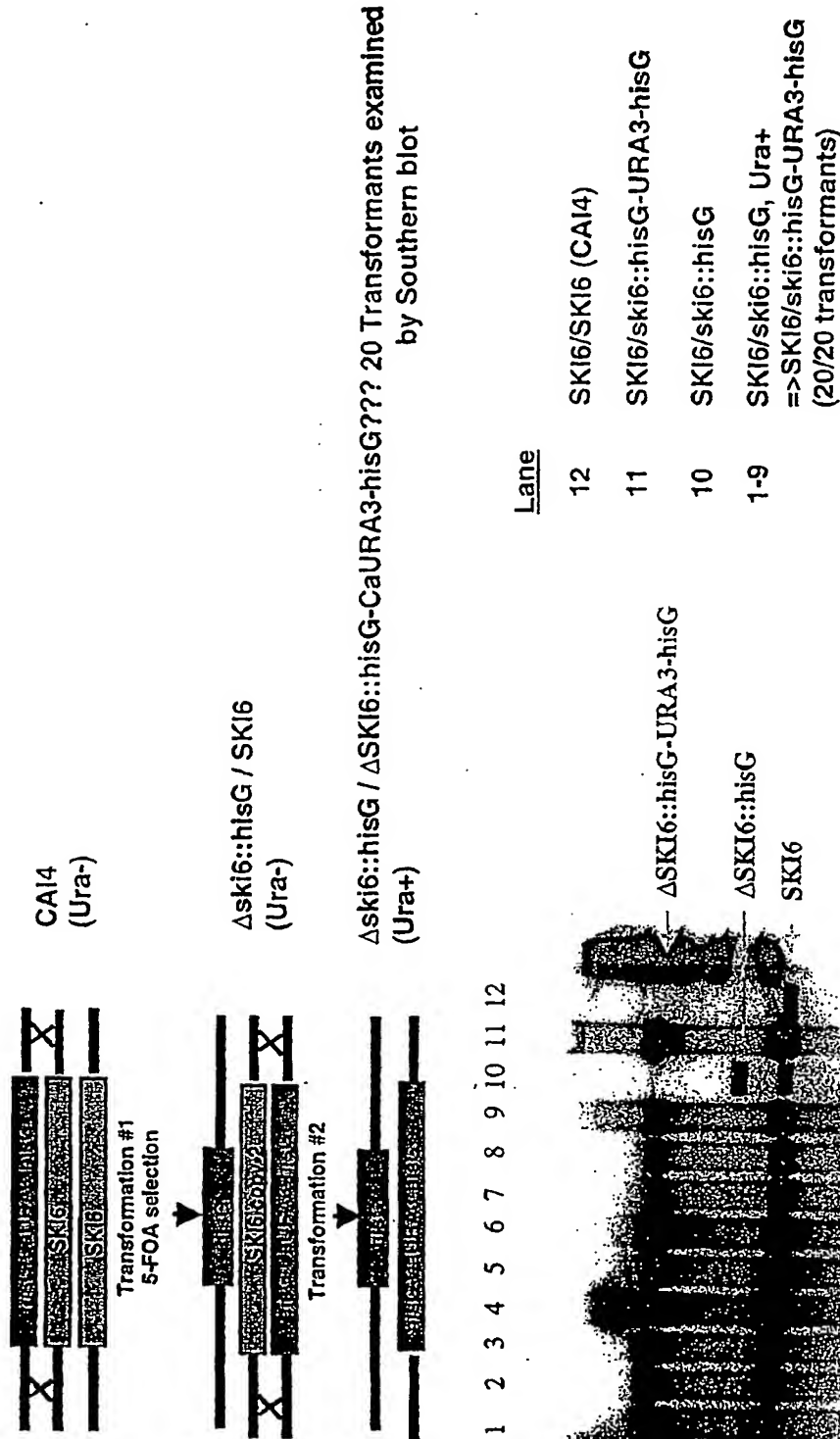


Figure 69A

C. albicans SKI6 deletion analysis



Unable to delete second copy of *CaSKI6*

Figure 69B

C. albicans NIP1 deletion analysis

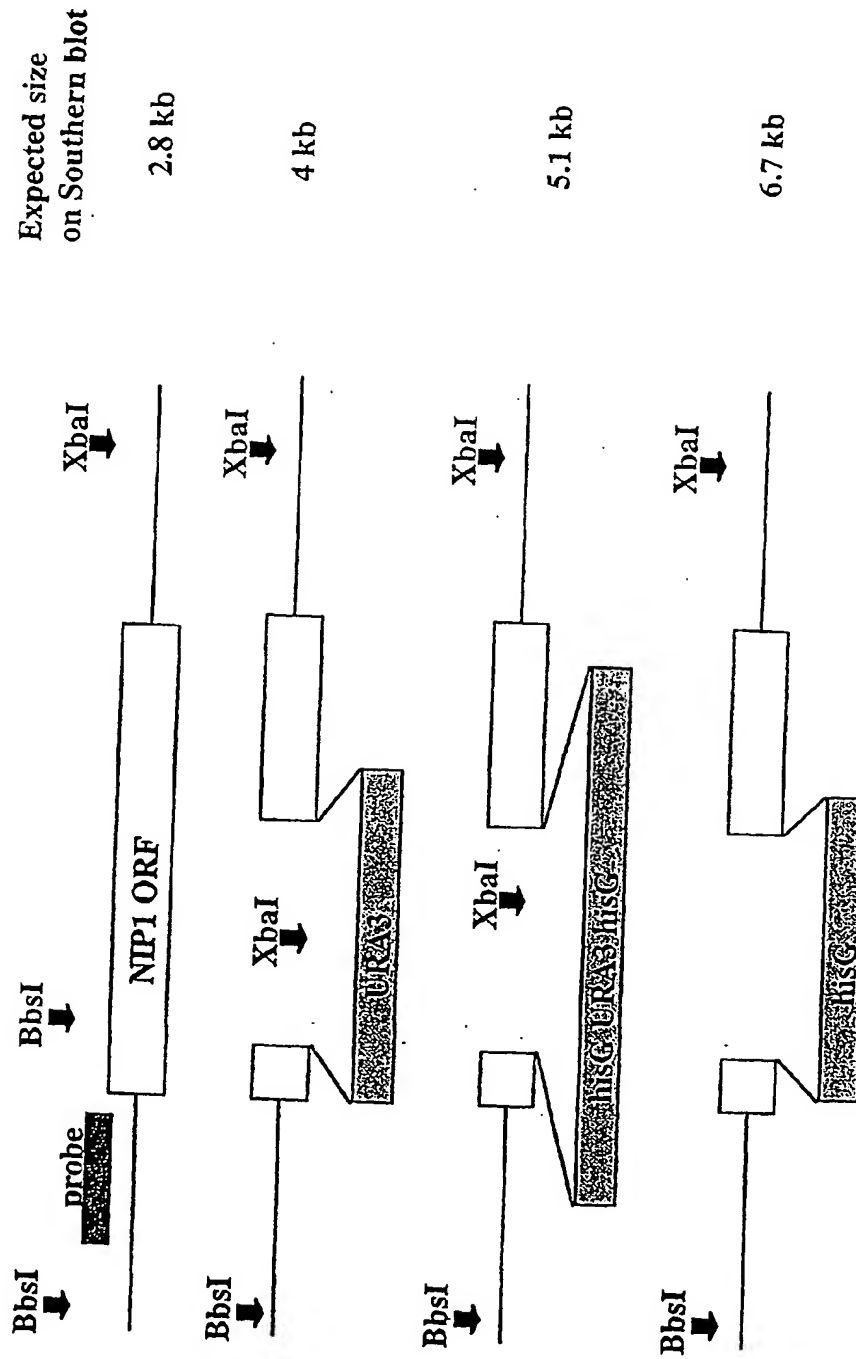
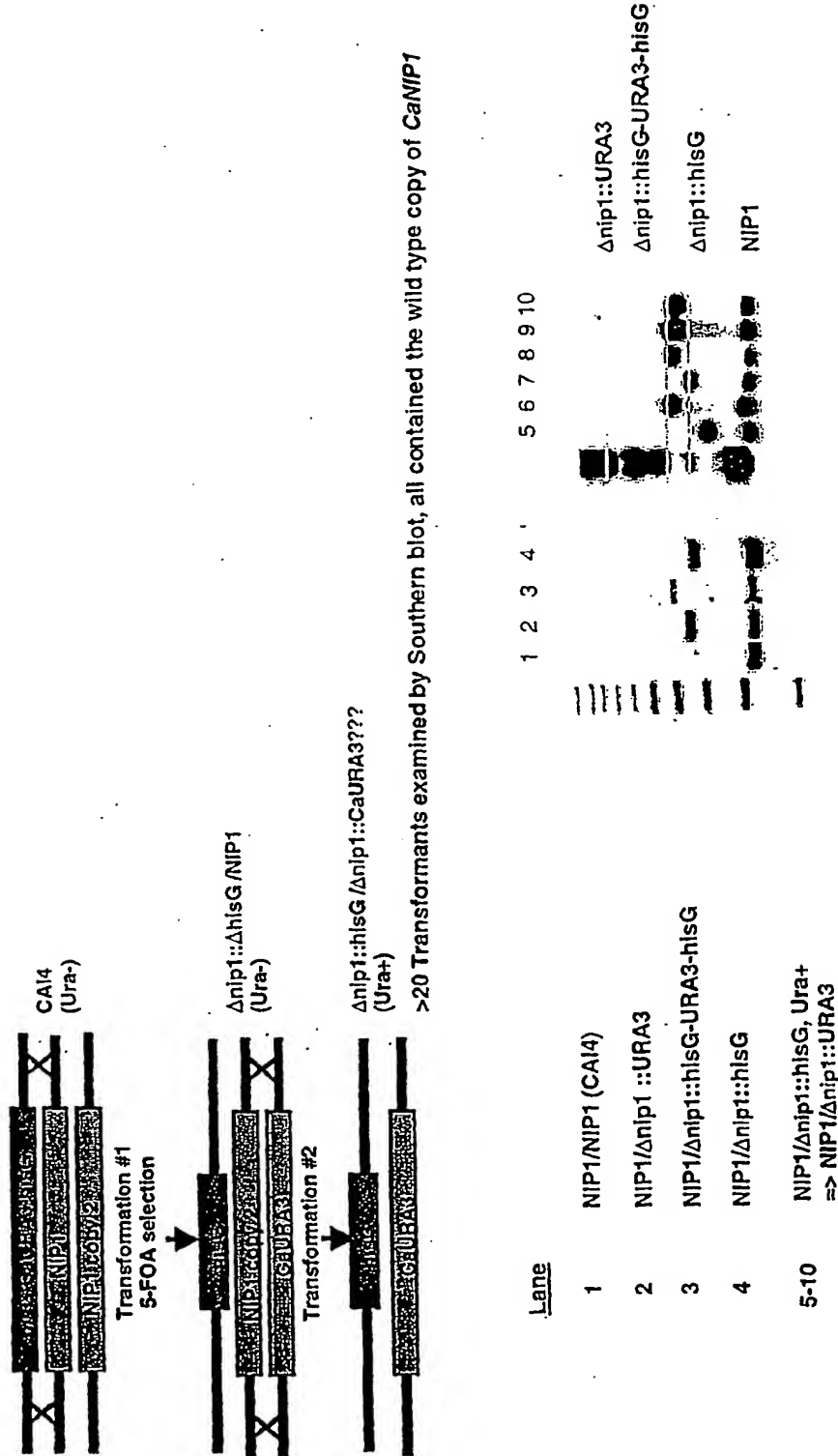


Figure 70A

C. albicans NIP1 deletion analysis



Unable to delete second copy of *CaNIP1*

Figure 70B

C. albicans LCP5 deletion analysis

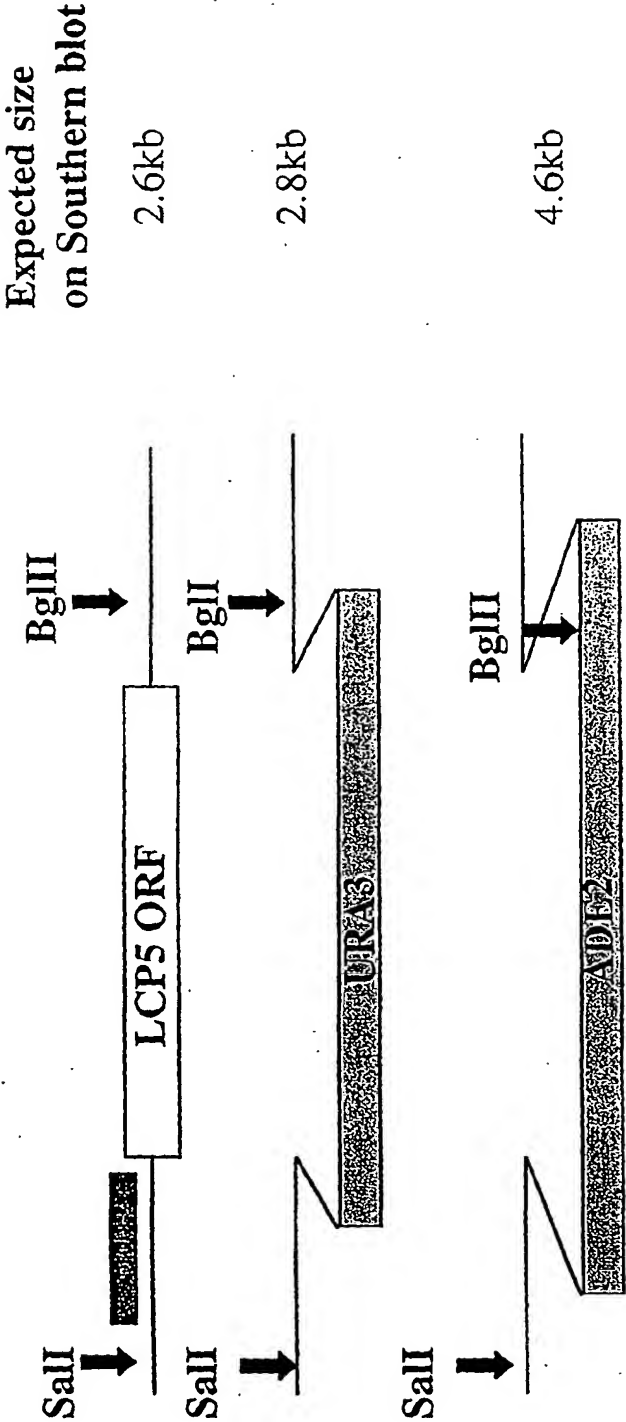
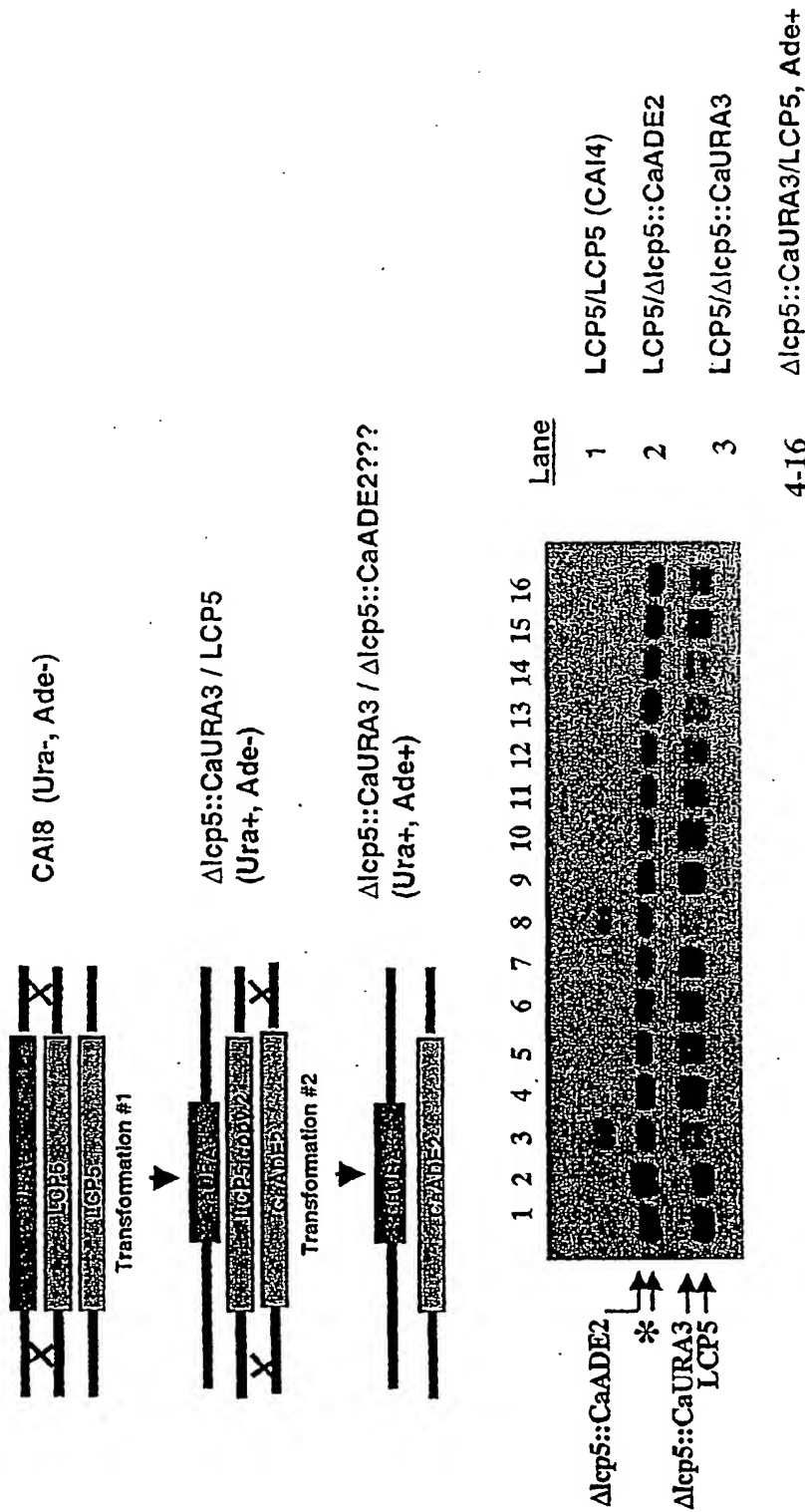


Figure 71A

C. albicans LCP5 deletion analysis



* Region 5' of LCP5 was used as probe
Region is repeated in genome (YER126)

Unable to delete second copy of CaLCP5

Figure 71B

C. albicans NCE103 deletion analysis

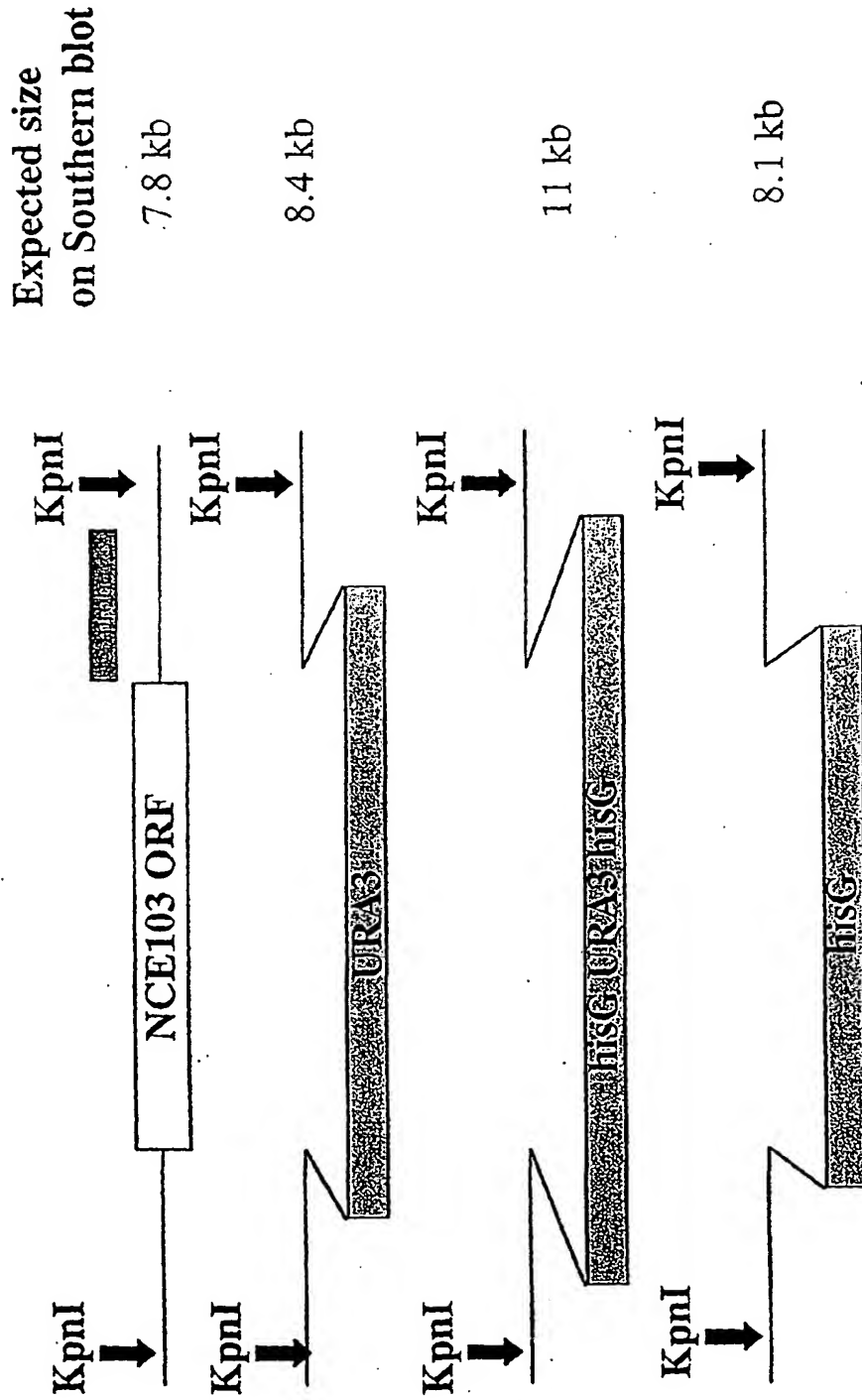
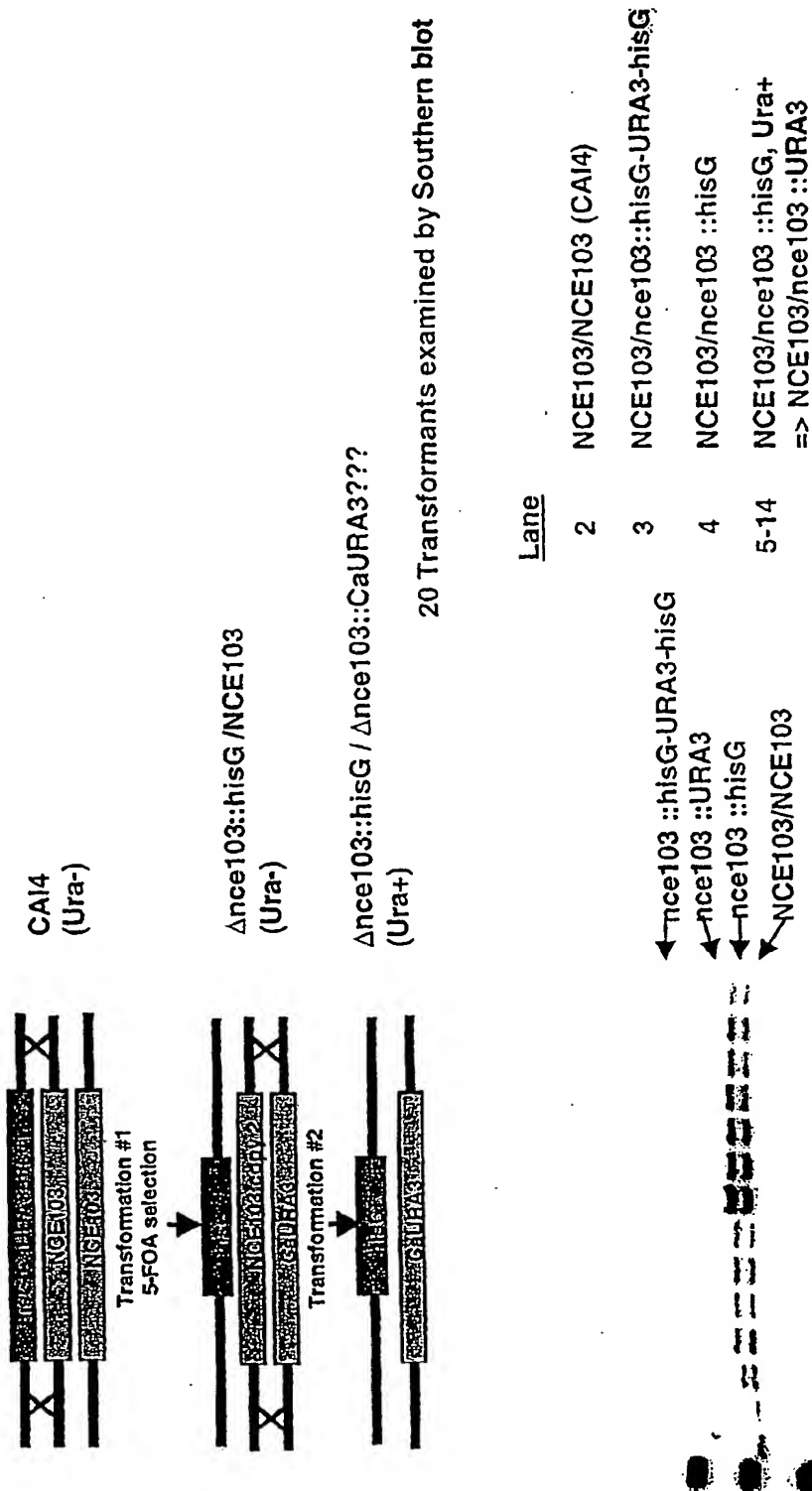


Figure 72A

C. albicans NCE103 deletion analysis



Unable to delete second copy of *CaNCE103*

Figure 72B

C. albicans ECO1 deletion analysis

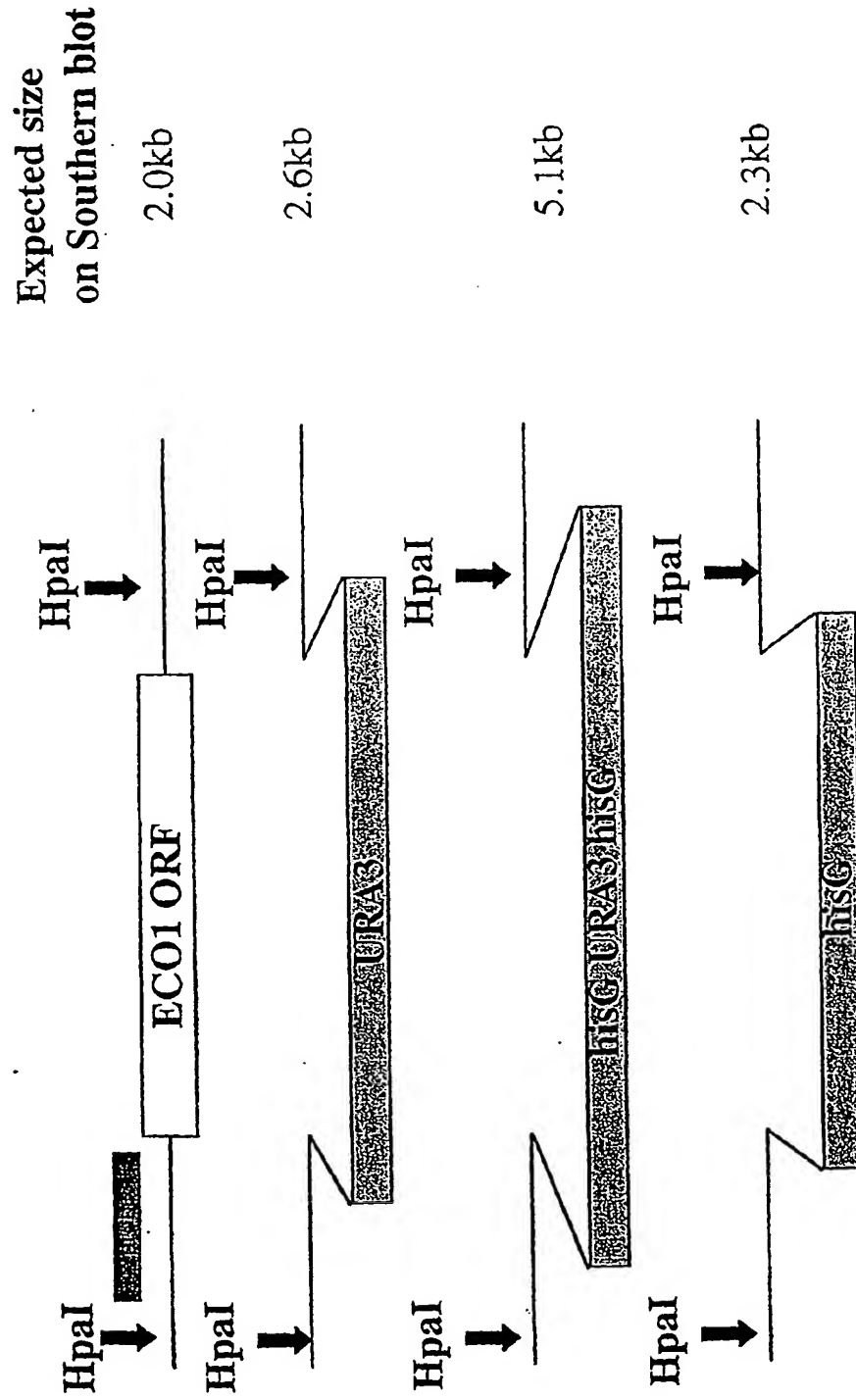
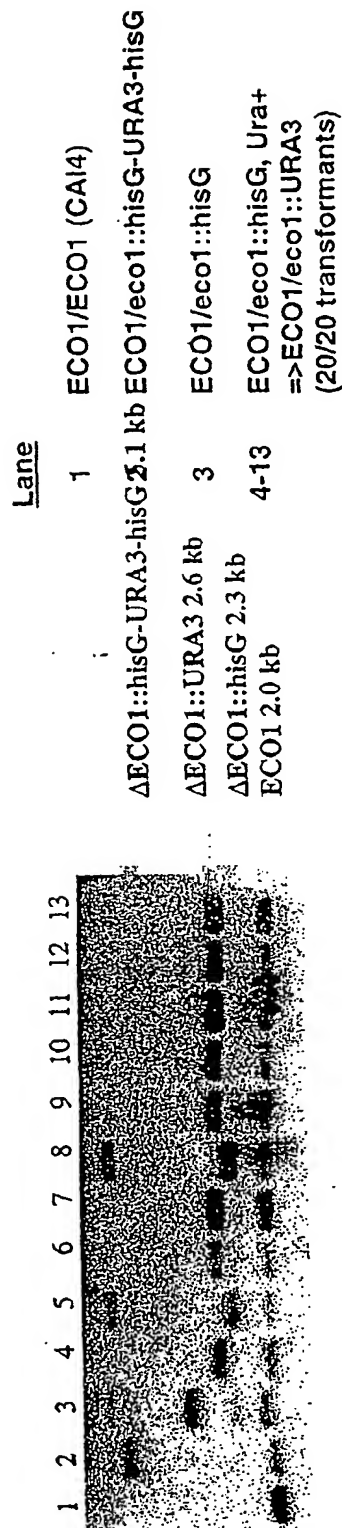
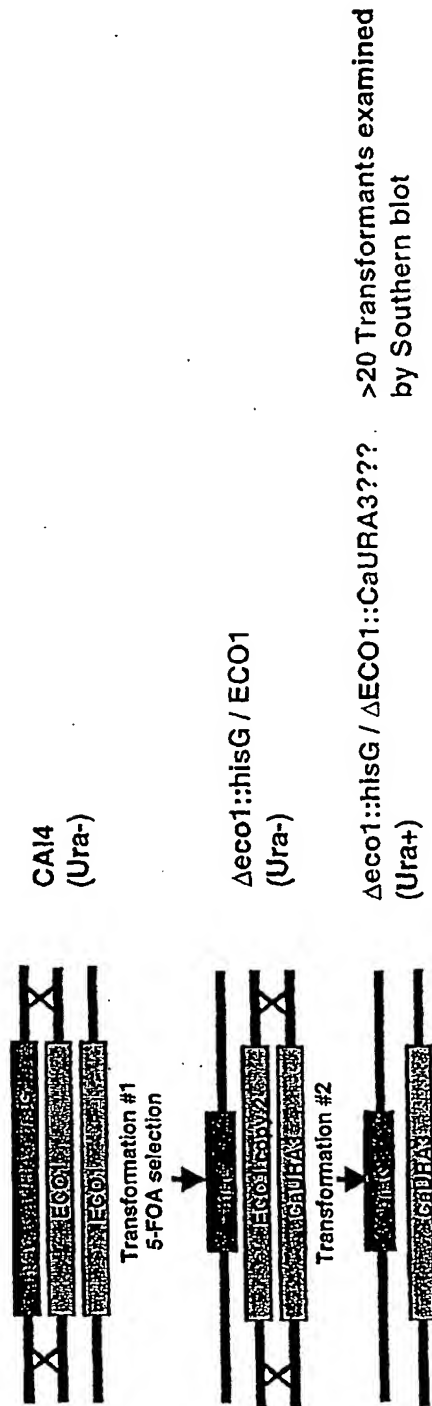


Figure 73A

C. albicans ECO1 deletion analysis



Unable to delete second copy of *CaECO1*

Figure 73B

C. albicans ORC2 deletion analysis

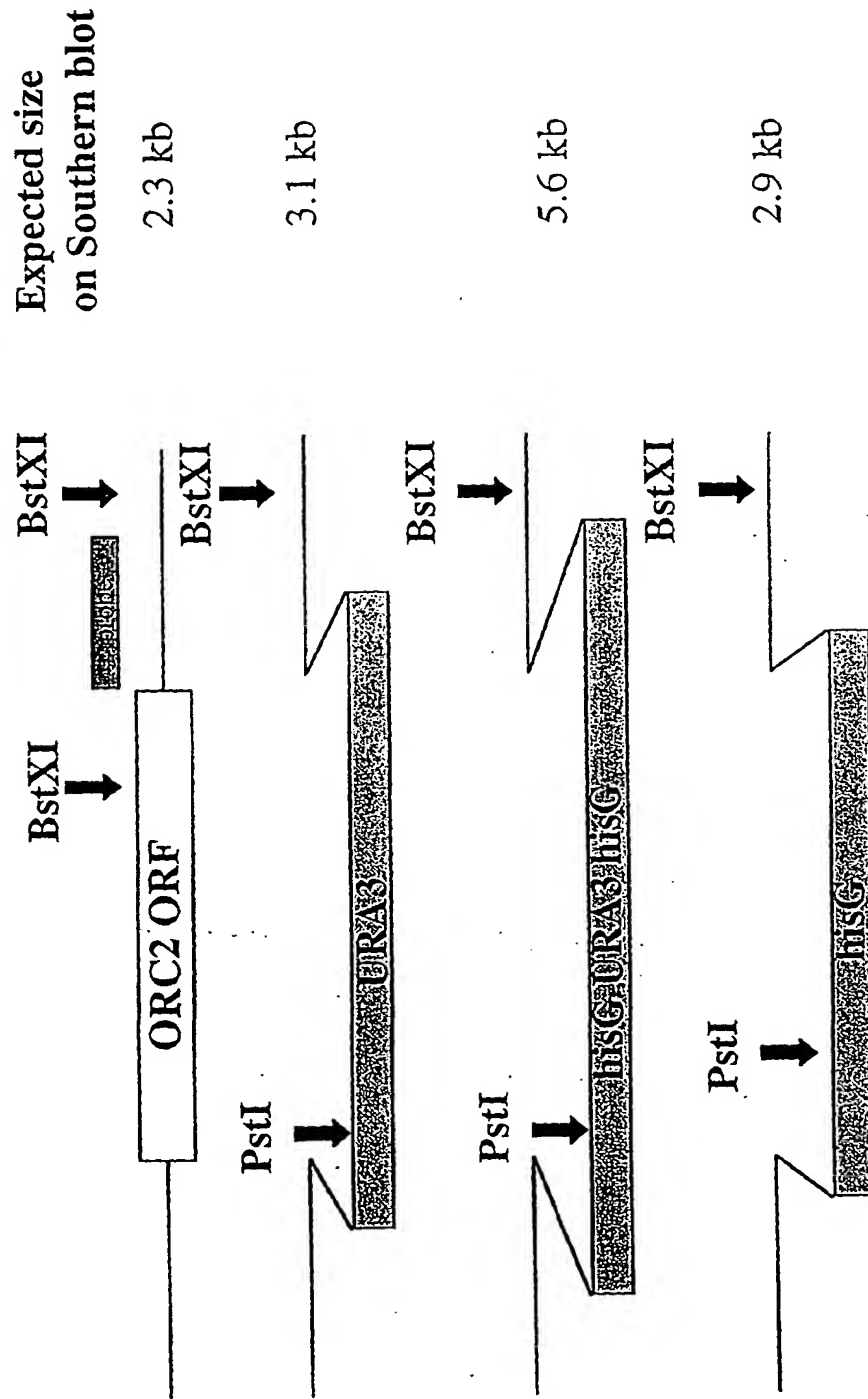
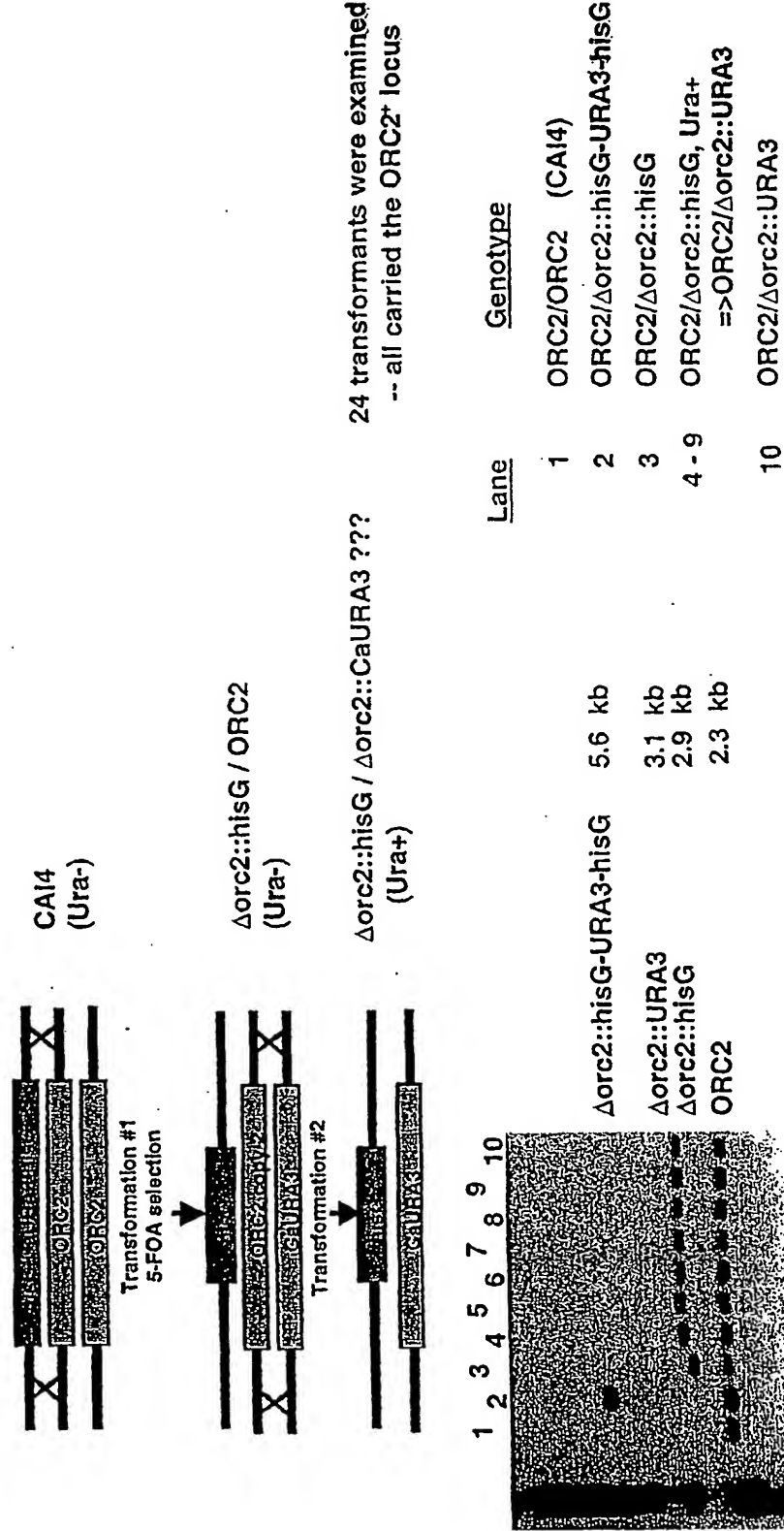


Figure 74A

C. albicans ORC2 deletion analysis



Unable to delete both copies of *CaORC2*

Figure 74B

C. albicans CNS1 deletion analysis

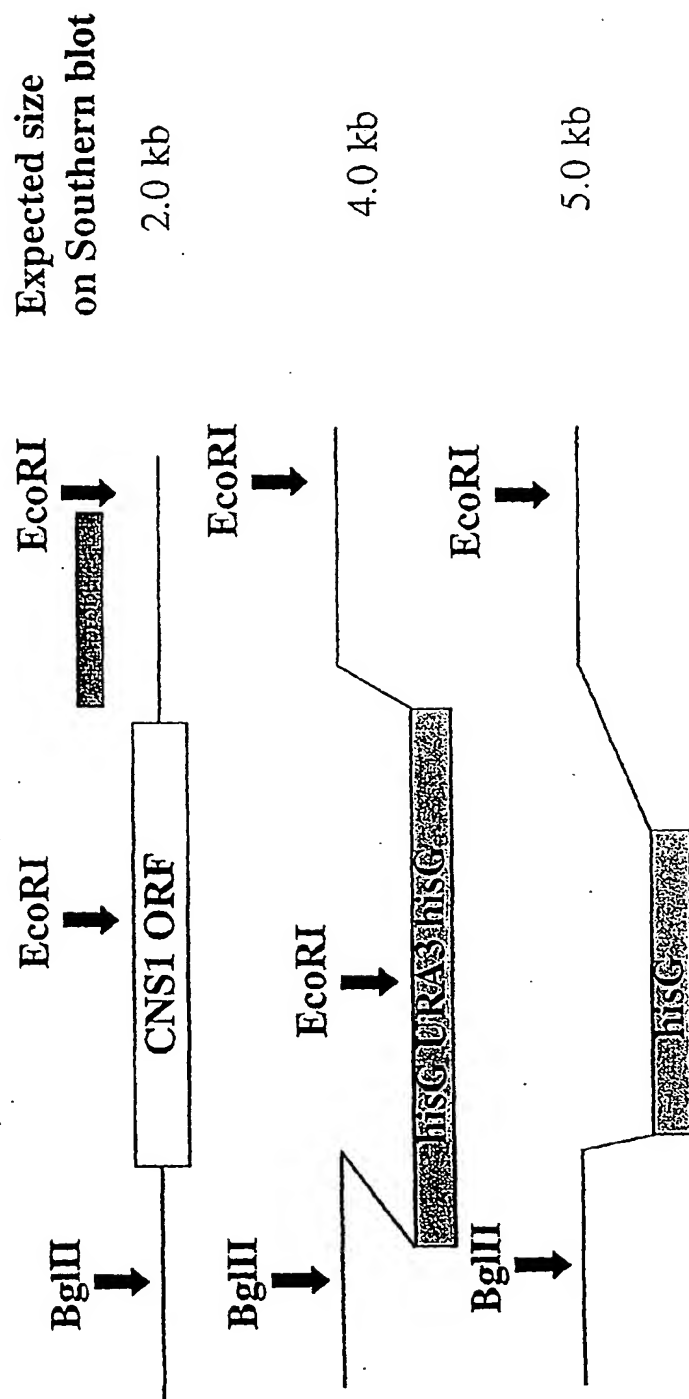
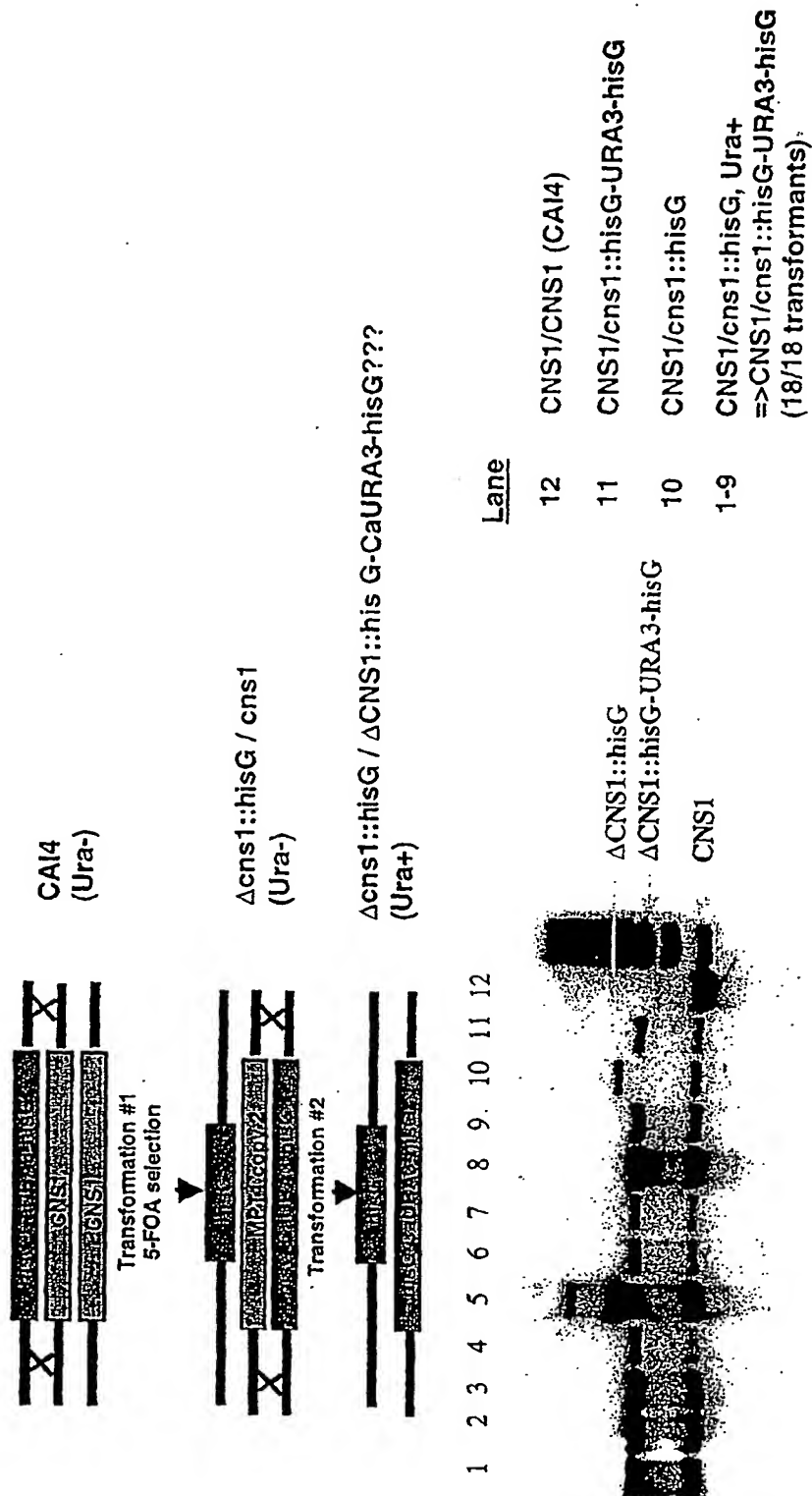


Figure 75A

C. albicans CNS1 deletion analysis



Unable to delete second copy of *CaCNS1*

Figure 75B

C. albicans YPD1 deletion analysis

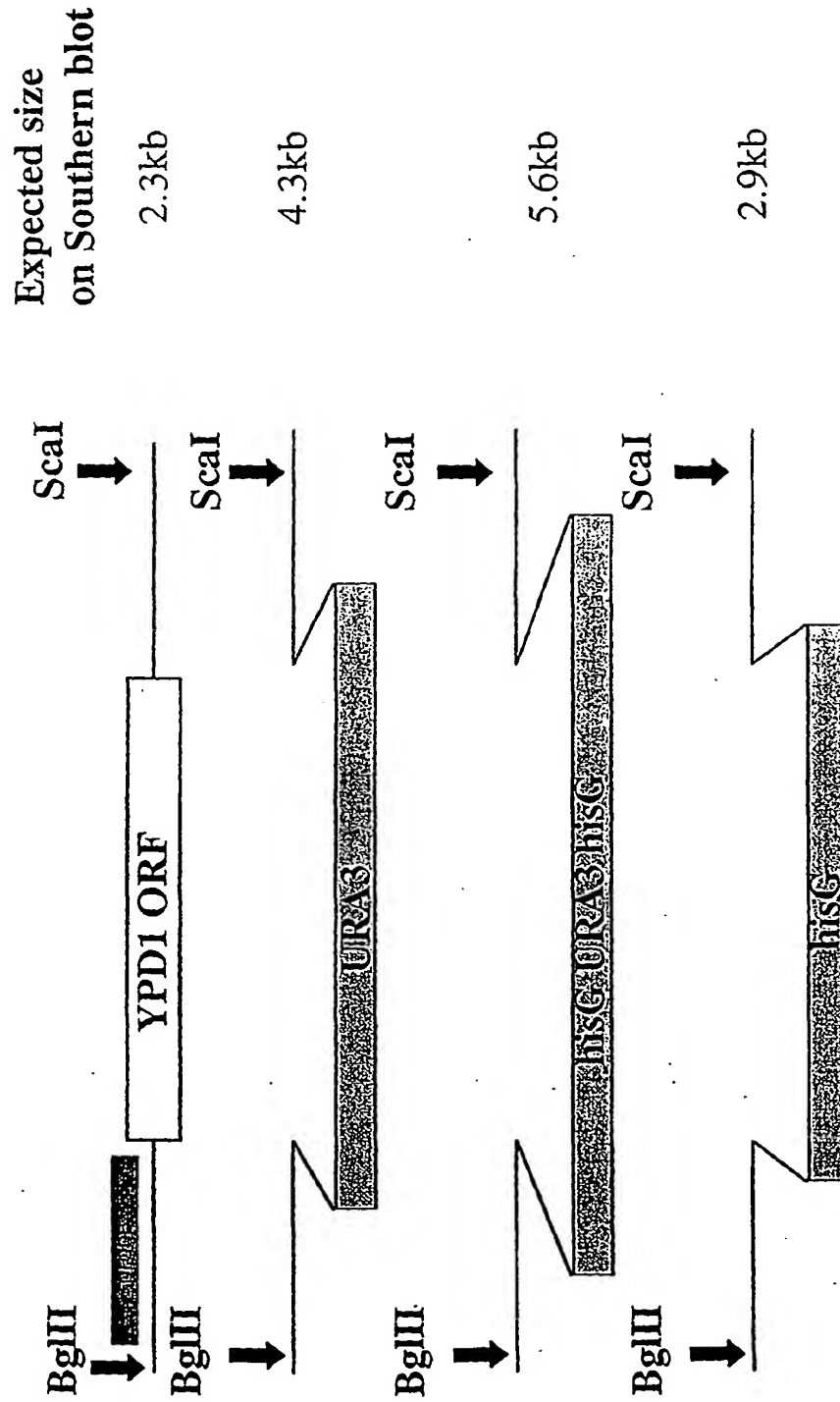


Figure 76A

C. albicans YPD1 deletion analysis

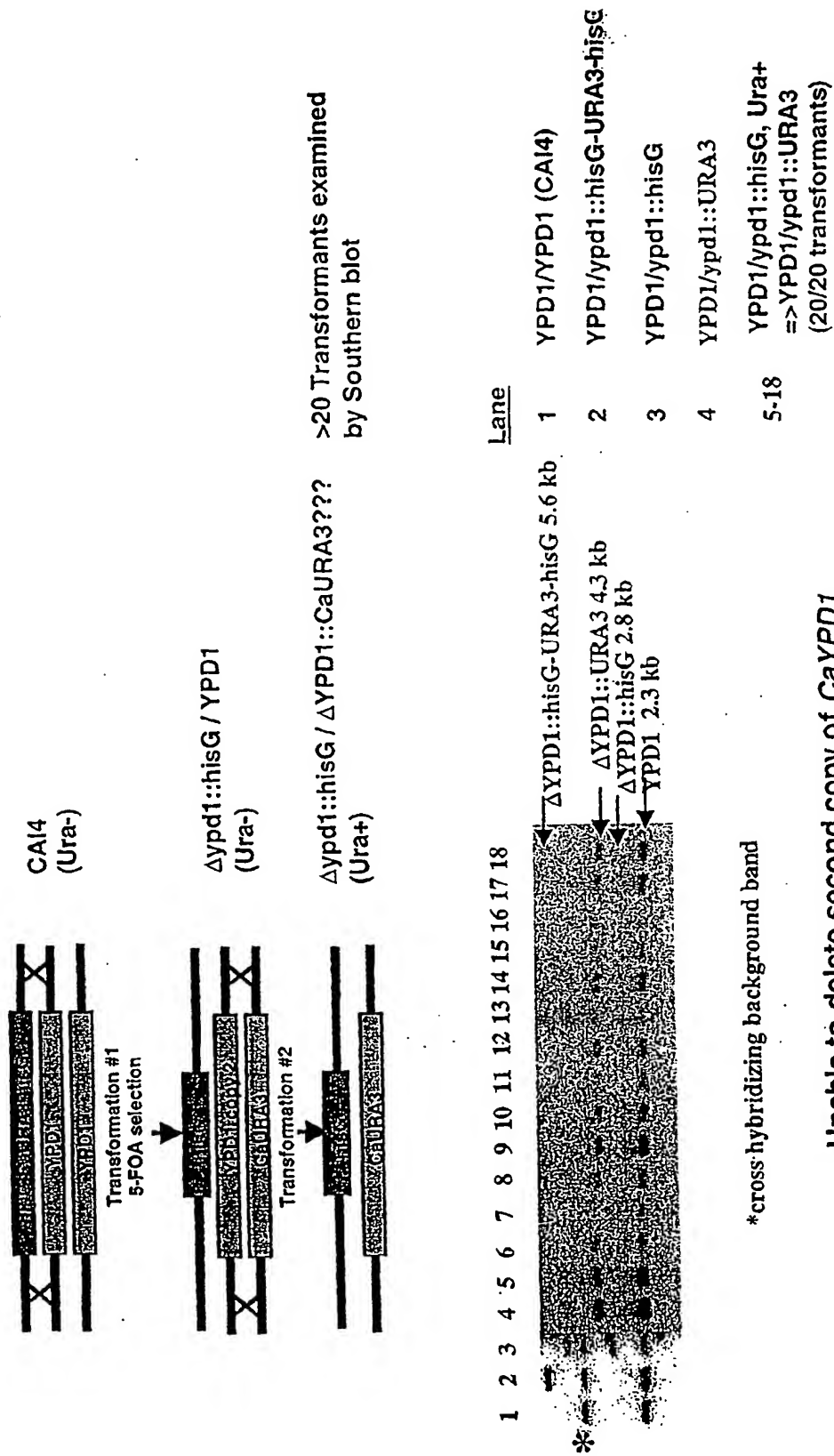


Figure 76B

C. albicans TIM10 deletion analysis

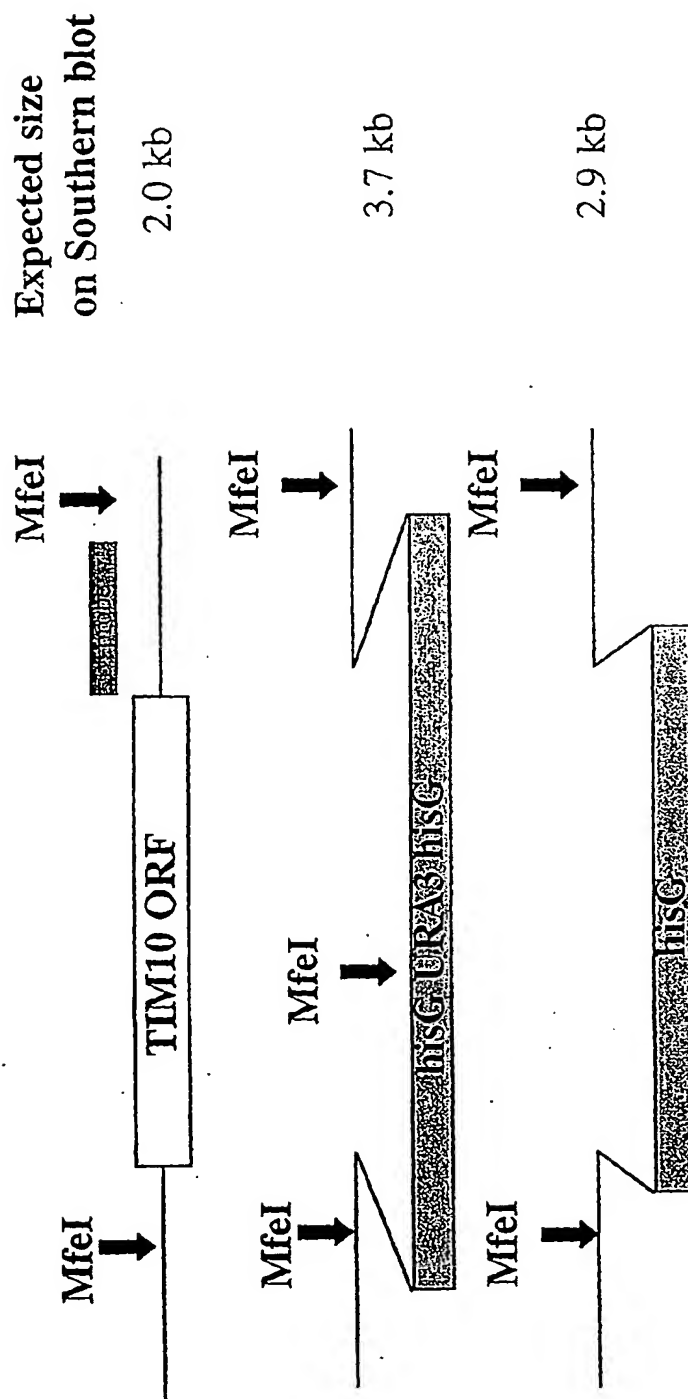
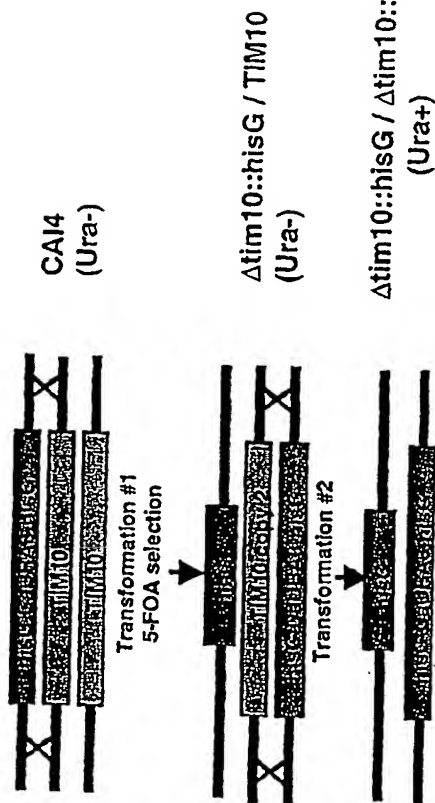
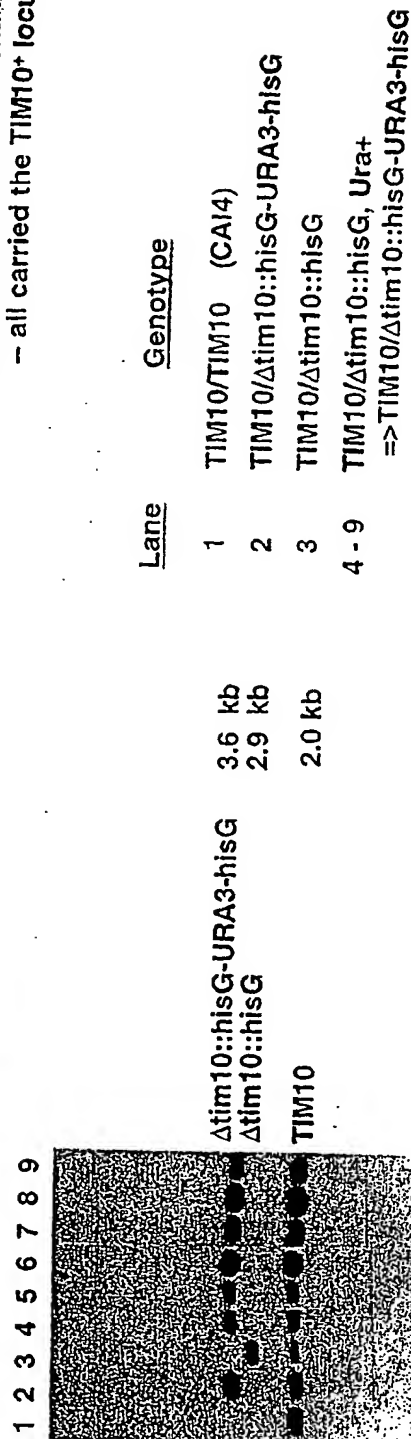


Figure 77A

C. albicans TIM10 deletion analysis



24 transformants were examined
- all carried the TIM10⁺ locus



Unable to delete both copies of *CaTIM10*

Figure 77B

C. albicans SRB4 deletion analysis

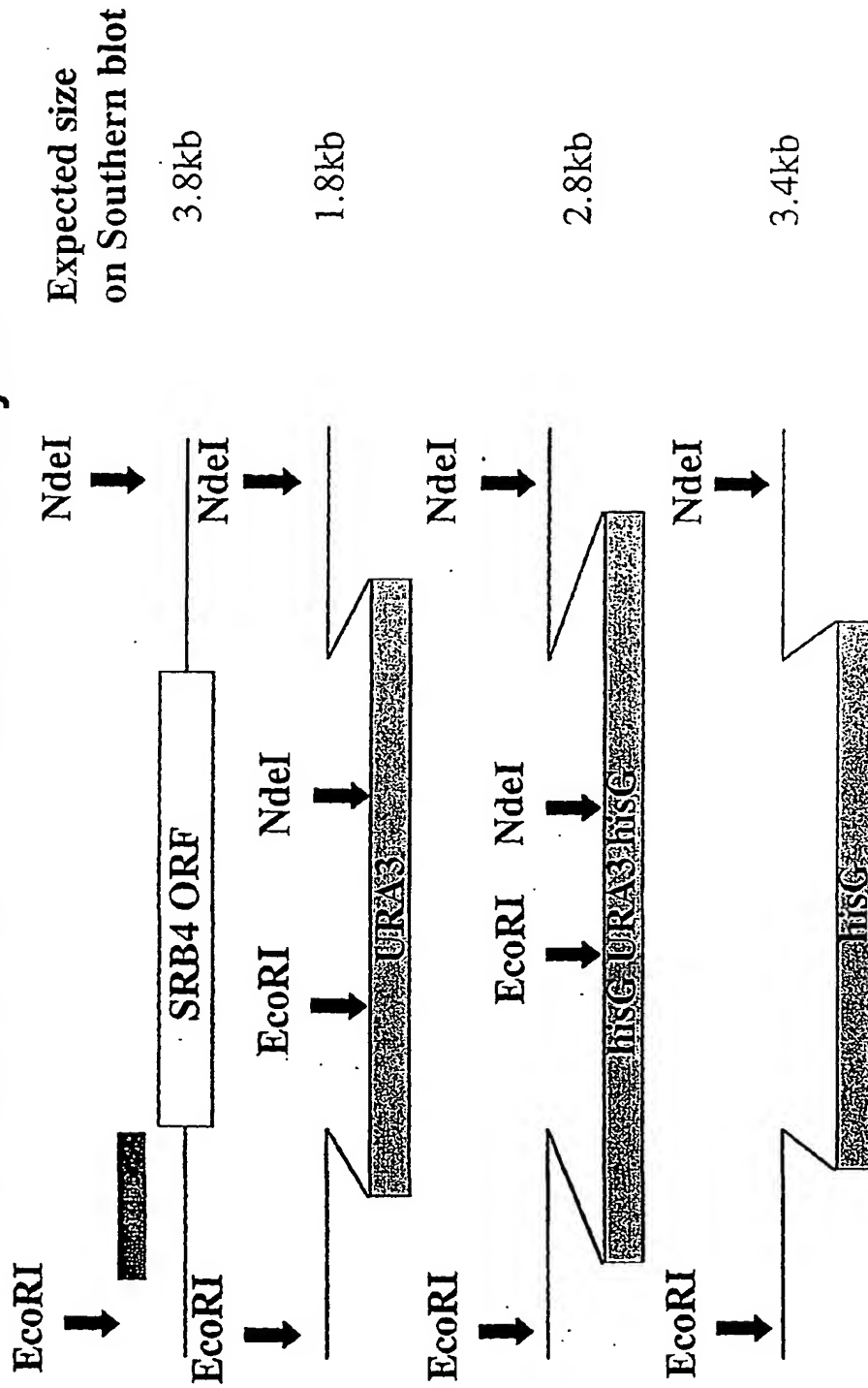


Figure 78A

C. albicans SRB4 deletion analysis

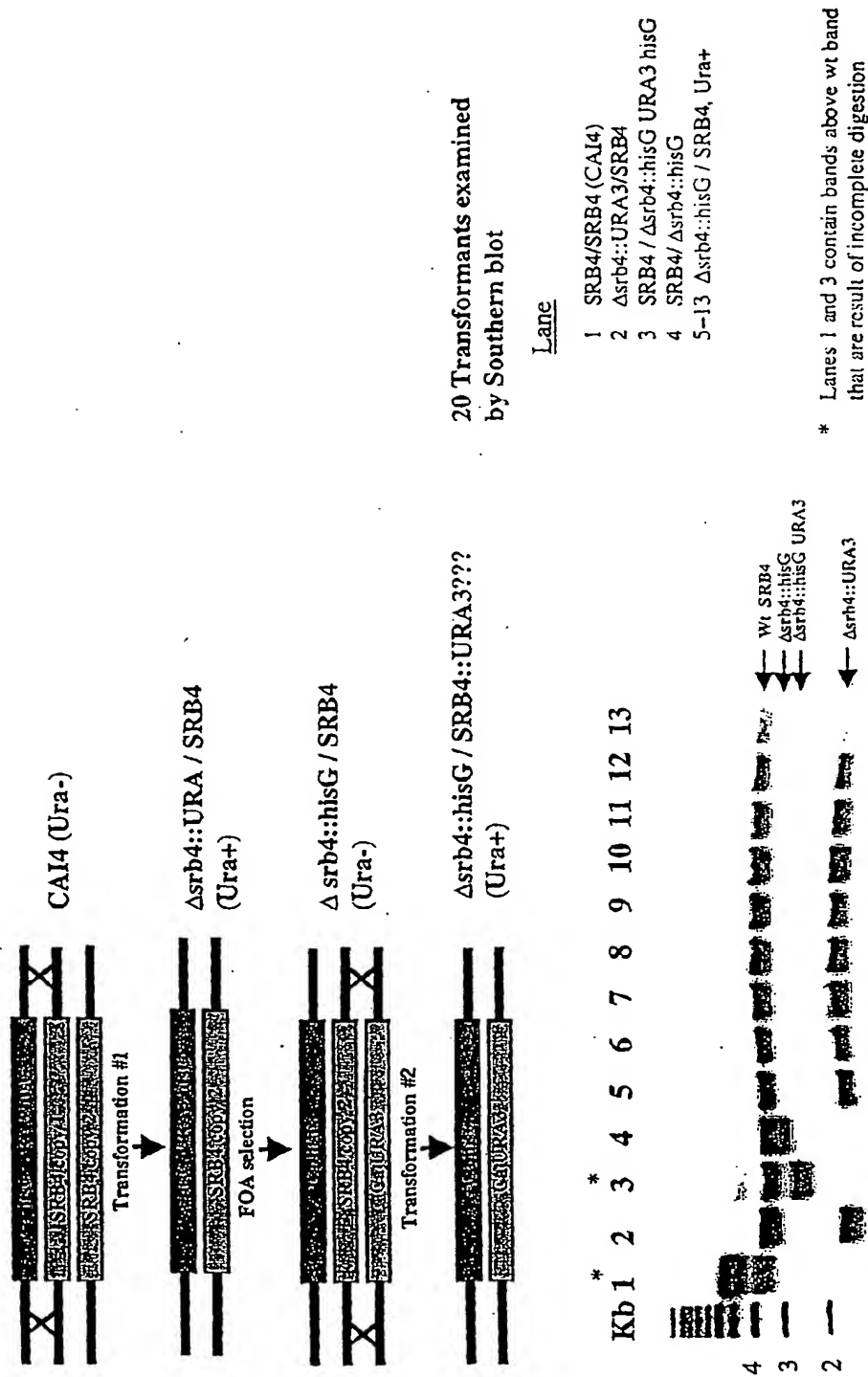


Figure 78B

Figure 79

Saccharomyces cerevisiae orf name: YAL034W-A

Saccharomyces cerevisiae gene name: MTW1

Candida albicans protein: SEQ ID NO: 30

MSDKTLDERTTAILTEHLEFAPLTLIDDVINAVNEIMYKGTTAIETYLKEQKQLMKNGITK
VTEDEIEIGMGKLESLESTIDKNFDKFELYCLRNIFNIPKDLIPYIQLSHQQGIEFKSDNVE
QKREFDQQIKNLQLKIMQELQLRKILKLVLKVQKLIKVLIAIDNDFKKIDFASGGGGNEE
SIRILKNLQPIDETLYFLISQIKNLINQIEQLSNKVNTNLKTQKFIPNLRDKFIDGRTRVLLQ
TGIWKDLEKNDIKILVQGNDDNNNNNNNNNNNTLTDLQNQDDIDMIPEQDDIDVDAIKNI
NAQIF

Saccharomyces cerevisiae protein:SEQ ID NO: 29

MSAPTMRSTSI TEHLGYPPISLVDDIINAVNEIMYKCTAAMEKYLLSKSKIGEEDYGEEI
KSGVAKLESLENSVDKNFDKLELYVLRNVLRIPPEYLDANVFRLENQKDLVIVDENELK
KSEEKLRKVNDVELAFKKNEMLLKRVTVKRLLFTIRGFKQKLNELLKCKDDVQLQKI
LESLKPIDDTMTLLTDSLRLKYVDSESTSTEEVEALLQRLKTNGKQNNKDFRTRYIDIR

Saccharomyces cerevisiae orf name: YBR060C

Saccharomyces cerevisiae gene name: ORC2

Candida albicans protein:SEQ ID NO: 60

MSHSNALPNSPFRSPKKQRMEVIGPLNASRFSFSPVKTPPHGRAGLSSPEKRLVKDLDKA
RKRANNSLYNRLMDEYLDTDYLDDEQDRILADRIKQSRGEPDEVNYGSDVELEIDLTQ
QRRTRRREKKVVYSSDSSNEYEDTGMPEESSSEEEAADDGDNVEFVYGPPKERKTSLS
SSPPTVKPTVRRTKRGRPSKSELVLGQIKSIFHQDDVLFSTDRTFTPTKPTAAKKPVSNY
LTSIFDQNFDRSKVPSLSGIPKSTNTHEEKKTFVPLPIPTLDADGNITDKEYISKYFDGVD
AKFKEGRFVDEKVFYLEGPEGYFEQQTTRVKQSGNSLTALAPQIEYKDFARLVKLGDNL
SFQRKRHLFELHKYTYHQWCFEMSQGFNLNFYGVGSKIDLLRDFATNYFGIWWENVVH
ADLPKVLVVGFNPSINIKKLILEIASILLPNELYPKHIAGTVPFVVDYLNHRLPCGSIGFH
KPKILLIHNLDGEVFRVDKTQTLLSQLMTLPEVWAMSSTDHINASLLWDLKVKNLNFI
WHNLTTYATYQRETSFRDVISLGKSKKFVGGGLGAKYVLRSLTDNHRNLYRELLIAQLDK

Saccharomyces cerevisiae protein:SEQ ID NO: 59

MLNGEDFVEHNDILSSPAKSRNVTPKRVDPHGERQLRRIHSSKKNLLERISLVGNERKNT
SPDPALKPKTPSKAPRKRGRPRKIQEELTDRIKKDEKDTISSKKKRKLDKDTSGNVNEES
KTSNNKQVMEKTGIKEKREREKIQAATTYEDNVTPTQDDNFVSNSPEPPEPATPSKKS
TTNHDFTSPLKQIIMNNLKEYKDSTSPGKLTLSRNFTPTVPKNKKLYQTSETKSASSFLD
TFEGYFDQRKIVRTNAKSRTMSMAPDVTREEFSLVSNNFNENFQKRPRQKLFEIQKCM
FPQYWFELTQGFSLLFYGVGSKRNFLEEFADYLSPKIAYSQLAYENELQONKPVNSIPCL
LNGYNPSCNYRDVFKEITDLLVPAELTRSETKYWGNHVLQIQKMIDFYKNQPLDKLILV
VHNLDGPSIRKNTFQTMLSFLSVIRQIAIVASTDHIYAPLLWDNMKAQNYNFVFDHISNFE
PSTVESTFQDVMKMGKSDTSSGAEGAKYVLQSLTVNSKKMYKLLIETQMOMNGNLSA
NTGPKRGTQRTGVLELKLFNHLCAADFIASNEIALRSMLREFIEHKMANITKNNSGMEIHW

Figure 79 (continued).

VPYTYAELEKLLKTVLNTL

human genbank accession #: Q13416

human protein:SEQ ID NO: 61

MSKPELKEDKMLEVHFVGDDVDLNLHILDREGGAKLKKERAQLLVNPKKUKKPEYDLEDDQEVLKI
FLEKEEEEA

Saccharomyces cerevisiae orf name: YBR088C

Saccharomyces cerevisiae gene name: POL30

Candida albicans protein:SEQ ID NO: 18

MLEGKFEEAALLKKVVEAIKDCVKKCNFNCSEHGITVQAVDDSRVLLVSLIGQTSFSER
CDRDVTLGIDLESFSKIISANNEDFLTLLAEDSPDQIMALEEKQKEKISEYSLKLMIDIDSE
FLQIDDMEYDAVVNMPPSSDFAKLVRDLKNLSESLRVVVTKDSVKFTSEGDSGSGSVILK
PYTNLKNERESVTISLDDPVDLTFGLKYLN DIVKAATLSDVITIKLADKTPALFEFKMQSG
GYLRFYLAPKFDDDEY

Saccharomyces cerevisiae protein:SEQ ID NO: 17

MLEAKFEEASLFRIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYR
CDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIA EYSLKLMIDIDA
DFLKIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIPFVD
MEHPETSIKLEMDQPVDLTFGAKYLLDIKGSLSRVRGIRLSSEAPALFQFDLKSGLQFF
LAPKFNDDEE

human genbank accession #: P12004

human protein:SEQ ID NO: 19

MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSHVSLVQLTLRSEGFDY
RCDRNLAMGVNLTSMKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKL
MDLDVEQLGIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNG
NIKLSQTSNVDKKEEA VTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLMSADVPLVVE
YKIADMGHLYLAPKJEDDEGS

Saccharomyces cerevisiae orf name: YBR155W

Saccharomyces cerevisiae gene name: CNS1

Candida albicans protein:SEQ ID NO: 63

MSKIEPVTEKEEEYVSEWDRRRYVPKAGEPELPPQLSEFSNKTTDEVIEELNRLPFFMTLD
ETDGDGGENVNLEALKSLAYEGDPDEIASNFKNQGNNCYKFKKYKDAIFYTKGLEVNC
DVDAINSALYLNRAACNLELKNYRRCIEDCKVLMLEKNIKACFRSGKAFFAIEKYDE
AIKVLEYGLNIEPENKDLQKLLQQVQKRQETLAQIKAKKAQEEERLKNIVLENSIKLR
HIEIVKSSSPPEVLKTAKIRLEDPKDYQSOLFAMILYPTTDEFDFIAEISELTTPLELL

Saccharomyces cerevisiae protein:SEQ ID NO: 62

MSSVNANGGYTKPQKYVPGPDPELPPQLSEFKDKTSDEILKEMNRMPFFMTKLDETGD

Figure 79 (continued)

AGGENVELEALKALAYEGEPHEIAENFKKQGNELYKAKRFKDARELYSKGLAVECEDK
 SINESLYANRAACELELKNYRRCIEDCSKALTINPKNVKCYRTSKAFFQLNKL EAKSA
 ATFANQRIDPENKSILNMLSVIDRKEQELKAKEEKQQREAQERENKKIMLESAMTLRNT
 NIKTHSPVELLNEGKIRLEDPMDFESQLIYPALIMYPTQDEFDFVGEVSELTTVQELVDLV
 LEGPQERFKKEGKENFTPKKVLVFMETKAGGLIKAGKKLTFHDILKKESPDVPLFDNALK
 IYTPKVESEGWISKWDKQKALERRSV

human genbank accession #: NP_004614

human protein:SEQ ID NO: 64

MEQPGQDPTSDDVMSDFLEKFQSQPYRGGFHEDQWEKEFEKVPLFMSRAPSEIDPRENP
 DLACLQSIIFDEERSPEEQAKTYKDEGNDYFKEKDYKKAVISYTEGLKKKCADPDLNAV
 LYTNRAAAQYYLGNFRSALNDVTAARKLKPCHLKAIIRGALCHLELIHFAEAVNWCDEG
 LQIDAKEKKLLEMRAKADKLKRIEQRDVRKANLKEKKERNQNEALLQAIKARNIRLSEA
 ACEDEDSASEGLGELFLDGLSTENPHGARLSLDGQGRLSWPVFLYPEY AQSDFISAFHE
 DSRFIDHLMVMFGETPSWDLEQKYCLIIWRSTLRMRTGQNYTGCLPRAPCYRFYSTRGT
 L
 --

Saccharomyces cerevisiae orf name: YDL235C

Saccharomyces cerevisiae gene name: YPD1

Candida albicans protein:SEQ ID NO: 66

MSEDKLQKLQDSGLVDWAVFSEIVTMDDEEGFSKSLVEVFVSQVEETFEEIDKYLKEK
 NLEKLSSSGHFLKGSAALGLTKISNQ CERIQNYGHKINFDFQLEDIKTKGDSAVSAEN
 VAVNDGETNPENGSGNETSNNKTNTSNIPDESSDDFWIALIEDALAKARDGFDQSRRA
 LDEYYY

Saccharomyces cerevisiae protein:SEQ ID NO: 65

MSTIPSEINWTLNEIISMDDDDSDFSKGLIIQFIDQAQTTF AQMQRQLDGEKNLTLDNL
 GHFLKGSSAALGLQRIAWVCERIQNLGRKMEHFFPNKTEL VNTLSDKSINGINIDEDDEEI
 KIQVDDKDENSIIYLLIAKALNQSRLEFKLARIELSKYYNTNL

human genbank accession #: CAA78727

human protein:SEQ ID NO: 67

TDKLSNMQKDLENSNAKLQEKIQELKANEHQ LITLKKDVNETQKKVSEMEQLKKQIKD
 QSLTSLKLEIENLNL AQELHENLEEMKSVMKERDNLRRVEETLKL ERDQLKESLQETKA
 RDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQISDIQKDLKSKDELQKKIQELQKK
 ELQLLRVKEDVNMSHKKINEMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAK
 ERD--

Saccharomyces cerevisiae orf name: YDR299W

Saccharomyces cerevisiae gene name: BFR2

Candida albicans protein:SEQ ID NO: 38

MSFFGLHFQLNSLT LNISNMAKKSLS EQISSLYTPKTDYDIEDHDL DVSKDNGIFQHHDG
 GSENESEDED TGLRNEHYVESSKSKLRQQNEG VNLGEKYVGNVTSR SKLYDDEDDKQP

Figure 79 (continued)

TEASSGEELDAESAEEDDEEDVADDDDDQESDRSSSSDAENDEDEDENISHKRELLKQ
 LMSKERSHIVNRLSQSATNDALKGYSIQQNKTFEKIIDVRLKFQKSVTSSNMLPINTSTY
 SETKSEDSDELVTAKKQLYSLDLHLFTLRNELDESTSVKTPKKRSFAKYSEVTSAAQAQ
 LNSRRNQILTKWSAKVANSSGRNAMNANKFKTINQSFEQQVNNNLSDMDRLIKRTKLN
 RRVNTPIGYTTKEEDDHENGKNKNSIDEDDDIPEDTSVRKKTQGLENDYFDDDFYRV
 LLNDLVDKKVQTSPTSGITISLRAAQKSNKLKNNVDTKASKGRKLRYHVQEPIANFETS
 RGS

Saccharomyces cerevisiae protein:SEQ ID NO: 37

MEKSLADQISDIAIKPVNKDFDIEDEENASLFQHNEKNGESDLSYDGNSTTEETKKAHYL
 EVEKSKLRAEKGLELNDPKYTGKGSQALYEEVSENEDEEEEEEEEEEEKEEDALSFR
 DSEDEEVEIDEEESDADGGETEEAQQKRHALSKLIQKETKQAINKLSQSVQRDASKGYSI
 LQQTCLFDNIIDRLIKLQKAVIAANKLPLTTESWEEAKMDDSEETKRLLKENEKLFNNLF
 NRLINFRIKFQLGDHITQNEEVAKHKLKSKRSLKELYQETNSLDSELKEYRTAVLNKWT
 KVSSASGNAALSSNKFKAINLPADVQVENQLSDMSRLMKRTKLNRRNITPLYFQKDCAN
 GRLPELISPVVKDSVDDNENSDDGLDIPKNYDPRRKDNNAIDITENPYVFDDDFYRVLL
 NDLIDKKISNAHNSESAATITSTNARSNNKLKKNIDTKASKGRKLNYSVQDPIANYEAPI
 TSGYKWSDDQIDEFFAGLLGQRVNFNENEDEEQHARJENDEELEAVKNDIDIQIFG

human genbank accession #: NM_000055

human protein:SEQ ID NO: 39

MGRPLALQLEQLLNPRPSEADPEADPEEATAARVIDRFDEGEDGEGDFLVVGSIRKLASA
 SLLDTDKRYCGKTTSRKAWNEHDHWEQTLPGSSDEEISDEEGSGDEDESEGLGLEEYDEDD
 LGAAEEQECGDHRESKKTSHSAKTPGFSVQSISDFEFTKGMDDLGSSEEEDEESGME
 EGDDAEDSQGESEEDRAGDRNSEDDGVVMTFSSVKVSEEVKGRAVKNQIALWDQLE
 GRIKLQKALLTTNQLPQPDVFPVFKDKGGPEFASALKNSHKALKALLRSLVGLQEELLFQ
 YPDTRYVVDGTPNAGSEEEISSEDELVEEKKQRRRVPKRKLEMEDYPSFMAKALPT
 LQSTGTTLQKWHDKTKLASGKLGKGFAGFERSILTQIDHILMCKERLLRTQTKRSVYR
 VLKPEPAAQVPESLPGEPEILPQAPANAHKDLDEEIFDDDDFYHQLLRELIERKTSSL
 DPNDQVAHGKAVACNPEVTEAKSTKKVDRKASKGRKLRFHVLSKLLSFMAPIDHTTMN
 DDARTELYRSLFGQLHPPDEGHGD

Saccharomyces cerevisiae orf name: YDR311W

Saccharomyces cerevisiae gene name: TFB1

Candida albicans protein:SEQ ID NO: 32

MDIRGACSVDKIGGMVYIREDLAPLMLEWKPIDEQEEDRAISIPNLSTTLQSTKETSPK
 MILKIVYKLTSGPPNTNADGTDNGGGGGGGEQKSFKLTFNRPMTNTIKDSLQITIVARSRT
 KGGLKVPVLQLQLQHQLHLSAPQADSTRDSTSSSTPIPTTSGTSTSSSLSLAASQSLS
 DANLLKNFELQQKLLLEDRLQDVFVKSVQFQKLSQVFWSSRLNQLRTPALTISQHKG
 PYNVLSTIKPVATSDNQVNVNVRTDTINEFTIYPIKKAFDDLVPNKFNEGEFWSRFFNSK
 LFRRLRGDKISISNSRGDVLDKYLIDQNYQEKLOKSSTLENNGSGGGGGGAGGGSGN
 SEQGIQTLESHPVKKFLDLGMNQDQNSQKLGNRPDFTMRYDEDNVDDDNKKPTLGNEN
 EMILMKNMNRLSSKMMSMSSTNGPEKPSETTIDGLSAAELNEEELDLHDLNDSNLQ

Figure 79 (continued)

YIKLNINTDIAKGTKLDSYEGSNTNNKISQDELHKYLSQTFQGQIELTETTYTCKSEEIEKT
SMEIAMLIKQNFRTFKLINKENDIAGTNVPNSLIQEITYNITTFEFLSHFWKIFLHGNNPGQ
LKKIFTSLKNCQSGLIELENKAIDQFKSMDILQKNQKLQDKVLKDFASCLQPMKIALDKA
CNE

Saccharomyces cerevisiae protein:SEQ ID NO: 31

MSHSGAAIFEKVSIGIINEDVSPAELTWRSTDGDKVHTVVLSTIDKLQATPASSEKMML
RLIGKVDESCKRKDNENGVVPPKQRHMFNFNRRTVMDNIKMTLQQIISRYKDADIYEE
KRRREESAQHTETPMSSSVTAGTPTPHLDTPQLNNGAPLINTAKLDDSLSKELLTNLK
LQQSLLKGNKVLKVFQETVINAGLPSEFWSTRIPLRAFALSTSQKVGPNVLSITKPV
ASSENKVNVLNLSREKILNIFENYPIVKKAYTDNVPKNFKEPEFWARFFSSKLFRKLRGEKI
MQNDRGDVIIDRYLTLDQEFDRKDDDMLLHPVKKIIDLGDNIQDDPVVRGNRPDFTMQP
GVDINGNSDGTVDILKGMNRLSEKMIMALKNEYSRTNLQNKSNITNDEEDEDNERNEL
KIDDLNESYKTNIAIHLKRNAHEKTTDNDKSSADSIKNADLKVSNNQMLQQLSLVM
NLINKLDLNQVVPNNVSNKINKRVITAINKAKQAKHNNVNNSALGSFVDNTSQANELEV
KSTLPIDLLESCRMHTTCCEFLKHFYHFSQSGEQKQASTVKKLYNHLKDCIEKLNELFQD
V

human genbank accession #: W19128

human protein:SEQ ID NO: 33

MATSSSEVLLIVKKVRQKKQDGALYLMAERIAWAPEGKDRFTISHMYADIKCQKISPEG
KAKIQLQLVLHAGDTTNFHFNSNESTAVKERDAVKDLLQQLLPFKRANKELEKNRCKIL
FCFSFIKLRTGEEQMLEDPVLFQLYKDVSQVISAEFEWNRLNVNATDSSTS NHKQDVGIS
AAFLADVPRQTDGCNGLRYNLTSDIIESIFRTYPAVKMKYAENVPHNMTKEFEWTRFFQ
SHYFHRDRLNTGSKDLFAECAKIDEKGLKTMVSLGVKNPLDLTALEDKPLDEGYGISSV
PSSNSKSIKENSNAAIKRFNHHSAMVLAAGLRKQEAQNEQTSEPSNMDGNSGDADCFQ
PAVKRAKLQESIEYEDLGKNNSVKTIALNLKKSDRYHGPPTIQSLQYATSQDIINSFQSIR
QEMEAYTPKLTQVLSSSAASSTITALSPGGALMQGGTQQAINQMVPNDIQTNLVSHIEM
LQTAYNKLHTWQSRRLMKKT

Saccharomyces cerevisiae orf name: YER022W

Saccharomyces cerevisiae gene name: SRB4

Candida albicans protein:SEQ ID NO: 72

MVEKQFNIDLELNDTGHI DPFLQDEYVCFLTLLVFLVLFSSLLTLPRDKLKLEELIPRIFER
KSFLNVTEDSLRKEIDNSLKISEEDALDTEESREDTVEADQQEVFNKHKFELSKNNINNAL
NETQLSLDFVSLISSVKPSLAKSTISPFLSKFVKPTSLNSDRLGQDSNDNQESKATDSFGQ
GWKLES LGKITDLFREASTNLNDQVIKERRYWNMINLVLANDEVLFMRDPQNNARAIG
VKYGYGDSGSNFHDQGLALLRKDNQTGEISFHPISSINNAKIVEKVSFRFIRVKILSQIDGDY
MLTGQSIFNFD FEKSKQSIINDIEKARFFLFEEDLFHQLIREAKLLVNYNVNIIISNKIIEINNII
IEIESIVYDELNEEELENYQNVNEYSTLHNKKCQLILNYLKLMLCCYYKYNLKLKQKVP
TALTWKWKQSN SHPLILRPLVGNMRHELNLNLMKSVLDRLMHAHESELSYSKLDVEKFIN
LATRSKKQNP FQKSIEKPISKFHLVLCNKTSNMLDVNIQLDNYELFVNLIINMTIIRFETEH
DFKNNVNGINVLQLGFSD FNEIEECLDWSIQNFVL

Figure 79 (continued)

Saccharomyces cerevisiae protein:SEQ ID NO: 71

MTTEDPDSNHLSSSETGIKLALDPNLITLALSSNPSSLSHSPTSDEPVPESAGKADTSIRLEG
DELENKTKKDNNDKNLKFKNKDSLVSNPHEIYGSMPLQLIPILRQRGPGFKFVDLNEKE
LQNEIKQLGSDSSDGHNSEKKD TDGADENVQIGEDFMEVDYEDKDNPVDSRNETDHKT
NENGETDDNIETVMTQE QFVKRRRDMLEHINLAMNESSLALEFVSLLLSSVKESTGMSS
MSPFLRKVVKPSSLNSDKIPYVAPTKEYIELDILNKGWKLQSLNESKDLLRASFNKLSSI
LQNEHDYWNKIMQSI SNKD VIFKIRDRTSGQKLLAIKYG YEDSGSTYKHDRGIANIRNNIE
SQNLDLIPHSSSVFKGTDFVHSVKKFLRVRIFTKIESEDDYILSGESVMDRSESEEAETKD
IRKQIQLLKKIIFEKELMYQIKKECALLISYGVSIENENKVIIELPNEKFEIELLSLDDDSIVN
HEQDLPKINDKRANLMLVMLRLLL VVIFKKTLRSRISSPHGLINLNVDDDILIRPILGKVR
FANYKLLLKKIKDYVLDIVPGSSITETEVEREQPQENKNIDDENITKLN

human genbank accession #: BAA88763

human protein:SEQ ID NO: 73

MYGSARSVGKVEPSSQSPGRSPRLPRSPRLGHRRTNSTGGSSGSSVGGGSGKTLSMENIQ
SLNAA YATSGPMYLS DHENVGSETPKSTMTLGRSGGRLPYGVRMTAMGSSPNIASSGV
ASDTIAFGHEHLPPVSMAS TVPHSLRQARDNTIMDLQTQLKEVLRENDLLRKDVEVKES
KLSSSMNSIKTFWSPELKKERALRKDEASKITIWKEQYRVVQEEHQHMQM TIQALQDEL
RIQRDLNQLFQQDSSSRTGEP CVAELTEENFQRLHAEHERQAKELFLLRK TLEEMELRIET
QKQTLNARDESIKKLLEMLQSKGLSAKATEEDHERTRRLAEAEMHVH HLESLEQKEKE
NSMLREEMHRRFENAPDSAKTKALQTVIEMKDSKISSMERGLRDLEEEIQMLKSNGALS
TEERBEEMKQMEVYRSHSKFMKNKIGQVKQELSRKDTELLALQTKLETLTNQFSDSKQH
IEVLKESLTAKEQRAAILQTEVDALRLRLEEKETMLNKKTKQIQDMAEEKGTQAGEIHD L
KDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLKERVKS LQADTTNTDTALTLEE
ALAEKERTIERLKEQRDRDEREKQEEIDNYKKDLKDLKEKVSLLQGD LSEKEASLLDLKE
HASSLASSDESSKAQAEVDRLLLEILKEVENEKNDKDKKIAELESLSRQVKDQNKKVAN
LKHKEQVEKKKSAQMLEEARREDNLNDSSQQLQVEELLMAMEKVKQELES MKAKLS
STQQSLAEKETHLTNLRAERRKHLEEVLEMKQEAALLAAJSEKDANIALLELSSSKKTQE
EVAALKREKDRLVQQLKQQTQNRMKLMADNYEDDHF KSSHSNQTNHKPSPDQDEEEG
IWA

--

Saccharomyces cerevisiae orf name: YER127W

Saccharomyces cerevisiae gene name: LCP5

Candida albicans protein:SEQ ID NO: 53

MSKVDTVLEKIISSSTKSTEASVKELIAFVKDSSSQHPELVRNLLAKSNSSLEGVSLGLKN
ESLVS YINNIVLVVL SHLERLESDSETGSSAVERSIIQRTLEKGVKPLEKKLSYQLDKMIR
AYGRMEQDEIKAEQKLNDRGSGENDENDENDSEEDSEEDSEDDSEDD ELAYRPDASSFA
KLTS AKTKSKPTSSAVSTSNEKYRPPKISAMAPPTAVKSHDL DANTTSSKNRKLQSMEEY
LQEQSDMPMV EASVGSTIVEHGRGGVKTHDRKKEREIQTYEEDNFVRLPTSQT KKS F

Saccharomyces cerevisiae protein:SEQ ID NO: 52

MSELNALLKDINGSLTATSESLERLSGIYSNSATDEIPESNQLHEHLFYDAKKPAEKVSLL
SLKNGSMLGYINSLMLIGNRLDDECKDPSAMDARERSIQHRVVLERG VVKPLEKKLAYQ

Figure 79 (continued)

LDKLTRAYVKMEKEYKDAEKRALEKSTLVNHSNDDSEDESSEDELA YRPNTSGIINT
 NKKSSAYRVEETAKQENGEENDNETGVYKPPKITAVLPPQQTHTFEDRFDAREHKDRSN
 KSNKAERKQKQRRERNARMNVIGGEDFGIFSSKRKLEDSTSRRGAKKTRSAWDRAQRR
 L

human genbank accession #: AL050003

human protein:SEQ ID NO: 54

MAALGVLESDLPSAVTLLKNLQEQVMAVTAQVKSLTQKVQAGAYPTEKGLSFLEVKDQ
 LLLMYLMDLTHLILDKASGSLQGHDAVLRLVEIRTVLEKLRLDQKLKYQIDKLIKTA
 TGSLSSENDPLRFKPHPSNMMSKLSSEDEEEDEAEDDQSEASGKKS VKGVSKKYVPPRLV
 PVHYDETEAEREKKRLERAKRRALSSSVIRELKEQYSDAPEEIRDARHPHVTRQS QEDQH
 RINYEESMMVRLSVSKREKGRRKRANVMSSQLHSLTHFSDISALTGGTVHLDEDQNPIK
 KRKKIPQKGRKKKGQ

Saccharomyces cerevisiae orf name: YFR027W

Saccharomyces cerevisiae gene name: ECO1

Candida albicans protein:SEQ ID NO: 58

MGSINSQKAQKIQSILALPSNFKKITCSTCDMTYNPHISQDKLLHNKYHTNFINGIPWNYK
 TDNDVLIENFTLVETPKLNSTGKSLKLTKTQTFKGSIIKINKSNKRHIQKVELLLNMVNO
 ELNASQDSGQWKKPEFDRSKAFVHDSKAIGLCTTDTIQPDQGRWMIHKTQSIVPNQINK
 NVVIGISRIWISRKWRQYGLGKLLNVVLKNSIYSVQLLKNQVAFSQPSFSGGMLAKSFN
 GVKHKS GEMLLPVYIE

Saccharomyces cerevisiae protein:SEQ ID NO: 57

MKARKSQRKAGSKPNLIQSKLQVNNGSKSNKIVKCDKCEMSYSSTSIEDRAIHEKYHTL
 QLHGRKWSPNWGSIVYTERNHSRTVHLSRSTGTTPLNSSPLKKSSPSITHQEEKIVYVRP
 DKSNGEVRAMTEIMTLVNNELNAPHDENVIWNSTTEEKGKAFVYIRNDRAVGIIENLY
 GGNGKTSSRGRWMVYDSRRLVQNVYPDFKIGISRIWVCRTARKLGIATKLIDVARENIV
 YGEVIPRYQVAWSQPTDSGGKLASKYNGIMHKS GKLLLPVYI

--

Saccharomyces cerevisiae orf name: YGL122C

Saccharomyces cerevisiae gene name: NAB2

Candida albicans protein:SEQ ID NO: 10

MQFAPDNQIGKELQQNLIQEIQRRFNKPADDAVDIADYIIYLVAKKSEQEIVAEVKDIADI
 SIDVGFIGDVYLEIRKLEVKNQPPAAVEEASQPQQEQQQSQASVVAPOPIGPKKQLTE
 EEKIALRSQRFGTTTTLSSGRGGRGGITKTRTDFRNHNNKNFLDPKKLDQIISGANNGAIK
 FVPLPPKGRCPDFPYCKNQNCEKAHPTKNCFNYPDCPNPPGTCNFLHPDQDQELIAKLET
 SKKEFEKKKNQLMVKQGSCKYGLKCAKENCNPFHPTANPESGKIETLEWCPQGKNC
 QDRNCTKSHPPPPTANSEKLLSAADLALEQCKFGSQCTNLKCPRRHATS AVPCRAGAEC
 RRVDCFTFSHPLKEPCRFGTKCTNKVCMYQHPEGRTIASHTWTRDGSNNNSTSNRSF

Saccharomyces cerevisiae protein:SEQ ID NO: 9

MSQEQYTENLKVIVAEKLAGIPNFNEDIKYVAEYIVLLIVNGGTVESVVDDELASLFDVS
 RDTLANVVQTAFFALEALQQGESAENTVSKIRMMNAQSLGQSDIAQQQQQQQQQQPDIA
 QQQPQQPQLQPLQPLGTQNAMQTDAPATPSPISAFSGVVNAAAPPQFAPVDNSQRFT

Figure 79 (continued):

QRGGGA VGKNRRGGRGGRGGRNNNSTRFNPLAKALGMAGESNMNFTPTKKEGRCL
 FPHCPLGRSCPHAHPTKVCNEYPCPKPPGTCEFLHPNEDEELMKEMERTREEFQKRKA
 DLLAAKRKPVQTGIVLCKFGALCSNPSCPFHPTANEDAKVIDLMWCDKNLTCDNPEC
 RKAHSSLSKIKEVKPISQKKAAPPPVEKSLEQCKFGTHCTNKRCKYRHARSHIMCREGAN
 CTRIDCLFGHPINEDCRFGVNCKNIYCLFRHPPGRVLPEKKGAAPNSNVPTNERPFALPEN
 AIEN

human genbank accession #: AAD42873

human protein:SEQ ID NO: 11

PQQLHLLSRQLEDPNGSFSNAEMSELSVAQKPEKLLERCKYWPACKNNGDECA YHHPISP
 CKAFPNCKFAEKCLFVHPNCKYDAKCTKPDPCPTHVSRRIQLCRYFPACKKMECPFYHP
 KHCRFNTQCTRPDCTFYHPTINVPPRHALKWIRPQTSE

--

Saccharomyces cerevisiae orf name: YGR195W

Saccharomyces cerevisiae gene name: SKI6

Candida albicans protein:SEQ ID NO: 47

MELYSPEGLRIDGRRWNELRRFECRINHPNSSDGSSYVEQGNTKVMCTVQGPIEPALRS
 QQHSERANIEVNLNIAFSSTFERKKRSRNERRLVELKTTLEKTFEESVMINLYPRTNIVNV
 QVLCQDGGMLAAVINSITLALIDAGISMYDYVSGVSCGLYDQTPLLDVNNLEEHDMS

Saccharomyces cerevisiae protein:SEQ ID NO: 46

MSRLEIYSPEGLRLDGRRWNELRRFESSINHPHAADGSSYMEQGNNKIITLVKGPKPR
 LKSQMDTSKALLNVSVNITKFSKFERSKSSHKNERRVLEIQTSLVRMFEKNVMLNIYPRT
 VIDIEIHVLEQDGGIMGSLINGITLALIDAGISMFDYISGISVGLYDTPPLDTSLEENAMS
 TVTLGVVGKSEKLSLLVEDKIPLDRLENVLAIGIAGHRVRDLMDEELRKHAQKRVS
 ASAR

human genbank accession #: BAA91279

human protein:SEQ ID NO: 48

MAGLELLSDQGYRVDGRRAGELRKIQARMGVFAQADGSAYIEQGNTKALAVVYGPHEI
 RSRARALPDRAVNLCQYSSATFSTGERKRRPHGDRKSCMGQLRQTFEAAILTQLHPR
 SQIDIYVQVLQADGGTYAACVNAATLAVLDAGIPMRDFVCACSAGFVDGTALADLSHV
 EEAAGGPQLALALLPASGQIALLEMDARLHEDHLERVLEAAAQAARDVHTLLDRVVRQ
 HVREASILLGDG

--

Saccharomyces cerevisiae orf name: YHR005C-A

Saccharomyces cerevisiae gene name: TIM10

Candida albicans protein:SEQ ID NO: 69

MFGLGGTTPQISSQKQLQAAEAELDMVTGMFNALVSQCHTKCINKSYNEADISKQESLC
 LDRCAVAKYFETNVQVGENMQKLQSGQFMGR

Saccharomyces cerevisiae protein:SEQ ID NO: 68

MSFLGFGGQQLSSQKIQAAEAELDLVTDMFNKLVNNCYKKCINTSYSEGELNKNES
 SCLDRCAVAKYFETNVQVGENMQKMGQSFNAAGKF

Figure 79 (continued)

human genbank accession #: NP_036588

human protein:SEQ ID NO: 70

MDPLRAQQLAAELEVEEMMADMYNRMTSACHRKCVPPHYKEAELSKGESVCLDRCVSK
YLDIHERMGKKLTELSMQDEELMKRVQQSSGPA

--

Saccharomyces cerevisiae orf name: YIR012W

Saccharomyces cerevisiae gene name:SQT1

Candida albicans protein:SEQ ID NO: 27

MSHQQEDVDDTQEEYINVNEVAEEVADDDQAPPDEEDEEMELDDEHETLEIDMSNNS
WTFYFDKHTDSIFTIFSHPKLPMVLTEGGDNTAYLWTTHTQPPRFVGEITGHKESVISGGFT
ADGKFVVTADMNGLIQVFKATKGGEQWVKFGELDEVEEVLFVTVHPTLPFFAFGATDG
SIWVYQIDESSKLLVQIMSGFSHTLKCNGAVFIQGKDENDLTLSISEDGTVVNWNCFGTG
QVNYKLQPHDDFKGVESPWVTVKVHGNLVAIGGRDGQLSIVNNDTGKIVHTLKTLDNV
DDIAELSIEALSWCESKNINLLAVGLVSGDXLLFDTQQWRLRKNLKVDDAITKLQFVGET
PILVGNMMDGKXYKWEPRTEKXFAGVGTNMGSYGLCYFKIEVKNWLLVDERCFHW
SLFMK

Saccharomyces cerevisiae protein:SEQ ID NO: 26

MEPQEEFITTEEVEQEIVPTVEVEQDVPVDIEGENDDDDEMMNDDEEAEVDMSNNSLT
YFDKHTDSVFAIGHHPNLPLVCTGGGDNLHLWTSHSQPPKFAGTLTGYGESVISCSFTS
EGGFLVTADMSGKVLVHMGQKGGAQWKLASQMQUEVEEIVWLKTHPTIARTFAFGATD
GSVWCYQINEQDGSLEQLMSGFVHQDCSMGEFINTDKGENTLELVTCSLDSTIVAWNC
FTGQQFLKITQAEIKGLEAPWISLSLAPETLTGKNSGVVACGSNNGLLAVINCNGGAILH
LSTVIELKPEQDELDASIESISWSSKFSLMAIGLVCGEILLYDTSAWRVRHKFVLEDSVTKL
MFDNDDLFASCINGKVYQFNARTGQEFVVCVGHNMGVLDIFILLHPVANTGTQKRKVI
TAGDEGVSLVFEVPN

human genbank accession #: NP_001078

human protein:SEQ ID NO: 28

MDSGRRLGPEKWIRRLRRMESESESGAAADTPPLETSLFHGDEEIEVVELDPGPPDPDDL
AQEMEDVDFEEEEEEGNEEGWVLEPQEGVVGSMGPDDESEVTFALHSASVFCVSLDP
KTNTLAVTGGEDDKAFVWRLSDGELLFECAGHKDSVTCAGFSHDSTLVATGDMGSLK
VWQVDTKEEVWSFEAGDLEWMEWHPRAPVLLAGTADGNTWMWKVPNGDCKTFQGP
NCPATCGRVLPDGKRAVVGYEDGTIRIWLKQGSPIHVLKGTEGHQGPLTCVAANQDG
SLILTGSVDCQAKLVSATTGKVVGVRFPETVASQPSLGEGESESNVESLGFCFSVMPLA
AVGYLDGTLAIYDLATQTLRHQCQHQSGIVQLLWEAGTAVVYTCSLDGIVRLWDARTG
RLTLDYRGHTAEILDFALSKDASLVVTTSGDHHKAKVFCVQRPDRDFSPDGALLATASYD
TRVYIWDPHNGDILMEFGHLFPPTPIFAGGANDRWVRSVSFSDGLHVASLADDKMVR
FWRIDEDYPVQVAPLSNGLCCAFSTDGSLAAGTHDGSVYFWATPRQVPSLQHLCRM
RRVMPTQEVQELPIPSKLLEFLSYRI

--

Saccharomyces cerevisiae orf name: YKL186C.

Figure 79 (continued)

Saccharomyces cerevisiae gene name: MTR2

Candida albicans protein:SEQ ID NO:16

MNQDPTQQLEPFLKRFLASLDLLYTQPTSQPFNVESYATQLGSNLKRSSAITVNGQPIIPS
 PQEDCKLQFQKKWLQTPLSHQLTSYDGHLP GTGTFFVHFSAKVRFDQSGRNRLGESA
 DLFQENNSIVSKTNQRPIWGSWFGVDVNLVVDENVMQDGEIINSM DYRFTYVPNDSSI KV
Saccharomyces cerevisiae protein:SEQ ID NO:15
 MNTNSNTMVMNDANQAQITATFTKKILAHLD DPDSNKLAQFVQLFNPNNCRIIFNATPF
 AQATVFLQMWQNQVVQTQHALTGVDYHAIPGSGTLCNVNCKVRFDESGRDKMGQDA
 TVPIQPNN TGNRNRPN DMNKPRLWGPYFGISLQLIIDRIFRND FNGVISGFNYNMVYK
 PEDSLLKI

--

Saccharomyces cerevisiae orf name: YKR062W

Saccharomyces cerevisiae gene name: TFA2

Candida albicans protein:SEQ ID NO:7

MSDLSAQLSAFKNKIKSGPSVIVPRKATFTQSPSSPLSSSTTTTTSKNDANVKKRSTTDSV
 TRVLKKQKANMGEMTGSHLSTQLHLAVEYIKEHDQPISVEKLQNYLSFDISHTLLPLLNEI
 DRVKYDESKGTLEYVSLHNIRSSDDVLEFLRRQTTFKGTSVKELKDGWAGCVA AIDELE
 SQGKILVLRNKKENAPRLVWANNGGELGYIDTEFKDMWDQVKLPEPDVLYQKLLDQGL
 KPTGADPNLIKKQPQQKEKKQKKARRGKITNTHMKGILKDYSQLV

Saccharomyces cerevisiae protein:SEQ ID NO:6

MSKNRDP LLANLNAFKSKVK SAPVIAPAKVGQKKTNDTVITIDGNTRKRTASERAQENT
 LNSAKNPVLVDIKKEAGSNSSNAISLDDDDDDDFGSSPSKKVRPGSIAAAALQANQTDI
 SKSHDSSKLLWATEYIQKKGKPV LVNELLDYLSMKKDDKVIELLKKLDRIEFDPKKGT
 KYLSTYDVHSPSELLKLLRSQVTFKGISCKDLKDGWPQCDETINQLEEDSKILVLR TKKD
 KTPRYVWYNSGGNLKCIDEEFVKMWENVQLPQFAELPRKLQDLGLKPASVDPATIKRQ
 TKRVEVKKKRQRKGKITNTHMTGILKDYSHRV

human genbank accession #: NP_002086

human protein:SEQ ID NO:8

MDPSLLRERELFKKRALSTPVVEKRSASSESSSSSSSKKKTKVEHGGSSGSKQNSDHSNG
 SFNLKALSGSSGYKFGVLAKIVNYMKTRHQRGDTHPLTLDEILDETQHLDIGLKQKQWL
 MTEALVNNPKIEVIDGKYAFKPKYNVRDKKALLRLDQHDQRGLGGILLEDIEEALPNSQ
 KAVKALGDQILFVNRPDKKKILFFNDKSCQFSVDEEFQKLWRSVTVD SMDEEKIEEYLK
 RQGISSMQESGPKKVAPIQRKKPASQKKRRFKTHNEHLA GVLKDYSDITSSK

--

Saccharomyces cerevisiae orf name: YLR078C

Saccharomyces cerevisiae gene name: BOS1

Candida albicans protein:SEQ ID NO:18

MNSIYNHGLKQTQTITKDLTQFEKNLSTSPSLQGAITTS LTAFRKTIKEYSDLLEKNVND
 TSYTKHENRLNKFNQDLNEFTLKFDTLKKQRDIQVQEANKQELLGRRHISTTATAALGST
 SSDNPYESSNPSQQQQQLQDEQNTMSYREGLYHEKNSLERGSEQLDRILEMGQQA FE

Figure 79 (continued)

DIVEQNEILRKVQTKFEESLITLGVSQGTIRSVERRAKQDKWLFWFCVVVMLVVFYYI
 Saccharomyces cerevisiae protein:SEQ ID NO:17
 MNALYNHAVKQKNQLQQELARFEKNSVTAPISLQGSISATLVSLEKTVKQYAEHLNRYK
 EDTNAEEIDPKFANRLATLTQDLHDFTAKFKDLKQSYNENNSRTQLFGSGASHVMDSDN
 PFSTSETIMNKRNVGGASANGKEGSSNGGGLPLYQGLQKEQSVFERGNAQLDYILEMGQ
 QSFENIVEQNKILSKVQDRMSNGLRTLGVSEQTITSINKRVFKDKLVFWIALILLIIGIYYVL
 KWLK

human genbank accession #: NP_003560

human protein:SEQ ID NO:19

MSYTPGVGGDPTQLAQRISNIQKITQCSVEIQRTLNLGTPQDSPELRQQQLQKQQYT
 QLAKETDKYIKEFGSLPTTPSEQRQRKIQKDRLEVAEFTTSLTNFQKVQRQAAEREKEFVA
 RVRASSRVSGSPEDSSKERNLVSWSQTQPQVQVQDEEITEDDLRLIHERESSIRQLEAD
 IMDINEIFKDLGMMIHEQGDVIDSIEANVENAEVHVQQANQQLSRAADYQRKSRKTLCH
 LILVIGVAIISLIWGLNH

--

Saccharomyces cerevisiae orf name: YLR291C

Saccharomyces cerevisiae gene name: GCD7

Candida albicans protein:SEQ ID NO:44

MSKLLTPEILALIDPVVSSLKRHLVDDKEIALTIAQLMKVISAARWSNTYDLIELIRQVG
 VIFTEAYPRKVIPGNIVRRVLALIRDETETETETETEQTNDIPMMSSMFSLATHNKNETIK
 EQTQLQLKKQTSMDRAIIQGIRDLVDEISNVNDGIETMAVDLIHDDEILLTPTPNSETVQH
 FLIKARLKRKFTVVVTENYPNDIKA AHKFVKTLAEHNIETILIPDTTIYAVMSRVGKVIIGT
 NAVFANGGCLSN SGVANVVECAKEHRTPVFAVAGLFKLSPLYPFTRNDLIEVGN SGKVL
 NYDDFELVQNV DVVTNPLEDYIPPHIDIFMTNIGGFSPSFIYRIVLDNYKAEDNKLE

Saccharomyces cerevisiae protein:SEQ ID NO:43

MSSQAFTSVHPNAATSDVNVITDTFVAKLKRRQVQGSYAIALETLLQLLMRFISAARWNH
 VNDLIEQIRDLGNSLEKAHPTAFSCGNVIRRLAVLRDEVEEDTMSTTVTSTVAEPLISSM
 FNLLQKPEQPHQNRKNSSGSSSMKTKTDYRQVAIQGIKDLIDEIKNIDEGIQQIAIDLIHDH
 EILLTPTPDSKTVLKFILITARERSNRTFTVLVTEGFPNNTKNAHEFAKKLAQHNIETLVVP
 DSAVFALMSRVGKVIIGTKAVFVNGGTISSNSGVSSVCECAREFRTPVFAVAGLYKLSPL
 YPFDVEKFVEFGGSQRILPRMDPRKRLDTVNQITDYVPPENIDIYITNVGGFNPSFIYRIAW
 DNYKQIDVHLDKNKA

human genbank accession #: AAC42002

human protein:SEQ ID NO:45

MPGSAAKGSEL SERIESFVETLKRGGGPRSSSEEMARETLGLLRQIITDHRWSNAGELMELI
 RREGRRMTAAQPSSETTVGNMVRRLKIREEYGR LHGRSDEDQQESLHKLLTSGGLNED
 FSFHYAQLQSNIEAINELLVELEGT MENIAAQALEHIHSNEVIMTIGFSRTVEAFLKEAAR
 KRKFHVIVAECAFP CQGHMAVNLSKAGIETTVM TAAIFAVMSRVN KVIIGTKTILANGA
 LRAVTGHTLALAAKHSTPLIVCAPMFKLS PQFPNEEDSFHKFVAPEEVL PFTGEDILEK
 VSVHCPVFDYVPELITLFISNIGGNAPS YTYRLMSEL YHPDDHVL

--

Figure 79 (continued)

Saccharomyces cerevisiae orf name: YMR005W

Saccharomyces cerevisiae gene name: MPT1

Candida albicans protein:SEQ ID NO:13

MSHKSMSTTPQESSNLKRQLENSDSSSPNKRSKTETTTENQSSWESDFNSLPVELLQTE
TNGTSPAPAPATPIDTTNASSTKERDQDTSKLNDAIAAAGVDIQQEEELLQQQLNRKSAE
GMASNLKSVIRSSKLPPFLHNYHLAAFIDKVAKQNGIQQNFLMDGEMLELISAACETWLS
NLATKTIILSRHRRRGIPVINKKSGSSSVPRSEISKELRSLALKQKEMEEKRVNKRVMGL
EKSTKDASKNDENGESKAGAEETLHRAANATAAMMTMNPGRKKYSWMTSSATAGGG
SDFGKSSGGSSKDSGKHQSPIISVRGDNGLRFREIRSGNSIIMKDLLGAIEDEKMGTRNA

Saccharomyces cerevisiae protein:SEQ ID NO:12

MANSPKKPSDGTGVSASDTPKYQHTVPETKPAFNLSPGKASELSHSLPSPSIKSTAHVSS
THNDAAGNTDDSVLPKNVSPTTNLRVESNGDTNNMFSSPAGLALPKKDDKKKNKGTSK
ADSKDGKASNSSGQNAQQQSDPNKMQDVLFSAAGIDVREEEALLNSSINASKSQVQTNN
VKIPNHLPLHPEQVSNYMRKVGKEQNFLTPTKNPEILDMMSACENYMRDILTNAIVI
SRHRRKAVKINSRRSEVSAALRAIALIQKKEEERRVKKRIALGLEKEDYENKIDSEETLH
RASNVTAGLRAGSKKQYGWLTSSVNKPTSLGAKSSGKVASDITARGESGLKFREAREEP
GIV

human genbank accession #: CAA72189

human protein:SEQ ID NO:14

MAAGSDLLDEVFFNSEVDEKVVSDLVGSLESLAASAHHHHHLAPRTPEVRAAAAGAL
GNHVVSAGSPAGAAGAGPAAPAEAGAPGAPEPPAGRARPGGGGPQRPGPPSPRRPLVPA
GPAPPAAKLRPPPEGSAGACAPVPAAAA VAAGPEPAPAGPAKPAAGPAALAAAGPGPGP
GPGPGPGPKPAGPGAAQTLNGSAALLNSHHAAAPAVSLVNNGPAALLPLPKPAAPGTV
IQTPPFVGAAPPAPAAPSPPAAPAPAPAAAPPPPPAPATLARPPGHPAGPPTAAPAVP
PPAAAQNGGSAGAAPAPAPAAAGGPAGVSGQPGPGAAAAAPAGVKAESPKRVVQAAP
PAAQTLAASGPASTAASMVIGPTMQGALPSPAAVPPPAPGTPTGLPKGAAGAVTQSLR
TPTATTSGIRATLTPTVLAPRLPQPPQNPTNIQNFQLPPGMVLVRSENGQLLMIPQQALAQ
MQAQAHAAQPQTMAPRPATPTSAPPVQISTVQAPGTPILARQVPTTTIKQVSQAQTTVQP
SATLQRSPGVQQLVLGGAAQTASLTATAVQTGTPQRTVPGATTTSSAATETMENVK
KCKNFLSTLIKLAASSGKQSTETAANVKELVQNLLDGKIEAEDFTSRLYRELNSSPQPYLVP
FLKRSPLALRQLTPDSAIFIQQSQQPPPTSQATTALTA VVLSSSVQRTAGKTAATVTS
ALQPPVLSLTQPTQVGVGKQGQPTPLVIQPPKPGALIRPPQVTLTQTPMVALRQPHNRI
MLTTPQQVNLSEESARILATNSELVGTLTRSKDETFLLQAPLQRRILEIGKKKHGTELHPD
VVSÝVSHATQORLQNLVEKISETAQQKNFSYKDDDRYEQASDVRAQLKFFEQLDQIEKQ
RKDEQEREILMRAAKSRSRQEDPEQLRLKQKAKEMQQQELAQMRQRDANLTALAAIGP
RKKRKVDCPGPGSGAEGSGPGSVVPGSSGVGTPRQFTRQRITRVNLRDLIFCLENERETS
HSLLLYKAFLK

--

Saccharomyces cerevisiae orf name: YMR131C

Saccharomyces cerevisiae gene name: RSA2

Candida albicans protein:SEQ ID NO:24

Figure 79 (continued)

MSKRS AEDDL SGN GSTSHTAVKTNKDSLPTTTNGKEE EPDNMDIGEFEDPYGDEFESDEI
 IELDDNNDEEDDEMIDENSTQAKIEELEAKEQEQQSSIYLP HKSKPLGPDEVLEADPTV
 YEMLHNINLPWPCLTV DILPDSLGNERRSY PATVYLATATQAAKAKDNELLAMKASSLA
 KTLVKDENEDEEDED DDDDDVSDPILDSESIPLRHTTNRIRVSPHAQQTGEYLTASMSE
 NGEVYIFDLLAQYKAFDTPGYMIPKSSKRPIHTIRAHGNVEGYGLDWSPLVNTGALLSGD
 MSGRIYLTNR TTSWTTDKTPFFASQSSIEDIQWSTGETTVFATGGCDGYICIWDTRSKKH
 KPALS VIASKSDVNVISWSSKINHLLASGHDDGSWGVWDLRNFTNNTTSNPSPVANYDF
 Saccharomyces cerevisiae protein:SEQ ID NO:23

MSKRSIEVNEEQDRVVS AKTESHSVPAIPASEEQDAPKNDLEEQLSDEFDS DGEIIEIDGD
 DEINDEDDL RKKQE EAETLVQKDQSEGNKEKIQELYLP HMSRPLGPDEVLEADPTVYEM
 LHNVNMPWPCLTLDVIPDTLGSERRNYPQSILLTTATQSSRKKENELMVLALS NLAKTLL
 KDDNEGEDDEEDED DDDVDPVIENENIPLRDTTNRLKVSPFAISNQEVLTATMSENGDVYI
 YNLAPQSKAFSTPGYQIPKSAKRPIHTVKNHGNVEGYGLDWSPLIKTGALLSGDCSGQIY
 FTQRHTSRWVTDKQPFTVSNNKSIEDIQWSRTESTVFATAGCDGYIRIWDTRSKKHKPAI
 SVKASNTDVNVISWSDKIGYLLASGDDNGTWGVWDLRQFTPSNADAVQPVAQYDFHK
 GAITSIAFNPLDESIVAVGSEDNTVTLWDL SVEADDEEIKQQAETKELQEIPPQLLFVHW
 QKEVKDVKWHKQIPGCLVSTGTDGLNVWKTISV

human genbank accession #: NP_005601

human protein:SEQ ID NO:25

MADKEAAFD DAVEERVINEEYKIWKKNTPFLYDLVMTHALEWPSLTAQWLPDVTRPEG
 KDFS IHLVLGTHTSDEQNH LVIASVQLPNDDAQFDASHYDSEKGEFGGFGSVSGKIEIEI
 KINHEGEVNRARYMPQNPCIIATKTPSSDVLVFDYTKHPSKPDPSGECNPDLRLRGHQKE
 GYGLSWNP NLSGHLLSASDDHTICLWDISAVPKEGKVVD AKTIFTGHTAVVEDVSWHLL
 HESLFGSVADDQKLMIWDTRSNNTSKPSHSVDAHTAEVNCLSFNPYSEFILATGSADKT
 VALWDLRN LKLKLSFESHKDEIFQVQWSPHNETILASSGTDRRLNVWDL SKIGEEQSPE
 DAEDGPPELLFIHGHTAKISDFS WNPNEPWWICSVSEDNIMQVWQMAENIYNDEDPEG
 SVDPEGQGS

--

Saccharomyces cerevisiae orf name: YMR235C

Saccharomyces cerevisiae gene name: RNA1

Candida albicans protein:SEQ ID NO:41

MASVEVELGVTPETTY SISGQLKFDSESDIAPYIKELTEKENVKKVDFSGNTIGIEASKA
 LSEALLKHKDTTVEINFSDLYTGR LNTEIPQSLEYLLPALS KLPNLKLNLSDNAFGLQTIDP
 IEAYLAKAVSIEHLILSNNGMGPFAGSRIGGS LFKLAKAKKAEGKESLKTFCGRNRLENG
 SVNYLSVGLRNH KDLEVRLYQNGIRPAGISKLVEQGLSNNKKLKVLDLQDNTITTRGAI
 HIAESLSNWPLLVELNLNDSLLKNKGS LKLVEAFHAGDEKPQLITLKLQYNELETDSL RV
 LADAIASKLPQLKFLELNGNRFEEDSEHIDKINGIFEERGYGEIDELDELEELDSEEEEDDE
 DDEGEDDTLEEDLDLTQLEEELAGVSLEDKDG NVDEIABELSKTHIKZ

Saccharomyces cerevisiae protein:SEQ ID NO:40

MATLHFVPQH EEEQVYSISGKALKLTTSDDIKPYLEELAALKTCTKLDLSGNTIGTEASEA
 LAKCIAENTQVRESLVEVNFADLYTSRLVDEVVDSLKFLLPVLLKCPHLEIVNLSDNAFG

Figure 79 (continued)

LRTIELLEDYIAHAVNIKHLILSNNGMGPFAGERIGKALFHQAQNKKAASKPFLETFCNTF
TKHASLILAKALPTWKDSL FELNLNDCLLKTAGSDEVFKVFTEVKFPNLHVLKFEYNEM
AQETIEVSFLPAMEKGNLPELEKLEINGNRLDESDALDLLQSKFDDLEVDDFEEVDS

human genbank accession #: CAA57714

human protein:SEQ ID NO:42

MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKEIEDFDSLEALRLEGNT
VGVEAARVIAKALEKKSELKRCHWSDMFTGRLRTEIPPALISLGEGLITAGAQLVELDLS
DNAFGPDGVQGFEALLKSSACFTLQELKLNNCGMGIGGGKILAAALTECHRKSSAQGKP
LALKVVFVAGRNRLNDGATALAEAFRVIGTLEEVMHPQNGINHPGITALAQAFVNPPL
RVINLNDNTFTTEKGAVAMAETLKLTRQVEVINFGDCLVRSKGAVAIADAIRGGLPKLKE
LNLSCFEIKRDAALAVAEAMADKAELEKLDLNGNTLGEEGCEQLQEVLEGFNMAKVLA
SLSDDEDEEPQQRGQGEKSATPSRKILDP
NTGEPAPVLSSPPPADVSTFLAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVSAFLKVSSV
FKDEATVRMAVQDAVDALMQKAFNSSFSNNTFLTRLLVHMGLLKSEDKVKAIANLYG
PLMALNHMVQQDYFPKALAPLLAFVTKPNSALESCSFARHSLQLTYKV

--

Saccharomyces cerevisiae orf name: YMR309C

Saccharomyces cerevisiae gene name: NIP1

Candida albicans protein:SEQ ID NO:50

MSRFFVSGYTSDSSEEDLLSTSEEELLSSSDEGEDNESDSSFFGEDDDSEESSDDDED
GRPSGPAYFLKKSFLKGAGGDDSDSDSDEGRKVVKSAKDKLLDDMKSSIEIINSNKYN
NNWSIVLGEFDKFRFLRCNQTNLGTPKFYKLLTSLDNSITETSNNERDDKTLKADEAR
AFNLTQRRIKKQIREFQVYDLYKENPEEFDENEDPLESVQAGLNDNVKNEADNSNVG
ALASNRVLSPIFHTLKTISESRGKKNDKLEQIATLEKLLLEANVSKSSPFELISTYQMLLSVR
FDASSNQAFMPLEQWQKNEHDLGKLLDLLEANVDTYQVSELGSTTDDIDIEPVANAQGV
KVIFGSITSSIDRLDELTKSLQHTDPHSIEYVERLKDESTIYNLIVRGQAYVESITPEDVKY
NSEQLARIVLRRLEHIYYKPKQLIKANEEBAWRNIEYNSSIVSKGSSVDEVIDQLTEFLQK
QQKNKTYGKHAILFSIYYYAVNSQYEKAKELFLRSQFYNSNINSAESSLQVQYNRALVQL
GLSAFRAGSIEESHKILNEIVNSQRSKELLGQGFNSKFPNQATVLERQKLLPFHQHINLELL
ECVFMTCSLLIEIPTLAAIANNHKDSKRKNASLSFKSKLDFHQRFFTGPPESIKDHIVHA
SIALQKGDWLKSYNLLSSIKIWKLPDNDKLLAMMKNQLQIEGLRTYIFTYKSVFKKLSIE
KLQQIFQLSKDEVVSILEKMITTGNVSGGEIIDNKFISFTSTTEPQRSKLQELAIVLNEKIQL
LTEKNEKTQSNGYGKKQKNKDQQNQQQNQNNQQNQNNQQNQNNQQNQNNQQNQSSQQSSNNI
LSEESANKFRYANVNSNDEFQATA

Saccharomyces cerevisiae protein:SEQ ID NO:49

MSRFFSSNYEYDVASSSSEEDLLSSSEEDLLSSSSSESELDQESDSSFFNESESESEADVDS
DDSDAKPYGPDWFKKSEFRKQGGGSKNFKLSSNYDSSDEESDEEDGKKVVKSAKEKLL
DEMQDVYNKISQAENSDDWLTISEFDLISRLLVRAQQQNWGTPNIFIKVVAQVEDAVN
NTQQADLKNKAVARA YNTTKQRVKVSRNEDSMKFRNDPESFDKEPTADLDISANG
FTISSSQGNDQAVQEDFFTRLQTIDSRGKKTVNQSSLISTLEELLTVAEKPYEFIMAYLTLI
PSRFDASANLSYQPIDQWKSSFNDISKLLSILDQTIDTYQVNEFADPIDFIEDEPKEDSDGV

Figure 79 (continued)

KRILGSIFSVERLDDEFMKSLNIDPHSSDYLRRLRDEQSIYNLILRTQLYFEATLKDEHDL
 ERALTRPFVKRLDHIYYKSENLIKIMETAAWNIIPAQFKSKFTSKDQLDSADYVDNLIDGL
 STILSKQNNIAVQKRAILYNIYYTALNKDFQTAKDMLLTSQVQTNNQFDSSLQILFNRRVV
 VQLGLSAFKLCLIEECHQILNDLLSSSHLREILGQQSLHRISLNSSNNASADERARQCLPYH
 QHINLDLIDVVFLTCSLLIEIPRMTAFYSGIKVKRIPYSPKSIRRSLEHYDSLKTYFFSFKRFY
 SSFSVAKLAELFDLPENKVVEVLQSVIAELEIPAKLNDEKTIFVVEK

human genbank accession #: AAD03462

human protein:SEQ ID NO:51

MSRFFTTGSDSESESSLSGEELVTKPVGGNYGKQPLLLSEDEEDTKRVVRSKDKRFEEL
 TNLIRTI RNAMKIRDVTKCLEEFELLGKAYGKAKSIVDKEGVPRFYIRILADLEDYLNELW
 EDKEGKKKMNNKNAKALSTLRQKIRKYNRDFESHITSYKQNPESADEDAEKNEEDSE
 GSSDEDEDEDGVSAATFLKKKSEAPSGESRKFLLKMDDEDEDESEDEDEDWDTGSTSS
 DSDSEEEEGKQTALASRFLKKAPTDDKKAEEKKREDKAKKKHDKSKRLDEEEEDN
 EGGEAAENNLGEGVIVKIKFNIIASLYDYNPNLATYMKPEMWGKCLDCINELMDILFANP
 NIFVGENILEESENHNADQPLRVGRCILTLVERMDDEFTKIMQNTDPHSQYVEHLKDE
 AQVCAIHERVQRYLEEKGTTEEVCRIYLLRLHTYKFDYKAHQRLTPPEGSSKSEQDQ
 AENEGEDSAVLMERLCKYIYAKDRTDRITCAILCHYHHALHSRWYQARDLMLMSHL
 QDNIQHADPPVQILYNRTMVQLGICAFRQGLTKDAHNALLDIQSSGRAKELLGQGLLRS
 LQERNQEKEKVERRRQVPFHLHNLELLECVYLVSAMLLEIPYMAAHESDARRRMISKQ
 FHHQLRVGERQPLLGPPEMREHVVAASKAMKMGDWKTCHSFIINEKMNGKVWDLFP
 EADKVRTMLVRKIQEESLRTYLFTYSSVYDSISMETLSDMFELDLPTVHSIISKMIINEELM
 ASLDQPTQTVVMHRTEPTAQQNLAQLAEKLGSLVENNERVFDHKQGTYYGGYFRDQK
 DGYRKNEGYMRRGGYRQQSQQTAY

--

Saccharomyces cerevisiae orf name: YNL036W

Saccharomyces cerevisiae gene name: NCE103

Candida albicans protein:SEQ ID NO:56

MGRENILKYQLEHDHESDLVTEKDQSLLLDNNNNLNGMNNTIKTHPVRVSSGNHNNFPF
 TLSSESTLQDFLNNKFFVDSIKHNHGNQIFDLNGQQSPHTLWIGCSDSRAGDQCLATL
 PGEIFVHRNIANTVNANDISSQGVQFAIDVLKVKKIIVCGHTDCGGIWASLSKKKIGGVLD
 LWLNPVRHIRAANLKLLEEYNQDPKLKAKKLAELNVISSVTALKRHPSASVALKKNEIEV
 WGMLYDVATGYLSQVEIPQDEFEDLFHVHDEHDEEEYNPH

Saccharomyces cerevisiae protein:SEQ ID NO:55

MSATESSSIFTLSHNSNLQDILAANAKWASQMNNIQTLPDHNAKGQSPHTLFIGCSDSR
 YNENCLGVLPGEVFTWKNVANICHSEDLTLKATLEFAHCLKVKNVVICGHTDCGGIKTCL
 TNQREALPKVNCISHLKYLDDIDTMYHEESQNLHLKTQREKSHYLSHCNVKRQFNRIE
 NPTVQTAVQNGELQVYGLLYNVEDGLLQTVSTYTKVTPK

--

Saccharomyces cerevisiae orf name: YNL126W

Saccharomyces cerevisiae gene name: SPC98

Figure 79 (continued)

Candida albicans protein:SEQ ID NO:35

MALNKVQLIKLYSNRLVKSLVPVEFGAIFIQSIINDLQTLLNTSSEEQNLSIINKLKMQF
LSNNLKNEWVEFQNIIVNSLSKFKSLDQICNYLAFLDALRDEKPEDILSTSTASLSPGKQNV
MINTVNTALTLSQLIEPYDITLSEQTILTYLPYTMGLGDSKIFTFSNNYTRLEIPKDINNSFS
SLLREVFEFAILYKQLAIVVDYKGTLLVLAIKTAIYAILEAQLNKYVNDINNIFNNKPNISIL
VVYNSIFPWSILRFLYRVSNRLNRLDGYEFLTFIYSFTNHGDPKIRGIAVTAFTEVVKPY
NIVEHWIVKGELIDNNNEFFIIFDQEQNEFNSIHKLLPKKIPAFIKSSDKIFQIGTTLIFLNKYC
RELKWWNQYNVVKYSAILFNNHQGLASMTTNEMIKLIDLQYNEILTFLTQIIQGNKLLTH
VYNIKRYFFMETNDFIDAIMVKGKDVFNESVNSISSTYLRKVLQDAIQISSVKNFYVDR
LDSRVLPQHGNGWESFTIEYKIDDLPMSTYLFEGHQHLQYLKMFHFLWKLRLQNNLLN
WHFEMFNELNHNVTKLSSRNRRPLAKSLSIITSIRFHFTQFLNELIAYLSYDVIEENFQQH
IVRKLFFYNKNDQDLLNKLFMNLLIEDPNNDLPKFNVNLLTIDELVELHGTIYDSIINSSLL
NEKLKGNETNISYIDQIFDILQTIFNFIIQVRNS

Saccharomyces cerevisiae protein:SEQ ID NO:34

MELEPTLFGIIEALAPQLLSQSHLQTFVSDVVNLLRSSTKSATQLGPLIDFYKLQSLDSPET
TIMWHKIEKFLDALFGIQNTDDMVKYLVSFQSLPSNYRAKIVQKSSGLNMENLANHEH
LLSPVRAPSIYTEASFENMDRFSERRSMVSSPNRYVPSSTYSSVTLRQLSNPYYVNTIPEE
DILKYVSYTLLATTSALFPDHEQIQIPSKIPNFESGLLHLIFEAGLLYQSLGYKVEKFRML
NISPMKKALIEISEELQNYTAFVNNLVSSGTVVSLKSLYREIYENIRLRIYCRFTEHLEELS
GDTFLIELNIFKSHGDLTIRKIATNLFNSMISLYEYLMNWLTKGLLRATYGEFFIAENTDT
NGTDDDDFIYHIPIEFNQERVPFIPKELAYKIFMIGKSYIFLEKYCKEVQWTNEFSKKYHVL
YQSNSYRGISTNFFEINDQYSEIVNHTNQILNQKFHYRDVVFALKNILLMGKSDFM DALI
EKANDILATPSDSLPNYKLTRVLQEAQVQLSSLRHLMNSPRNSSVINGLDARVLDLGHGSV
GWDVFTLDYILYPPLSLVLNVNRPFGKKEYLRIFNFWRFKKNNYFYQKEMLKSNDIIRS
FKKIRGYNPLIRDIINKLSRISILRTQFQQFNSKMESYLYNCIIEENFKEMTRKLQRTENKSQ
NQFDLIRLNNGTIELNGILTPKAEVLTKSSSSKPQKHAIEKTLNIDELESVHNTFLTNL SHK
LFATNTSEISVGDYSGQPYPTSLVLLNSVYEFVKVYCNLNDIGYEIFIKMNLNDHEASNG
LLGKFNTNLKEIVSQYKNFKDRLYIFRADLKNDDGEELFLLSKSLR

human genbank accession #: AAC39727

human protein:SEQ ID NO:36

MATPDQKSPNVLLQNLCRILGRSEADVAQQFQYAVRVIGSNFAPTVERDEFLVAEKIK
KELIRQRREADAALFSELHRKLHSQGVLKNKWSILYLLSLSEDPRRQPSKVSSYATLFA
QALPRDAHSTPYYYARPQTLPLSYQDRSAQSAQSSGSGVSSGIISGLCALS GPAPAPQSL
LPGQSNQAPGVGDCLRQQLGSR LAWTLTANQPSSQATTSGVPSAVSRNMTRSREGD
TGGTMEITEAALVRDILYVFQGDGKNKMNTENCYKVEGKANLSRSLRDTAVRLSEL
GWLHNKIRRYTDQRSIDRSFGLVGQSFCALHQELREYRLLSVLHSQLQLEDDQGVNL
GLESSLTLRLLVWTYDPKIRLKTALALVDHCQGRKG GELASAVHAYTKTGDPYMRSL
VQHILSLVSHPVLSFLYRWYDGELEDYHEFFVASDPTVKTDRLWHDKYTLRKSMIPSF
MTMDQSRKVLLIGKSINFLHQVCHDQPTTKMIAVTKSAESPQDAADLFTDLENAFQGKI
DAAYFETSKYLLDVLNKKYSLLDHMQAMRRYLLLGQGFIRHLMDLLKPELVRPATTL
YQHNLTGILETAVRATNAQFDSPEILRRLDVRLLLEVSPGDTGWDVFSLDYHVDGPATVF
TRECMSHYLRVFNFLWRAKRMEYILTDIRKGHMCNAKLLRNMPFSGVLHQCHILASE

Figure 79 (continued)

MVHFHQMQYYTTFEVLECSWDELWNKVQQAQDLHDHILAAHEVFLDTIISRCLLSDSRA
LLNQLRAVFDQIIELOQAQDAIYRAALEELQRRLQFEEKKKQREIEGQWGVTAEEEEEN
KRIGEFKESIPKMCSQLRILTHFYQGIVQQFLVLLTTSSDESLRFLSFRL--

Saccharomyces cerevisiae orf name: YNL282W

Saccharomyces cerevisiae gene name: POP3

Candida albicans protein:SEQ ID NO:5

MNKS NKVKKPSVAKVSTKAASSSLKSQEAQRQVFRPILDNSFTQSNQWPFIEPTIANDIV
DLLEVLLKMQDSTFKYRGFNPTVSALEKQAAANRGIHKNACVQIKYVVFVCKYDISPATL
TNVFPTLCFTASKSAEDRVKLIQLPRGSLERLSKALGVDRVGIFGLTKDTEGAQPLFDLIN
ENVKDIEAPWLDCIFREEMVFNQPN TKHVASTVGRKKKK

Saccharomyces cerevisiae protein:SEQ ID NO:4

MSGSLKSLDKKIAKRRQVYKPVLDNPFTNEAHMWPRVHDQPLIWQLLQSSIINKLIHIQS
KENYPWELYTDFNEIVQYLSGAHGNSDPVCLFVCNKDPDVPVLVLLQQIPLLCYMAPMTV
KLVQLPKSAMDTFKSVSKYGMILLRCDDRVDKKFVSQIQKNVDLLQFPWLNAIKYRPTS
VKLLKTTVPVSKKRQK

--

Saccharomyces cerevisiae orf name: YNR003C

Saccharomyces cerevisiae gene name: RPC34

Candida albicans protein:SEQ ID NO:2

MSEMLVSDKARHLYTKMREYPTSKLFDQDELQTLFDIKKGSELMEYLQELVNGKYVKIS
KMGDQLKFQTVAAAAKKVSSMSDDEAMISYIEASGREGIWTKTIKAKTNLHQHIVQK
CLKNLENNRYIKSIKSVKHPTRKIYMLYNLQPSIDVTGGPWFTDSELDTEFIETLLEV CWR
FIVGKTMKYKDEEADNEDINPLQTTYHNHHPGVNLDQLVEFINNSNITSVELGINDIRSLC
DVLIIYDDRIEEEVGGNQENSGIFKATWQSIIDKGNITLQNNYQDLKNVSEDCFNLYLQNNQ
SDFS VFQYKSTIQDLQDESDLVYLD SWMNE

Saccharomyces cerevisiae protein:SEQ ID NO:1

MGEVKVKVQPPDADPVEIENRIELCHQFPHGITDQVIQNEPHIEAQQRAVAINRLLSM
GQLDLLRSNTGLLYRIKDSQNAGKMKGSDNQEKL VYQIIE DAGNKGIWSRDIRYKSNLP
LTEINKILKNLESKKLIKAVKSVAAASKKKVYMLYNLQPD RSVTGGA WYSDQDFESEFVE
VLNQQCFKFLQSKAETARESKQNP MIQRNSSFASSHEVWKYICELGISKVELSMEDIETIL
NTLIYDGKVMETIAAKEGTVGSVDGHMKLYRAVNPIIPPTGLVRAPCGLCPVFDDCHEG
GEISPSNCIYMTEWLEF

human genbank accession #: U93869

human protein:SEQ ID NO:3

MSGMIENGLQLSDNAKTLHSQMMSKGIGALFTQQELQKQMGIGSLDLM SIVQELLDKN
LIKLVKQNDLKFQGVLESEAQKKATMSAEEALVYSYIEASGREGIWSKTIKARTNLHQ
HVVLKCLKSLESQRYVKS VKSVKFPTRKIYMLYSLQPSVDITGGPWFTD GELDIEFINSLL
TTVWRFISENTFPNGFKNFENGPKKNVFYAPNVKNYSTTQEILEFITAAQVANVELTPSNI
RSLCEVLVYDDKLEKVTHDCYRVTL ESILQMNQGEGEPEAGNKALEDEEEFSIFNYFKM
FPASKHDKEVVYFDEWTI

FIGURE 80

Saccharomyces cerevisiae orf name: YAL034W-A

Saccharomyces cerevisiae gene name: MTW1

GENBANK Accession Number: BAA77792.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 102

ATGTCTGCTCCCACTATGAGATCCACCTCAATATTGACAGAGCATTTGGGATATCCGCCC
ATCTCGCTTGTTGATGATATCATTAAATGCTGTAAATGAAATTATGTACAAGTGCCTGCT
GCCATGGAAAAATATCTGCTATCCAAGAGCAAAATCGGCGAGGAAGATTATGGAGA
AGAGATCAAAAGTGGAGTTGCTAAGTTGGAATCACTTTTGGAAAACCTCCGTGGATAA
GAATTTTGACAACTAGAACTATATGTTTTGAGGAACGTCCTTCGAATCCCTGAAGA
GTATTTGGACGCCAATGTTTTTAGATTGGAGAACCAAAAGGATCTGGTCATTGTAGA
TGAGAATGAGTTGAAGAAAAGTGAGGAGAACTTCGAGAGAAAAGTGAACGACGTGG
AGTTAGCGTTCAAAAAGAATGAAATGCTATTGAAAAGAGTTACAAAAGTGAAGAAGAC
TGTTGTTTACGATAAGAGGATTCAAACAAAAGCTAAACGAGTTACTGAAATGCAAAG
ACGATGTACAATTGCAGAAAATTTTGGAGTCGTTAAACCTATAGATGACACAATGA
CTCTACTGACTGATTCAATTACGTAACTATATGTTGATAGTGAAAGTACCAGTTCAAC
AGAGGAGGTAGAGGCACTACTGCAGAGATTGAAGACCAACGGGAAGCAAAAATAATA
AGGATTTTCAAGACACGATATATCGATATAAGGACGAATAATGTCCTACGAAAATTGG
GGCTACTAGGTGATAAAGAGGACGAAAAACAGTCTGCCAAGCCGGATGCGAGGACG
CAAGCAGGGGATATAGTTAGTATAGATATTGAAGAGCCT

Candida albicans nucleic acid: SEQ ID NO: 103

ATGTCAGATAAACTTTAGACGAACGTACTACAGCAATTCTTACTGAACATTTAGAAT
TTGCTCCCTTGACACTTATTGATGACGTGATCAATGCGGTGAATGAAATCATGTACAA
GGGAACAACAGCTATTGAAACATATTTAAAAGAACAAAAACAATTAATGAAAAATGG
GATATTTACCAAAGTTACTGAAGATGAAATAGAAATTGGTATGGGGAAATTAGAATC
ATTATTAGAATCGACTATAGATAAGAATTTTGATAAATTTGAATTATATTGTTAAGA
AATATTTTCAATATACCTAAAGATCTAATACCATATATACAGTTAAGCCATCAACAAG
GAATTGAATTTAAAAGTGATAATGTTGAACAAAAACGTGAATTTGATCAACAAATTA
AAAATTTACAATTGAAAATCATGCAAGAATTACAACCTTCGAAAAATCTTAAATTTAC
AACTTGTCAAAGTCCAAAAATTAATTAAGTATTAATAGCCATTGATAATGATTTCAA
GAAAATAGATTTTGCTAGTGGTGGTGGTGAATGAAGAATCAATAAGAATTTTGAA
AAATCTTCAACCTATTGATGAAACATTATATTTTTTAATTAGTCAAATTAATAATCTA
ATAAATCAAATTTGAACAATTATCAAATAAAGTTAATACCAATTTGAAAACCTCAAAAA
TTTATACCAATTTGCGTGATAAATTCATTGATGGTAGAACATTTAGAGTTTACAAC
AAACGGGGATTTGGAAAGATTTGGAAAAAATGATATCAAGATTCTGGTGCAGGGA
AATGACAATAATAATAATAATAATAATAATAATAATACCTTAACAGATTTACAA
AATCAAGACGACATTGATATGATAATACCAGAACAAGACGATATAGATGTGGATGCA
ATAAAGAATATAAATGCTCAAATTTAA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YBR060C

Saccharomyces cerevisiae gene name: ORC2

GENBANK Accession Number: CAA85003.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 132

```
ATGCTAAATGGGGAAGACTTTGTAGAGCATAATGATATCCTATCGTCTCCGGCAAAA
AGCAGGAATGTAACCCCAAAAAGGGTTGACCCACATGGAGAAAGACAACCTGAGAAG
AATTCATTCATCAAAGAAGAATTTGTTGGAAAGAATCTCGCTTGTAGGCAACGAAAG
GAAAAATACATCTCCAGATCCGGCACTCAAACCTAAAACGCCAAGTAAAGCTCCCCG
TAAACGTGGAAGACCAAGAAAGATACAGGAAGAATTAAGTATAGGATCAAGAAGG
ATGAGAAAGATACAATTTCTCTAAGAAAAAGAGGAAATTGGACAAAGATACATCAG
GTAATGTCAATGAGGAAAGCAAGACTTCTAACAACAAGCAGGTGATGGAAAAGACG
GGGATAAAAGAGAAAAGAGAACGCGAAAAAATACAGGTAGCGACCACAACATATGA
AGATAATGTGACTCCACAACTGATGATAATTTTGTATCAAATTCACCCGAGCCACCA
GAACCTGCAACACCATCTAAGAAGTCTTTAACCCTAATCATGATTTTACTTCGCCCC
TAAAGCAAATTATAATGAATAATTTAAAAGAATATAAAGACTCAACCTCCCCAGGTA
AATTAACCTTGAGTAGAAATTTTACTCCAACCCCTGTACCGAAAAATAAAAAGCTCTA
CCAACTTCGGAAACCAAGTCAGCAAGCTCGTTTTTGGATACTTTTGAAGGATATTTT
GACCAAAGAAAAATGTGTCAGAACTAATGCGAAGTCAAGGCACACCATGTCAATGGCA
CCTGACGTTACCAGAGAAGAGTTTTCCCTAGTATCAAACTTTTTCAACGAAAATTTT
AAAAACGTCCCAGGCAAAAGTTATTTGAAATTCAGAAAAAATGTTTCCCCAGTATT
GGTTTGAATTGACTCAAGGATTCTCCTTATTATTTTATGGTGTAGGTTGAAACGTAA
TTTTTTGGAAGAGTTTGCCATTGACTACTTGTCTCCGAAAATCGCGTACTCGCAACTG
GCTTATGAGAATGAATTACAACAAAACAAACCTGTAAATTCATCCCATGCCTTATTT
TAAATGGTTACAACCTAGCTGTAACCTATCGTGACGTCTTCAAAGAGATTACCGATCT
TTTGGTCCCCGCTGAGTTGACAAGAAGCGAAACTAAGTACTGGGGCAATCATGTGAT
TTTGCAGATCCAAAAGATGATTGATTTCTACAAAAATCAACCTTTAGATATCAAATTA
ATACTTGTAGTGCATAATCTGGATGGTCTAGCATAAGGAAAAACACTTTTCAGACGATG
CTAAGCTTCCTCTCCGTCATCAGACAAATCGCCATAGTCGCCTCTACAGACCACATTTAC
GCTCCGCTCCTCTGGGACAACATGAAGGCCCAAACTACAACCTTTGTCTTTCATGATATT
TCGAATTTTGAACCGTCGACAGTCGAGTCTACGTTCCAAGATGTGATGAAGATGGGT
AAAAGCGATACCAGCAGTGGTGCTGAAGGTGCGAAATACGTCTTACAATCACTTACT
GTGAACTCCAAGAAGATGTATAAGTTGCTTATTGAAACACAAATGCAGAATATGGGG
AATCTATCCGCTAACACAGGTCCTAAGCGTGGTACTCAAAGAACTGGAGTAGAACTT
AAACTTTTCAACCATCTCTGTGCCGCTGATTTTATTGCTTCTAATGAGATAGCTCTAA
GGTCGATGCTTAGAGAATTCATAGAACATAAAATGGCCAACATAACTAAGAACAATT
CTGGAATGGAAATTATT
```

Candida albicans nucleic acid: SEQ ID NO: 133

```
ATGTCACACTCAAATGCTCTACCAAATAGTCCATTCCGGTCACCTAAAAAACAACGTA
TGGAGGTCATAGGACCACTCAATGCGTCTCGTTTTTCCTTTTCGCCGGTAAAGACACC
TCCTCATGGGAGAGCTGGTCTATCATCTCCAGAGAAAAGATTAGTCAAAGACCTTGA
```


FIGURE 80 (CONT'D)

CAAGTCGGCGAGAAAAAGAGCCAACAATAGCTTATATAACCGATTAATGGATGAGTA
TCTGGACACAGATGATTATTTGGATGAACAAGATAGGATATTGGCCGACAGAATTAT
CAAACAGTCGAGGGGAGAACCCGACGAAGTCAATTATGGCAGCGACGTGGAATTGG
AAATTGATCTAACTCAGCAGAGACGAACCCGAAGAAGAGAAAAAGAAAGTTGTTTACT
CGAGCGATAGTAGCAACGAATATGAGGATACAGGAATGCCAGAAGAATCTTCAAGC
GAGGAAGAAGAGGCAGATGATGATGATGGCAATGTGGAGTTTGTATGGACCACCC
AAAGAAAGAAAAACGTCGTTATCAAGCTCACCACCCACAGTCAAGCCTACTGTGCGC
CGAACCAAGCGAGGTAGACCAAGCAAGAGTGAGCTTGTCTGGGTCAAATCAAAAGT
ATATTCCATCAAGATGACGTGTTGTTTCAAGTACAGATAGAAAAACGTTACACCCGACT
AAACCAACCGCAGCGAAAAAACAGTCAGCAATTATTTGACATCTATTTTTGATCAA
AATTTGATAGAAGCAAGGTGCCAAGTCTAAGTGGAATTCCCAAATCAACCAACACG
CATGAAGAGAAGAAAACGTTTGTGCCGCTTCTTATCCACCCCTCGATGCTGACGGA
AATATCACTGACAAGGAGTACATCTCCAAATACTTTGATGGAGTTGACCCTGCAAAG
TTCAAAGAAGGCAGGTTTGTGGACGAAAAAGTATTTTACTTAGAAGGGCCAGAAAGGA
TACTTTGAACAGCAAACTACCAGAGTTAAACAAAGTGGCAACTCTTTAACAGCATTG
GCACCCAGATTGAGTACAAAGATTTTGCCAGGTTAGTAAAGTTGGGCGACAACCTC
AGTTTCCAACGCAACGCCACCTTTTTCGAATTGCACAAGTATATCTATCACCAGTGGT
GTTTTGAAATGTCACAAGGGTTCAATTTGAATTTCTACGGAGTCGGATCCAAAATCGATC
TACTCCGAGATTTTGGCACAACCTATTTTGGCATCTGGTGGGAAAATGTGGTACACGCCG
ATTTGCCAAAGGTTTTGGTGGTTAACGGTTTTAACCTAGCATCAATATCAAAAACTAA
TTCTCGAAATCGCTTCCATCTTTTGGCAAACGAAGTGTACCCAAAACATATAGCTGGAA
CGGTTCCCTTTGTGGTTGATTATCTAAACAACCATAGACTGCCCTGTGGAAGTATCGGTT
TCCATAAACCCAAAATCTTGTGATTATTCACAATCTTGATGGGGAAGTTTTAGAGTAG
ACAAGACACAGACGCTTTTGTGCAATTAATGACACTACCAGAAGTATGGGCCATGT
CATCTACCGACCACATCAATGCATCATTGTTATGGGACCTGTCCAAAGTTAAAACTT
GAATTTCTCTGGCATAATCTCACAACATATGCCACTTACCAACGAGAAACATCTTTC
CGAGACGTGATAAGTTTAGGCAAATCCAAAAAATTTGTGGGTGGCCTTGGTGCCAAG
TATGTCTTGCGCTCGCTTACCGACAATCACCAGAACCTTACCGCGAGCTATTGATTG
CACAATTGGATAAAATGGAGAAAGCTGTCCCATCTGCTTCTGGAAGAGTGGGTTTGA
AAGGTAATGCCAAGGTTGCTGTTGACCTAAAAAGCCTATACAATACATGTTTGGACG
AGTTCATTACTTCCAACGAGATGAACCTTTAGAACATTCTTAAAAGAGTATGTTGAGCA
TAAAATGTGTCAGCTAGTAAAAGATCCTTCAGGAGTTGAGAAGGTATTCATTCCGTT
CACATACGAAGAGATACAAAACATATATAAGCAAGAATTTGATGTATAGTGGGTACC
CTACACGTATGCGGAACCTTGAAAACTTCTGAAAACCGTTTTAAATACTCTATAA

Human GENBANK Accession Number: GI:4433811

Human nucleic acid sequence: SEQ ID NO: 134

GGCGCGAATTACTGGAAATTGGCTTTTCCCGTTGGGGCCGAAGGTACCTTCCCTGCG
GCGGCGACTCAGCGGGGTGTCGTTCCGGCCGGCGTGACGCAGCCGGATCGGCGCCAG
ACGGAACCTAGCGGTGACTGTATCTGAATTTTGCAGCTGCAGAATGTGTAGTACCT
TAAAAGGTTGGCAACAATGAGTAAACCAGAATTAAAGGAAGACAAGATGCTGGAGG

FIGURE 80 (CONT'D)

TTCAC TTTGTGGGAGATGATGATGTTCTTAATCACATTCTAGATAGAGAAGGAGGAG
CTAAATTGAAGAAGGAGCGAGCGCAGCTTTTGGTCAACCCCAAAAAATAATAAAGA
AGCCAGAATATGATTTGGAGGAAGATGACCAGGAGGTCTTAAAAGATCAGAACTATG
TGGAAATTATGGGAAGAGATGTTCAAGAATCATTGAAAAATGGCTCTGCTACAGGTG
GTGGAAATAAAGTTTATTCTTTTCAGAATAGAAAACACTCTGAAAAGATGGCTAAAT
TAGCTTCAGAACTAGCAAAAACACCACAAAAAAGTGTTTCATTTCAGTTTGAAGAATG
ATCCTGAGATTACGATAAACGTTCTCTCAAAGTAGCAAGGGCCATTCTGCTTCAGACA
AGGTTCAACCGAAGAACAATGACAAAAGTGAATTTCTGTCAACAGCACCTCGTAGTC
TAAGAAAAAGATTAATAGTTCCAAGGTCTCATTCTGACAGTGAAAGCGAATATTCTG
CTTCCAACCTCAGAGGATGATGAAGGGGTTGCACAGGAACATGAAGAGGACACTAAT
GCAGTCATATTCAGCCAAAAGATTCAAGCTCAGAATAGAGTAGTTTCAGCTCCTGTT
GGCAAAGAAACACCTTCTAAGAGAATGAAAAGAGATAAAACAAGTGACTTAGTAGA
AGAATATTTTGAAGCTCACAGCAGTTCAAAAGTTTTAACCTCTGATAGAACACTGCA
GAAGCTAAAGAGAGCTAAACTGGATCAGCAAACCTTTGCGTAACTTATTGAGCAAGGT
TTCCCTTTCCTTTTCTGCCGAACCTTAAACAACCTAAATCAACAGTATGAAAAATTATTT
CATAAATGGATGCTGCAATTACACCTTGGGTTCAACATTGTGCTTTATGGTTTGGGTTCT
AAGAGAGATTTACTAGAAAGGTTTCGAACCACTATGCTGCAAGATTCCATTACGTTGTC
ATCAATGGCTTCTTTCTGGAATCAGTGTGAAATCAGTCCTGAATTCTATAACAGAAGAA
GTCTCTGATCATATGGGTACTTTCCGCAGTATACTGGATCAGCTAGACTGGATAGTAAAC
AAATTTAAAGAAGATTCTTCTTTAGAACTCTTCCTTCTCATCCACAATTTGGATAGCCAG
ATGTTGAGAGGAGAGAAGAGCCAGCAAATCATTGGTCAGTTGTCATCTTTGCATAAC
ATTTACCTTATAGCATCCATTGACCACCTCAATGCTCCTCTCATGTGGGATCATGCAA
AGCAGAGTCTTTTAACTGGCTCTGGTATGAACTACTACATACAGTCCTTATACTGA
AGAAACCTCCTATGAGAACTCTCTTCTGGTAAAGCAGTCTGGATCCCTGCCACTTAGC
TCCCTTACTCATGTCTTACGAAGCCTTACCCCTAATGCAAGGGGAATTTTCAGGCTAC
TAATAAAATACCAGCTGGACAACCAGGATAACCCCTTCTTACATTGGCCTTTCTTTTCA
AGATTTTACCAGCAGTGTGCGGAGGCATTCTCGTCAATAGTGATCTGACACTCCG
GGCCAGTTAACTGAATTTAGGGACCACAAGCTTATAAGAACAAGAGGGGAAGTGA
TGGAGTAGAGTATTTATTAATTCCTGTTGATAATGGAACATTGACTGATTTCTTGGAA
AAGGAAGAAGAGGAGGCTTGAAGCTTTCCTTTATTCTTGAATCTCCCATGGAAGGGT
TGTAACCCAGCTGCCACTCCTCTAGTTGAAAAGTGTTGTGTTTACATCTGACATTAAT
TATTTTCCAGCATACAAGATTTAAATTTGGGAAGGGGGGATGTCTCAATTAGAA
CTTTTGTATCAGCCTGGCTGGTACCGTCTAGTACTATGCAGCGGTCTCAAGTTGGAG
AAAATGTGCCTTTCATTTCATTACCTCTCTGGAGACTTCTTGCTGGAATGAACAGTGTG
CTCAGGGACTATTTGGAACCTGGATGTTTTTGAATTATTTTATACTTAGAGATATTCTG
AATTTTTTGAAGGCTTTTAACTCCCGAGCTGATTGTTTGCAAGTGTGTTTGTTC
CAGAGTGTGGAAGTATAAAGACATGGGCATCACGTAAATTGGTTTTGTTTGTCTATTC
TGTGTGTCAGAACCAACGAGTGTAATGGAGAGGGCAGGTCATCTTATTGTTTCTA
AAACAACCTAAAAGGTGTAGATTGGGAAGAGGTGAGTGATCCAGCTTTCTCCTTTTG
GATTGAGGCTATGACTTGGTGGGGCAGGGGAGGGAATATATTATAATACTATTCA
GTTGGGATAATGGGAAAAACAGAGTATATAGGGTATCTACCCAGCCTAGAAAGCACA
GGAACAATACGTCATATATTTGGAACAGTTATTGTCTGTGCCATGACCTTCA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YBR088C

Saccharomyces cerevisiae gene name: POL30

GENBANK Accession Number: CAA85038.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 93

ATGTTAGAAGCAAATTTGAAGAAGCATCCCTTTTCAAGAGAATAATTGATGGTTTCAAA
GATTGTGTCCAGTTGGTCAATTTCCAATGTAAGAAGATGGTATCATTGCACAAGCTGTC
GATGACTCAAGAGTTCTATTGGTCTCCTTGGAATAGGTGTCTGAAGCCTTCCAAGAATAT
AGATGTGACCATCCTGTTACGTTAGGTATGGATCTAACCTCACTAAGTAAAATCCTACGT
TGTGGTAACAACACCGATACATTAACACTAATTGCTGACAACACACCGGATTCCATCATC
TTATTATTTGAGGATACCAAGAAAGACCGTATAGCCGAATACTCTCTGAAATTGATGGAT
ATCGATGCTGATTTCTTAAAGATTGAAGAATTACAGTACGACTCCACCCTGTCATTGCCA
TCTTCCGAATTCTCTAAAATTGTTTCGTGACTTGTCCCAATTGAGTGATTCTATTAATATC
ATGATCACCAAAGAAACAATAAAGTTTGTAGCTGACGGTGATATCGGATCAGGTTCA
GTCATAATAAAACCATTTCGTGGATATGGAACATCCTGAAACAAGCATCAAACCTTGAA
ATGGATCAACCTGTCGACTTGACGTTTCGGAGCTAAATATTTATTGGACATCATTAAG
GGCTCCTCCCTTTCTGATAGAGTTGGTATCAGGCTCTCCAGCGAAGCTCCTGCTTTAT
TCCAATTTGAT

Candida albicans nucleic acid: SEQ ID NO: 94

ATGTTAGAAGGTAAATTTGAAGAAGCTGCTTTATTAAAAAAAGTTGTTGAAGCCATT
AAAGATTGTGTTAAAAAATGTAACCTCAATTGTTTCAGAGCATGGGATTACTGTACAA
GCAGTGGATGATTCTCGTGTATTATTAGTTTCATTATTAATTGGTCAAACCTTCTTTCA
GTGAATATAGATGTGACAGAGACGTTACATTAGGTATTGACTTGGAAGTTTCAGTA
AGATTATCAAATCTGCTAACAATGAAGATTTCTTGACCCTTTTAGCTGAAGATTCACC
AGATCAAATAATGGCTATTCTTGAAGAAAAACAAAAAGAGAAAATCAGTGAATATTC
TTTAAATTAATGGATATTGATTCTGAATTTTACAAATTGATGATATGGAATACGAT
GCTGTTGTGAATATGCCAAGTAGTGATTTTGCTAAACTTGTGAGGGATTGAAAAAT
TTAAGTGAATCTTTACGTGTTGTTGTTACTAAAGATTCCGTCAAGTTTACATCTGAAG
GTGATTCTGGTTCCGGAAGTGTTATCTTGAAACCTTACACCAACTTGAAAAATGAAA
GAGAAAGTGTCACTATTAGTTTAGATGACCCAGTTGATTTGACTTTTGGTTTGAAATA
CTTGAATGATATTGTGAAGGCAGCTACATTATCCGATGTCATCACCATCAAATTGGCC
GATAAACTCCTGCATTGTTTGAATTTAAATGCAATCTGGAGGTTATTTGAGATTCT
ACTTGGCACCAAAATTCGATGATGATGAGTAG

Human GENBANK Accession Number: GI:181271

Human nucleic acid sequence: SEQ ID NO: 95

AGGTCTCAGCCGGTCGTCGCGACGTTCCGCCGCTCGCTCTGAGGCTCCTGAAGCCGA
AACTAGCTAGACTTTCTCCTTCCCGCCTGCCTGTAGCGGCGTTGTTGCCACTCCGCC
ACCATGTTTCGAGGCGCGCCTGGTCCAGGGCTCCATCCTCAAGAAGGTGTTGGAGGCA
CTCAAGGACCTCATCAACGAGGCCTGCTGGGATATTAGCTCCAGCGGTGTAACCTG

FIGURE 80 (CONT'D)

CAGAGCATGGACTCGTCCACGTCTCTTTGGTGCAGCTCACCCCTGCGGTCTGAGGGC
TTCGACACCTACCGCTGCGACCGCAACCTGGCCATGGGCGTGAACCTCACCAGTATG
TCCAAAATACTAAAATGCGCCGGCAATGAAGATATCATTACACTAAGGGCCGAAGAT
AACGCGGATACCTTGGCGCTAGTATTTGAAGCACCAAACCAGGAGAAAGTTTCAGAC
TATGAAATGAAGTTGATGGATTAGATGTTGAACAACCTTGAATTCCAGAACAGGAG
TACAGCTGTGTAGTAAAGATGCCTTCTGGTGAATTTGCACGTATATGCCGAGATCTCA
GCCATATTGGAGATGCTGTTGTAATTTCCCTGTGCAAAAGACGGAGTGAAATTTTCTG
CAAGTGGAGAACCTTGGAAATGGAAACATTAAATTGTACAGACAAGTAATGTGCGATA
AAGAGGAGGAAGCTGTTACCATAGAGATGAATGAACCAGTTCAACTAACTTTTGCAC
TGAGGTACCTGAACTTCTTTACAAAAGCCACTCCACTCTCTTCAACGGTGACACTCAG
TATGTCTGCAGATGTACCCCTTGTGTAGAGTATAAAATTGCGGATATGGGACACTTA
AAATACTACTTGGCTCCCAAGATCGAGGATGAAGAAGGATCTTAGGCATTCTTAAAA
TTCAAGAAAATAAACTAAGCTCTTTGAGAACTGCTTCTAAGATGCCAGCATATACT
GAAGTCTTTTCTGTACCAAATTTGTACCTCTAAGTACATATGTAGATATTGTTTTCT
GTAAATAACCTATTTTTTTTCTCTATTCTCTCCAATTTGTTTAAAGAATAAAGTCCAAA
GTCTGATCTGGTCTAGTTAACCTAGAAGTATTTTTGTCTCTTAGAAATACTTGTGATT
TTTATAATAAAAAGGGTCTTGACTCTAAATGCAGTTTTAAGAAGTGTTTTT

Saccharomyces cerevisiae orf name: YBR155W

Saccharomyces cerevisiae gene name: CNS1

GENBANK Accession Number: CAA85114.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 35

CCAATCAAAGGATTGACCCAGAGAACAAATCAATTTTGAATATGTTATCAGTGATTG
ATAGAAAAGAACAAGAATTGAAAGCAAAGAAGAAAAACAGCAAAGAGAAGCTCAG
GAACGTGAAAACAAGAAAATTATGTTAGAGAGCGCAATGACGCTGAGAAACATAAC
TAACATCAAACTCACTCTCCAGTAGAGTTACTTAATGAGGGTAAAATAAGGCTAGA
AGACCCAATGGATTTTGAATCTCAATTGATCTATCCCGCATTAATTATGTACCCACG
CAAGATGAATTTGATTTTGTAGGTGAAGTAAGTGAGTTAACTACTGTGCAAGAACTT
GTTGACCTAGTTTGGAAAGGGCCGCAAGAACGCTTCAAAAAGAAGGTAAAGGAAAA
CTTCACACCAAAGAAAGTGTTGGTGTTCATGGAAACAAAGGCAGGTGGTTTGATTAA
AGCTGGTAAGAACTGACATTTACGATATCTTGAAGAAAGAGTCGCCAGATGTACC
ATTGTTGATAACGCTTTGAAAATATATATTGTGCCAAAGGTAGAAAGTGAAGGGTG
GATTTCCAAGTGGGATAAGCAAAAAGCCTTAGAAAGAAGATCTGTGTGA

Candida albicans nucleic acid: SEQ ID NO: 36

ATGTCCAAAATAGAGCCAGTCACTGAAAAAGAAGAATAACGTTTCCGAATGGGAT
AGAAGAAGATATGTTCCCAAAGCAGGTGAACCTGAATTACCTCCCCAATTATCAGAA
TTCTCTAACAAGACCACAGACGAGGTTATTGAGGAATTGAATAGATTGCCATTTTTTA
TGACAAAAGTTAGATGAACTGATGGAGATGGCGGAGAAAATGTAACTTGGAAAGCA
CTTAAAAGTTTGGCATATGAAGGTGATCCTGACGAAATTGCCTCAAATTTCAAAAAT

FIGURE 80 (CONT'D)

CAGGGGAATAATTGTTACAAATTTAAAAAATACAAAGATGCAATTATATTTTATACG
AAAGGTCTTGAAGTAACTGTGACGTGGACGCAATCAATTCAGCATTATACTTGAAT
CGTGCTGCTTGTAACTTGGAGTTGAAAAATTACCGTCGGTGCATTGAAGATTGTAAG
AAAGTATTAATGCTTGATGAGAAGAATATTAAGGCTTGTTCCGTTTCAGGAAAGGCA
TTCTTTGCAATTGAAAAATACGATGAAGCAATCAAAGTGCTTGAATACGGTCTAAAT
ATAGAACCAGAAAACAAAGATTTACAGAAATTATTACAGCAAGTTCAAAAGAGGCAA
GAAACTTTAGCTCAAATAAAAAGCTAAAAAGGCACAAGAAGAGGAACAAGAGCGGTT
GAAAAATATCGTGTTGGAGAATTCTATAAAATTAAGACACATTGAAATAGTGAAGTC
CTCATCTCCTCCAGAAGTCTTGAAGACTGCCAAGATACGATTGGAAGACCCCAAAGA
TTATCAGTCACAATTAATATTCCCTGCTATGATACTATACCCCACCACCGATGAATTT
GACTTTATTGCAGAAATAAGCGAATTAAGTACTCCTTTGGAATTGCTAGAGATGGTAT
TAAATAGACCTAGGGAATGGTTTGATGATCCAAAACACAAGGATTTCAATGTCAAAA
AATTGGAATGCTTTATGGAACTGAATCTGGTGGGTTGATTAAAGTGGGCAAGAAAA
TTGAAGTTAACAATGCTTTGATGAATGAAAAACCTAAGGCACCATTGTTTGATAACG
CTTTAAGACTTTATGTCGTTCCAAAATTAGACGTCGCCAAATGGACATCTGAATGGA
ATAAAGAAACCGCCTTGGCAGCTCGTAAATAG

Human GENBANK Accession Number: NM_004623.1

Human nucleic acid sequence: SEQ ID NO: 37

CTGGGACCCGGGCTGGAAGGCAGGGCATCAGCTATGGAACAACCTGGGCAGGATCC
CACCTCAGACGACGTCATGGACTCGTTCCTGGAAAAGTTCCAGAGCCAGCCTTACCG
TGGCGGCTTTCATGAGGACCAGTGGGAGAAGGAATTTGAAAAGGTCCCCCTATTTAT
GTCGAGAGCGCCATCAGAAATTGATCCCAGGGAGAATCCTGACTTGGCTTGTCTCCA
GTCAATTATTTTTGATGAGGAGCGTTCTCCAGAAGAACAGGCCAAGACCTATAAAGA
TGAGGGCAATGATTACTTTAAAGAAAAAGACTACAAGAAAGCTGTAATTTCATACAC
TGAAGGCTTAAAGAAGAAATGTGCAGATCCTGATTTGAATGCTGTCCTTTATACCAA
CCGGGCAGCAGCACAGTACTATCTGGGCAATTTTCGTTCTGCTCTCAATGATGTGACA
GCTGCCAGAAAGCTAAAACCCTGCCACCTCAAAGCAATAATAAGAGGTGCCTTATGC
CATCTGGAAGTATACACTTTGCCGAGGCCGTGAAGTGGTGTGATGAGGGACTGCAA
ATAGATGCCAAAGAGAAGAAGCTTCTGGAAATGAGGGCTAAAGCAGACAAGCTGAA
GCGAATTGAACAGAGGGATGTGAGGAAAGCCAACTTGAAAGAAAAGAAGGAGAGGA
ATCAGAATGAGGCTTTACTCCAGGCCATCAAGGCTAGGAATATCAGGCTCTCAGAAG
CTGCCTGTGAGGATGAAGATTCAGCCTCAGAAGGTCTAGGTGAGCTTTTCCTGGATG
GACTCAGCACTGAGAACCCCATGGAGCCAGGCTGAGTCTAGATGGCCAGGGCAGG
CTGAGCTGGCCTGTGCTCTTTCTGTACCCAGAGTATGCCAGTCGGACTTCATCTCTG
CTTTTCATGAGGACTCCAGGTTTATTGATCATCTAATGGTGATGTTTGGTGAAACACC
TTCTTGGGACCTAGAGCAAAAATATTGCCTGATAATTTGGAGGTCTACTTTGAGGAT
GAGGACAGGGCAGAACTATACCGGGTGCCTGCCAAGAGCACCTTGCTACAGGTTCTA
CAGCACCAGAGGTACTTTGTAAAAGCCCTGACACCAGCATTTTTGGTCTGTGTAGGAT
CCTCTCCTTTTTGCAAGAATTTCTCCGGGGGAGAAAGGTGTACCAGATACGATGACTAA
GCCAGGGCCCCTGGATCTCCTCCCTTACCCTCCTCTGCTGGGAACCTAGCACACCTGAAT

FIGURE 80 (CONT'D)

CAGCTGGACATACTGCTGGAGTCCAGTGCTTTCTTTCCGTCACCCTGGGGATAGTCCTTC
CTGGCATCGTGGTGGGGGAGGAGCCTCTGGCTTCCCTAAACTGCAGCTCTCTGGCTG
GTCTTCACTTTCTCAGTTGATATAAACTCTGGTCTTGGCCATGATGTCCTTGGATT
CCATCGCTAAAGGGACCATCTGCTGCAGTTACCACAGCAACTGACTTGAGCGGCACC
TGGTCTGTGGAGATGGACTCAGGATCCAGTGACATGATTCTGAACTTTTGTGGAGTT
TGACACCTTAGAGAAGCTACCCCTCAAAGTGCACATCTACACACAAACAAACAATGC
ATAGGATTCCAAGGCTTTAAAGCTGAGAGACCCTGGCCTCAAGTTATTTTCATGCGCA
CAGAGGGAAGCCATGTGGGGTTGCTGAAGATGCCTTGAGGTGAAATGGGGGCAGGA
AAGCCACATCTTGCTCTGCATTTATAAAGACCGTACAAACTCAGATCCTTGGTACCCC
TAAAAAGATTGCCAATTTTCTTCATCTTTGCCATATGGAGGACTGTGACAGACTTTGG
ACAGTGGCCTCTTGAGTTCCTCTGCAGTTTGTGACATTTAGGATTTTGTGTCTTTTAAA
CTGGAAAATCTTCTAGCATGTTGGGTTGTTACAGAGTATATTTTTGTCTGCAGCTGTT
TGTTGCCCCATTCTAAGAGGAGTTTATCCATCCTGAAAAAAAAAAAAAAAAAAAAA

Saccharomyces cerevisiae orf name: YDL235C

Saccharomyces cerevisiae gene name: YPD1

GENBANK Accession Number: CAA98815.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 138

ATGTCTACTATTCCTCAGAAATCATCAATTGGACCATCTTAAATGAAATTATATCTATG
GATGACGATGATTCCGATTTTTCTAAAGGTCTAATTATTCAATTTATCGACCAGGCACAA
ACAACTTTTGCTCAAATGCAACGACAGCTGGACGGTGAAAAAATCTTACCGAATTA
GACAATCTGGGCCATTTTTTAAAGGGTTCTTCTGCTGCATTAGGCTTACAAAGAATTG
CCTGGGTTTGTGAAAGAATTCAAACTTGGGAAGAAAAATGGAACATTTCTTCCCCA
ACAAGACCGAATTGGTCAACACTCTGAGCGATAAATCGATTATTAATGGAATCAATA
TTGATGAAGATGACGAGGAAATAAAGATACAAGTGGACGATAAAGACGAAAATTCC
ATATATCTCATCTTGATAGCAAAAGCTTTGAACCACTAGGTTGGAGTTCAAAGTGG
CGAGAATTGAGTTATCTAAATATTACAACACAAACCTATAA.

Candida albicans nucleic acid: SEQ ID NO: 139

ATGTCAGAAGATAAATTACAAAAATTACAAGACTCAGGACTTGTGCGACTGGGCAGTG
TTTAGTGAAATAGTGACCATGGACGAGGATGAAGAAGGGTTTTCCAAATCACTAGTA
GAAGTCTTTGTTAGCCAAGTGGAAGAAACATTTGAAGAAATTGATAAATATTTAAAG
GAAAAGAATTTGGAGAAATTGTCATCGTCGGGTCATTTTTTGAAGGATCTGCTGCT
GCTTTGGGGTTGACCAAAATTTCAAATCAATGCGAACGAATTCAAAATATGGCCAT
AAGATCAACTTTGACAATTTCAATTGGAAGATATAAAAACTAAAGGCGATTGCGCC
GTAAGTGCGGAAAATGTGGCCGTTAATGATGGTGAACTAATCCAGAAAATGGATCC
AATGGCAACGAAACAAGTAATAACAAAACAAATACTAGCAATATACCGGATGAATCA
AGCGATGACTTTTGGATAGCATTAAATTGAGGATGCATTAGCCAAGGCGAGAGATGGA
TTCGACCAATCTAGAAGAGCATTGGACGAATATTACGAATAG

FIGURE 80 (CONT'D)

Human GENBANK Accession Number: Z15005.1

Human nucleic acid sequence: SEQ ID NO: 140

ATGGCGGAGGAAGGAGCCGTGGCCGTCTGCGTGCGAGTGCGGCCGCTGAACAGCAG
AGAAGAATCACTTGGAAGTAAATCCTTCAATTTTGATCGTGCTTTTCATGGTAATGAA
TATCAAGTTGATGGAAGTAAATCCTTCAATTTTGATCGTGCTTTTCATGGTAATGAA
ACTACCAAAAATGTGTATGAAGAAATAGCAGCACCAATCATCGATTCTGCCATACAA
GGCTACAATGGTACTATATTTGCCTATGGACAGACTGCTTCAGGAAAAACATATACC
ATGATGGGTTCAGAAGATCATTTGGGAGTTATACCCAGGGCAATTCATGACATTTTC
CAAAAAATTAAGAAGTTTCCTGATAGGGAATTTCTCTTACGTGTATCTTACATGGAAA
TATACAATGAAACCATTACAGATTTACTCTGTGGCACTCAAAAAATGAAACCTTTAAT
TATTCGAGAAGATGTCAATAGGAATGTGTATGTTGCTGATCTCACAGAAGAAGTTGT
ATATACATCAGAAATGGCTTTGAAATGGATTACAAAGGGAGAAAAGAGCAGGCATTA
TGGAGAAACAAAAATGAATCAAAGAAGCAGTCGTTCTCATACCATCTTTAGGATGAT
TTTGGAAAGCAGAGAGAAGGGTGAACCTTCTAATTGTGAAGGATCTGTAAAGGTATC
CCATTTGAATTTGGTTGATCTTGCAGGCAGTGAAGAGCTGCTCAAACAGGCGCTGC
AGGTGTGCGGCTCAAGGAAGGCTGTAATATAAATCGAAGCTTATTTATTTTGGGACA
AGTGATCAAGAACTTAGTGATGGACAAGTTGGTGGTTTCATAAATTATCGAGATAG
CAAGTTAACACGAATTCCTCAGAATTCCTTGGGAGGAAATCCAAAGACACGTATTAT
CTGCACAATTACTCCAGTATCTTTTGATGAAACTCTTACTGCTCTCCAGTTTGCCAGT
ACTGCTAAATATATGAAGAATACTCCTTATGTTAATGAGGTATCAACTGATGAAGCTC
TCCTGAAAAGGTATAGAAAAGAAATAATGGATCTTAAAAAACAATTAGAGGAGGTTT
CTTTAGAGACGCGGGCTCAGGCAATGGA AAAAGACCAATTGGCCCAACTTTTGGAAAG
AAAAAGATTTGCTTCAGAAAGTACAGAATGAGAAAATTGAAAACCTTAACACGGATG
CTGGTGACCTCTTCTCCCTCACGTTGCAACAGGAATTAAGGCTAAAAGAAAACGA
AGAGTTACTTGGTGCCTTGGCAAAATTAACAAAATGAAGAACTCAAATATGCAGAT
CAATTTAATATACCAACAAATATAACAACAAAAACACATAAGCTTTCTATAAATTTAT
TACGAGAAATTGATGAATCTGTCTGTTTCAGAGTCTGATGTTTTTCAGTAACACTCTTGA
TACATTAAGTGAGATAGAATGGAATCCAGCAACAAAGCTACTAAATCAGGAGAATAT
AGAAAGTGAGTTGAACTCACTTCGTGCTGACTATGATAATCTGGTATTAGACTATGA
ACAACTACGAACAGAAAAAGAAGAAATGGAATTGAAATTA AAAAGAAAAGAATGATT
TGGATGAATTTGAGGCTCTAGAAAAGAAAACTAAAAAAGATCAAGAGATGCAACTA
ATTCATGAAATTTGAACTTAAAGAATTTAGTTAAGCATCGAGAAGTATATAATCAA
GATCTTGAGAATGAACTCAGTTCAAAAGTAGAGCTGCTTAGAGAAAAGGAAGACCAG
ATTAAGAAGCTACAGGAATACATAGACTCTCAAAAGCTAGAAAATATAAAAATGGAC
TTGTCATACTCATTGGAAGCATTGAAGACCCAAAAACAAATGAAGCAGACTCTGTTT
GATGCTGAAACTGTAGCCCTTGATGCCAAGAGAGAATCAGCCTTTCTTAGAAGTGAA
AATCTGGAGTTGAAGGAGAAAATGAAAGAACTTGCAACTACATACAAGCAAATGGA
AAATGATATTCAGTTATATCAAAGCCAATTGGAGGCCAAAAAGAAAATGCAAGTTGA
TCTGGAGAAAAGATTACAATCTGCTTTTAATGAGATAACAAAACCTCACCTCCCTTATA
GATGGCAAAGTTC AAAAGATTTGCTCTGTAATTTGGAATTGGAAGGAAAGATTACT
GATCTTCAGAAAGAACTAAATAAAGAAGTTGAAGAAAATGAAGCTTTGCGGGAAGA

FIGURE 80 (CONT'D)

AGTCATTTTGCTTTCAGAATTGAAATCTTTACCTTCTGAAGTAGAAAAGGCTGAGGAAA
GAGATACAAGACAAATCTGAAGAGCTCCATATAATAACATCAGAAAAAGATAAATTG
TTTTCTGAAGTAGTTCATAAGGAGAGTAGAGTTCAAGGTTTACTTGAAGAAATTGGG
AAAACAAAAGATGACCTAGCAACTACACAGTCGAATTATAAAAGCACTGATCAAGAA
TTCCAAAATTTCAAAACCCTTCATATGGACTTTGAGCAAAAGTATAAGATGGTCCTTG
AGGAGAATGAGAGAATGAATCAGGAAATAGTTAATCTCTCTAAAGAAGCCCCAAAAT
TTGATTTCGAGTTTGGGTGCTTTGAAGACCGAGCTTTCTTACAAGACCCAAGAACTTCA
GGAGAAAACACGTGAGGTTCAAGAAAGACTAAATGAGATGGAACAGCTGAAGGAAC
AATTAGAAAATAGAGATTCTCCGCTGCAAACTGTAGAAAGGGAGAAAACACTGATTA
CTGAGAACTGCAGCAAACTTTAGAAGAAGTAAAACTTTAACTCAAGAAAAAGATG
ATCTAAAACAACTCCAAGAAAGCTTGCAAATTGAGAGGGACCAACTCAAAGTGATA
TTCACGATACTGTTAACATGAATATAGATACTCAAGAACAATTACGAAATGCTCTTGA
GTCTCTGAAACAACATCAAGAAACAATTAATACACTAAAATCGAAAATTTCTGAGGA
AGTTTCCAGGAATTTGCATATGGAGGAAAATACAGGAGAAAATAAAGATGAATTTCA
GCAAAAGATGGTTGGCATAGATAAAAAACAGGATTTGGAAGCTAAAAATACCCAAA
CACTAACTGCAGATGTTAAGGATAATGAGATAATTGAGCAACAAAGGAAGATATTTT
CTTTAATACAGGAGAAAAATGAACTCCAACAAATGTTAGAGAGTGTTATAGCAGAAA
AGGAACAATTGAAGACTGACCTAAAGGAAAATATTGAAATGACCATTGAAAACCAG
GAAGAATTAAGACTTCTTGGGGATGAACTTAAAAAGCAACAAGAGATAGTTGCACAA
GAAAAGAACCATGCCATAAAGAAAGAAGGAGAGCTTTCTAGGACCTGTGACAGACT
GGCAGAAGTTGAAGAAAACTAAAGGAAAAGAGCCAGCAACTCCAAGAAAAACAGC
AACAACTTCTTAATGTACAAGAAGAGATGAGTGAGATGCAGAAAAAGATTAATGAAATA
GAGAATTTAAAGAATGAATTAAGAACAAGAATTGACATTGGAACATATGGAAACA
GAGAGGCTTGAGTTGGCTCAGAACTTAATGAAAATTATGAGGAAGTGAAATCTATA
ACCAAAGAAAGAAAAGTTCTAAAGGAATTACAGAAGTCATTTGAAACAGAGAGAGA
CCACCTTAGAGGATATATAAGAGAAATTGAAGCTACAGGCCTACAAACCAAGAAGA
ACTAAAAATTGCTCATATTCACCTAAAAGAACCAAGAACTATTGATGAACTAAG
AAGAAGCGTATCTGAGAAGACAGCTCAAATAATAAATACTCAGGACTTAGAAAAATC
CCATACCAAATTACAAGAAGAGATCCCAGTGCTTCATGAGGAACAAGAGTTACTGCC
TAATGTGAAAAAAGTCAGTGAGACTCAGGAAACAATGAATGAACTGGAGTTATTAAC
AGAACAGTCCACAACCAAGGACTCAACAACACTGGCAAGAATAGAAATGGAAAGGC
TCAGGTTGAATGAAAAATTTCAAGAAAGTCAGGAAGAGATAAAATCTCTAACCAAGG
AAAGAGACAACCTTAAAACGATAAAAAGAAGCCCTTGAAGTTAAACATGACCAGCTGA
AAGAACATATTAGAGAACTTTGGCTAAAATCCAGGAGTCTCAAAGCAAACAAGAAC
AGTCCTTAAATATGAAAGAAAAAGACAATGAACTACCAAAATCGTGAGTGAGATGG
AGCAATTCAAACCCAAAGATTTCAGCACTACTAAGGATAGAAATAGAAATGCTCGGAT
TGTCCAAAAGACTTCAAGAAAGTCATGATGAAATGAAATCTGTAGCTAAGGAGAAAG
ATGACCTACAGAGGCTGCAAGAAGTTCTTCAATCTGAAAGTGACCAGCTCAAAGAAA
ACATAAAAGAAATTGTAGCTAAACACCTGGAACTGAAGAGGAACTTAAAGTTGCTC
ATTGTTGCCTGAAAGAACAAGAGGAACTATTAATGAGTTAAGAGTGAATCTTTCAG
AGAAGGAACTGAAATATCAACCATTCAAAGCAGTTAGAAGCAATCAATGATAAAT
TACAGAACAAGATCCAAGAGATTTATGAGAAAGAGGAACAACCTTAATATAAAACAAATT

FIGURE 80 (CONT'D)

AGTGAGGTTTCAGGAAAACGTGAATGAACTGAAACAATTCAAGGAGCATCGCAAAGC
CAAGGATTCAGCACTACAAAGTATAGAAAGTAAGATGCTCGAGTTGACCAACAGACT
TCAAGAAAGTCAAGAAGAAATACAAATTATGATTAAGGAAAAAGAGGAAATGAAAA
GAGTACAGGAGGCCCTTCAGATAGAGAGAGACCAACTGAAAGAAAACACTAAAGAA
ATTGTAGCTAAAATGAAAGAATCTCAAGAAAAAGAATATCAGTTTCTTAAGATGACA
GCTGTCAATGAGACTCAGGAGAAAATGTGTGAAATAGAACACTTGAAGGAGCAATTT
GAGACCCAGAAGTTAAACCTGGAAAACATAGAAACGGAGAATATAAGGTTGACTCA
GATACTACATGAAAACCTTGAAGAAATGAGATCTGTAACAAAAGAAAGAGATGACCT
TAGGAGTGTGGAGGAGACTCTCAAAGTAGAGAGAGACCAGCTCAAGGAAAACCTTA
GAGAACTATAACTAGAGACCTAGAAAAACAAGAGGAGCTAAAAATTGTTACATGC
ATCTGAAGGAGCACCAAGAACTATTGATAAACTAAGAGGGATTGTTTCAGAGAAAA
CAAATGAAATATCAAATATGCAAAAGGACTTAGAACACTCAAATGATGCCTTAAAG
CACAGGATCTGAAAATACAAGAGGAACCTAAGAATTGCTCACATGCATCTGAAAGAGC
AGCAGGAACTATTGACAACTCAGAGGAATTGTTTCTGAGAAGACAGATAAACTAT
CAAATATGCAAAAAGATTTAGAAAATTCAAATGCTAAATTACAAGAAAAGATTCAAG
AACTTAAGGCAAATGAACATCAACTTATTACGTTAAAAAAAGATGTCAATGAGACAC
AGAAAAAAGTGTCTGAAATGGAGCAACTAAAGAAACAAATAAAAGACCAAAGCTTA
ACTCTGAGTAAATTAGAAATAGAGAATTTAAATTTGGCTCAAGAACTTCATGAAAAC
CTTGAAGAAATGAAATCTGTAATGAAAGAAAGAGATAATCTAAGAAGAGTAGAGGA
GACACTCAAACCTGGAGAGAGACCAACTCAAGGAAAAGCCTGCAAGAAAACCAAAGCTA
GAGATCTGGAAATACAACAGGAACTAAAACTGCTCGTATGCTATCAAAAAGAACACA
AAGAACTGTTGATAAACTTAGAGAAAAAATTCAGAAAAGACAATTCAAATTTTCAG
ACATTCAAAAGGATTTAGATAAATCAAAAAGATGAATTACAGAAAAAGATCCAAGAAC
TTCAGAAAAAAGAACTTCAACTGCTTAGAGTGAAAGAAGATGTCAATATGAGTCATA
AAAAAATTAATGAAATGGAACAGTTGAAGAAGCAATTTGAGCCAACTATCTATGCA
AGTGTGAGATGGATAACTTCCAGTTGACTAAGAACTTCATGAAAGCCTTGAAGAAA
TAAGAATTGTAGCTAAAGAAAGAGATGAGCTAAGGAGGATAAAAGAATCTCTCAA
ATGGAAAGGGACCAATTCATAGCAACCTTAAGGGAATGATAGCTAGAGACCGACA
GAACCACCAAGTAAAACCTGAAAAAAGGTTACTAAGTGATGGACAACAGCACCTTAT
GGAAAGCCTGAGAGAAAAGTGCTCTAGAATAAAAGAGCTTTTGAAGAGATACTCAG
AGATGGATGATCATTATGAGTGCTTGAATAGATTGTCTCTTGACTTGGAGAAGGAAA
TTGAATTCCACAGAATCATGAAGAACTGAAGTATGTGTTAAGCTATGTTACAAAAA
TAAAGAAGAACAACATGAATGCATCAATAAATTTGAAATGGATTTTATTGATGAAG
TGGAAAAGCAAAAGGAATTGCTAATTAATAACAGCACCTTCAACAAGATTGTGATG
TACCATCCAGAGAATTAAGGGATCTCAAATTGAACCAGAATATGGATCTACATATTG
AGGAAATTCTCAAAGATTTCTCAGAAAGTGAGTTCCCTAGCATAAAGACTGAATTTT
AACAACTACTAAGTAATAGGAAAGAAATGACACAGTTTTTGAAGAGTGGTTAAATACT
CGTTTTGATATAGAAAAGCTTAAAAATGGCATCCAGAAAGAAAATGATAGGATTTGT
CAAGTGAATAACTTCTTTAATAACAGAATAATTGCCATAATGAATGAATCAACAGAG
TTTGAGGAAAGAAGTGCTACCATATCCAAAGAGTGGAACAGGACCTGAAATCACTG
AAAGAGAAAAATGAAAACTATTTAAAACTACCAAACATTGAAGACTTCCTTGGCA
TCTGGTGCCCAGGTTAATCCTACCACACAAGACAATAAGAATCCTCATGTTACATCAA

FIGURE 80 (CONT'D)

GAGCTACACAGTTAACCACAGAGAAAATTCGAGAGCTGGAAAATTCAGTGCATGAAG
CTAAAGAAAGTGCTATGCATAAGGAAAGCAAGATTATAAAGATGCAGAAAGAACTT
GAGGTGACTAATGACATAATAGCAAACTTCAAGCCAAAGTTCATGAATCAAATAAA
TGCCTTGAAAAACAAAAGAGACAATTCAAGTACTTCAGGACAAAGTTGCTTTAGGA
GCTAAGCCATATAAAGAAGAAATTGAAGATCTCAAAATGAAGCTTGTGAAAATAGAC
CTAGAGAAAATGAAAATGCCAAAGAATTTGAAAAGGAAATCAGTGCTACAAAAGC
CACTGTAGAATATCAAAAGGAAGTTATAAGGCTATTGAGAGAAAATCTCAGAAGAAG
TCAACAGGCCCAAGATACCTCAGTGATATCAGAACATACTGATCCTCAGCCTTCAA
TAAACCTTAACTTGTGGAGGTGGCAGCGCATTGTACAAAACACAAAAGCTCTTAT
TTTGAAAAGTGAACATATAAGGCTAGAAAAAGAAATTTCTAAGTTAAAGCAGCAAAA
TGAACAGCTAATAAAACAAAAGAATGAATTGTTAAGCAATAATCAGCATCTTTCCAA
TGAGGTCAAACTTGGAAGGAAAGAACCCTTAAAAGAGAGGCTCACAAACAAGTAA
CTTGTGAGAATTCTCCAAAGTCTCCTAAAGTGACTGGAACAGCTTCTAAAAAGAAAC
AAATTACACCTCTCAATGCAAGGAACGGAATTTACAAGATCCTGTGCCAAAGGAAT
CACCAAAATCTTGTTTTTTTGTAGCCGATCAAAGTCTTTACCATCACCTCATCCAGTT
CGCTATTTTGATAACTCAAGTTTAGGCCTTTGTCCAGAGGTGCAAAATGCAGGAGCA
GAGAGTGTGGATTCTCAGCCAGGTCCTTGGCACGCCTCCTCAGGCAAGGATGTGCCT
GAGTGCAAACTCAGTAG

Saccharomyces cerevisiae orf name: YDR299W

Saccharomyces cerevisiae gene name: BFR2

GENBANK Accession Number: AAB64735.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 110

ATGGAAAATCACTAGCGGATCAAATTTCCGATATCGCCATTAAACCGGTCAATAAA
GACTTCGATATTGAAGATGAGGAAAATGCATCTTTATTTCAACACAATGAAAAAAT
GGAGAAAGTGATTTAAGCGACTATGGAAATAGCAACACAGAAGAAACCAAGAAGGC
GCACTATTTGGAGGTGGAAAAGTCTAAGTTAAGAGCAGAAAAAGGTTTAGAACTAAA
CGATCCAAAATATACAGGTGTTAAAGGTTCAAGACAAGCATTATATGAAGAAGTTTC
CGAGAATGAGGACGAAGAAGAAGAAGAAGAAGAGGAAGAAGAAAAAGAGGAAGAT
GCTCTTTCATTACAGGACAGATTCTGAAGATGAAGAAGTAGAGATTGATGAAGAAGAA
TCAGACGCGGACGGCGGTGAAACGGAGGAGGCTCAACAGAAAAGGCATGCACTATC
GAACTAATTCAACAAGAGACTAAACAAGCTATTAACAACTGTCTCAATCAGTTCA
AAGAGATGCTTCGAAGGGTTATTCCATTTTACAACAGACAAAATTATTTGACAACAT
CATTGATTTGAGAATAAACTACAAAAAGCTGTAATTGCAGCAAATAAGCTCCCATT
AACTACAGAGTCCTGGGAAGAGGCTAAAATGGATGATTACAGAGGAAACAAAGCGTT
TGCTGAAGGAAAACGAAAACTGTTCAATAATTTATTCAATCGGTTGATAAATTTCA
GAATAAAATTCCAACTTGGCGATCATATCACTCAAAATGAAGAGGTGGCGAAGCATA
AATTGTCCAAAAAAGATCTCTCAAAGAGCTTTACCAAGAACTAATAGCTTAGACT
CAGAACTAAAAGAGTACAGGACTGCCGTATTAACAAGTGGTCTACCAAGTTTCTT
CTGCATCAGGTAACGCTGCTTTATCATCTAACAATTCAAAGCTATCAACTTACCTGC

FIGURE 80 (CONT'D)

AGATGTACAAGTCGAAAACCAATTATCCGATATGTCCCGTTTGATGAAAAGAACAAA
GTTGAACAGGAGAAACATAACGCCTTTGTATTTCCAAAAAGACTGTGCTAATGGCAGG
CTACCAGAATTGATTTCTCCCGTTGTCAAAGATAGTGTTGATGACAATGAGAATTCGGAT
GATGGGCTTGATATCCCGAAAACTATGACCCAAGAAGAAAGGATAACAATGCCATT
GACATTACCGAAAACCCATATGTTTTTGATGACGAAGATTTTTACCGTGTTTTACTAA
ACGATTTAATTGACAAAAAGATTTCCAACGCTCACAATTCTGAAAGTGCAGCAATTA
CAATCACCTCAACTAATGCTCGTTTGAACAACAAGCTAAAGAAGAATATCGATACTA
AGGCTTCCAAGGGTAGGAAATTGAACTACTCAGTTCAAGATCCAATTGCGAATTATG
AAGCCCCCATCACATCCGATACAAATGGTCAGACGACCAAAATCGATGAATTCCTTG
CGGGATTGTTAGGTCAACGAGTGAACCTTAATGAAAATGAGGATGAGGAACAACATG
CCAGAATAGAAAATGACGAA

Candida albicans nucleic acid: SEQ ID NO: 111

ATGAGCTTCTTCGGCTTACACTTTCAACTTAATTCATTGACATTGAACATTTCAAATA
TGGCAAAAAAGTCTTTATCAGAGCAAATTTCTAGTTTATATACACCAAAGACTGATTA
TGATATTGAGGATCATGATTTAGATGTATCTAAAGACAATGGCATTTTTCAGCATCAT
GACGGTGGTTCTGAAAACGAATCTGAAGACGAGGATACTGGCTTAAGAAATGAGCAT
TATGTTGAATCTTCAAAATCAAAGTTGAGACAACAGAATGAAGGTGTGAACCTGGGG
GAAAAATACGTGGGCAATGTCACAAGCAGAAGCAAATTGTATGACGATGAGGATGA
CAAACAACCAACAGAAGCTAGCTCCGGAGAGGAGTTAGATGCTGAATCAGCGGAAG
AAGAAGAGGATGAAGAATCTGAAGATGTAGCAGATGATGATGAAGATGACCAAGAG
TCAGATCGCAGTAGCTCAAGTGATGCAGAGAATGACGAGGACGAGAACATTTACAC
AAAAGGGAATTATTAACAATTAATGAGCAAAGAGAGAAGTCACATCGTTAACAGA
TTATCCCAATCAGCAACAAATGATGCATTAAGGTTATTCAATACAACAGCAAAAC
AAAACTTTTGAAAAATCATTGATGTGAGGTTGAAATTTGAGAAATCGGTAACCTCA
AGTAATATGTTACCTATAAATACAAGTACATATTCAGAAACCAAATCTGAAGATAGC
GATGAATTAGTGACTAAAGCCAAGAAACAATTGTATAGTTTGTGGATCATTATTAC
ACTTAGAAACGAAGTAGACGAAAGTACCTCAGTCAAGACCCCCAAAAACGATCATT
TGCTAAATATTCGGAGGTTACATCTGCTGCAGATGCACAATTGAATTCCTCGTAAAC
CAAATATTAACCAAGTGGTCAGCTAAAGTTGCCAATTCATCCGGTAGAAATGCCATG
AATGCTAATAAATTCAAACTATAAACCAATCTTTTGAACAACAGGTTAACAACAAC
TTGTCTGACATGGATAGATTAATCAAAGAACAATAATTGAACCGAAGAAACGTAAC
CCCATTGGTTATACCACCAAGAGGAGGATGATCATGAAAATGGCAATAAAAAACAA
TCTATCGACGAGGACGACGACGATATCCCGAAGATACTTCTGTTTCGTAAGAAAACC
CAAGGCTTGGAATGATTATATATTTGATGACGAAGATTTCTATAGAGTATTGTTG
AATGATTTAGTCGACAAGAAAGTGCAAACAAGTGATCCAACATCAGGTATAACTATC
AGTTTAAGAGCTGCTCAAAAGTCCAATAAATTGAAAAATAATGTTGATACAAAAGCA
TCTAAAGGTAGGAAATTGAGATATCACGTGCAAGAACCAATTGCTAATTTTGAACT
TCAAGAGGCAGCTGGAGATGGAATGATGATCAAATTGACGAGTTTTTCGCATCTTTA
TTGGGCCAAAAGGTCAATATGAATGAGATAGATGATGAACAAGAAGAACAAGA
GAATGATGATAATGATATTATCCAGAGGATAACCGAATCCAGTTGTTTGGTTAA

FIGURE 80 (CONT'D)

Human GENBANK Accession Number: NM_000055

Human nucleic acid sequence: SEQ ID NO: 112

AGTAACAGTTGATTGTTACATTACAGTAACACTGAATGTCAGTGCAGTCCAATTTACAGGC
TGGAGCAGCAGCTGCATCCTGCATTTCCCCGAAGTATTACATGATTTTCACTCCTTGCAA
ACTTTACCATCTTTGTTGCAGAGAATCGGAAATCAATATGCATAGCAAAGTCACAATCAT
ATGCATCAGATTTCTCTTTTGGTTTCTTTTGCTCTGCATGCTTATTGGGAAGTCACATAC
TGAAGATGACATCATAATTGCAACAAAGAATGGAAAAGTCAGAGGGATGAACTGA
CAGTTTTTGGTGGCACGGTAACAGCCTTTCTTGGAATTCCCTATGCACAGCCACCTCT
TGGTAGACTTCGATTCAAAAAGCCACAGTCTCTGACCAAGTGGTCTGATATTTGGAA
TGCCACAAAATATGCAAATTCCTTGCTGTCAGAACATAGATCAAAGTTTTCCAGGCTTC
CATGGATCAGAGATGTGGAACCCAAACACTGACCTCAGTGAAGACTGTTTATATCTA
AATGTATGGATTCCAGCACCTAAACCAAAAAATGCCACTGTATTGATATGGATTTAT
GGTGGTGGTTTTCAAACCTGGAACATCATCTTTACATGTTTATGATGGCAAGTTTCTGG
CTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTGGGTGCCCTAGGAT
TCTTAGCTTTGCCAGGAAATCCTGAGGCTCCAGGGAACATGGGTTTATTTGATCAAC
AGTTGGCTCTTCAGTGGGTTCAAAAAATATAGCAGCCTTTGGTGGAAATCCTAAAA
GTGTAACCTCTCTTTGGAGAAAGTGCAGGAGCAGCTTCAGTTAGCCTGCATTTGCTTTC
TCCTGGAAGCCATTCAATTGTTCAACAGAGCCATTCTGCAAAGTGGATCCTTTAATGCT
CCTTGGGCGGTAACATCTCTTTATGAAGCTAGGAACAGAACGTTGAACTTAGCTAAA
TTGACTGGTTGCTCTAGAGAGAATGAGACTGAAATAATCAAGTGTCTTAGAAATAAA
GATCCCCAAGAAATTCCTCTGAATGAAGCATTTGTTGTCCCCTATGGGACTCCTTTGT
CAGTAAACTTTGGTCCGACCGTGGATGGTGATTTTCTCACTGACATGCCAGACATATT
ACTTGAACCTTGGAACAATTTAAAAAAACCCAGATTTTGGTGGGTGTTAATAAAGATGA
AGGGACAGCTTTTTTAGTCTATGGTGCTCCTGGCTTCAGCAAAGATAACAATAGTATC
ATAACTAGAAAAGAATTTCAAGGAAGGTTTAAAAATATTTTTTCCAGGAGTGAGTGAG
TTTGGAAAGGAATCCATCCTTTTTTATTACACAGACTGGGTAGATGATCAGAGACCT
GAAAACCTACCGTGAGGCCTTGGGTGATGTTGTTGGGGATTATAATTTTCATATGCCCT
GCCTTGGAGTTACCAAGAAGTTCTCAGAATGGGGAAATAATGCCTTTTTTCTACTATT
TTGAACACCGATCCTCCAAACTTCCGTGGCCAGAATGGATGGGAGTGATGCATGGCTA
TGAAATTGAATTTGTCCTTTGGTTTACCTCTGGAAAGAAGAGATAATTACACAAAAGCCGA
GGAAATTTTGAGTAGATCCATAGTGAAACGGTGGGCAAATTTTGCAAAATATGGGAA
TCCAAATGAGACTCAGAACAATAGCACAAGCTGGCCTGTCTTCAAAAAGCACTGAACA
AAAATATCTAACCTTGAATACAGAGTCAACAAGAATAATGACGAAACTACGTGCTCA
ACAATGTCGATTCTGGACATCATTTTTTCCAAAAGTCTTGGAATGACAGGAAATATT
GATGAAGCAGAATGGGAGTGGAAAGCAGGATTCCATCGCTGGAACAATTACATGAT
GGACTGGAAAAATCAATTTAACGATTACACTAGCAAGAAAGAAAGTTGTGTGGGTCT
CTAATTAATAGATTTACCTTTATAGAACATATTTTCTTTAGATCAAGGCAAAAATA
TCAGGAGCTTTTTTACACACCTACTAAAAAAGTTATTATGTAGCTGAAACAAAAATGC
CAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTACCTAGCATTTCAA
AACCCAAATGGCTAGAACATGTTTAAATTAATTTTACAATATAAAGTTCTACAGTTAA
TTATGTGCATATTAACAATGGCCTGGTTCAATTTCTTTCTTTCTTAATAAATTTAA
GTTTTTCCCCCAAATATCAGTGCTCTGCTTTTAGTCACGTGTATTTTCATTACCA

FIGURE 80 (CONT'D)

CTCGTAAAAAGGTATCTTTTTTAAATGAATTAAATATTGAAACACTGTACACCATAGT
TTACAATATTATGTTTCCTAATTAAAATAAGAATTGAATGTCAATATGAGATATTTAA
ATAAGCACAGAAAATC

Saccharomyces cerevisiae orf name: YDR311W

Saccharomyces cerevisiae gene name: TFB1

GENBANK Accession Number: AAB64747.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 104

ATGTCACATTCCGGAGCTGCCATTTTTGAGAAAGTTTCTGGGATAATTGCCATAAATGAG
GATGTTTCACCCGCAGAATTGACATGGAGGTCTACGGACGGTGACAAGGTTACACA
GTTGTCTTATCCACTATTGACAAGTTACAAGCTACCCCTGCTTCCAGTGAAAAATGA
TGTTGAGGCTAATCGGGAAGTGGATGAGTCAAAAAAGAGAAAAGACAACGAAGGA
AATGAGGTTGTGCCCCAACCGCAACGTCATATGTTTTCGTTTAAACAATAGAACAGTT
ATGGATAATATCAAGATGACCCTTCAACAAATCATCTCACGGTATAAAGATGCAGAT
ATCTACGAAGAAAAGAGAAGAAGAGAGGAGTCTGCGCAACACACAGAAACACCAAT
GAGCTCTTCTTCTGTTACTGCAGGGACTCCCACACCACATCTCGATACACCACAATTG
AATAATGGGGCTCCGTTGATTAATACAGCCAACTAGATGATTCTCTCTCTAAAGAA
AAATTGTTGACCAATTTAAAGCTACAGCAATCTTTACTGAAAGGAAACAAAGTTCTA
ATGAAGGTTTTTCAGGAAACAGTCATTAACGCCGGTTTGCCTCCATCTGAATTTTGGT
CAACTAGAATTCCGTTATTGAGGGCTTTTGCCTTATCTACTTCTCAAAAAGTTGGGCC
TTACAACGTTTTGTCAACTATCAAGCCGGTGGCTTCATCGGAAAACAAAGTCAATGTT
AATTTGTCAAGAGAAAAAATTTTGAATATTTTGAAGAACTATCCAATTGTAAAGAAA
GCTTACACTGATAATGTGCCCCAAAATTTCAAAGAACCAGAGTTCTGGGCAAGGTTT
TTCTCTTCGAAGTTATTCAGAAAATTAAGGGGTGAAAAGATCATGCAAAATGATAGA
GGTGACGTAATCATTGACAGGTACTTGACATTGGATCAAGAGTTTCGACAGAAAAGAT
GATGACATGCTATTGCATCCTGTGAAAAAAATTATAGATTTAGATGGTAACATACAG
GACGACCCAGTTGTACGAGGCAACAGGCCCGACTTCACTATGCAGCCAGGTGTGGAT
ATTAATGGTAATAGCGATGGTACCGTGGACATCTTAAAGGGTATGAATAGATTGAGT
GAAAAAATGATTATGGCTTTGAAGAATGAGTATTCAAGGACAAATCTACAGAAC
AAATCTAATATTACAAACGATGAGGAAGATGAAGATAATGATGAAAGAAATGAACT
GAAAATCGATGACTTAAACGAAAGCTACAAGACAACTATGCAATCATACATCTGAA
AAGGAACGCACATGAAAAGACAACCGACAACGATGCGAAAAGCTCGGCAGACTCGA
TAAAGAATGCAGATTTGAAGGTTTCTAATCAACAAATGTTACAACAGTTGTCATTGG
TCATGGATAATTTAATTAATAAGCTAGACTTGAACCAAGTAGTTCCTAACACGAAG
TCAGCAACAAGATCAATAAAAAGAGTCATAACTGCAATCAAGATTAACGCCAAACAGG
CTAAGCATAACAATGTTAATTCAGCACTCGGCTCTTTTGTGACAACACTTCTCAAGC
AAATGAATTAGAGGTGAAAAGTACCCTACCAATAGACCTATTAGAAAGTTGTAGAAT
GCTACACACAACGTGCTGTGAATTTCTAAAGCACTTTTATATTCAATTTTCAGAGCGGT
GAACAAAAGCAAGCCAGTACCGTCAAAAACTTTATAATCATTTGAAGGACTGTATT
GAAAAGCTGAATGAGCTATTTCAAGACGTCCTTAATGGTGATGGTGAATCTATGTCA
AACACATGTACCGCCTATTTGAAGCCAGTTTTGAAGTCCATTACTTTGGCTACTCATA

FIGURE 80 (CONT'D)

AGTACGATGAGTACTTCAACGAATATAACAACAATTCGAACTAGGATGTTTCACCCG
CAGAATTGACATGGAGGTCTACGGACGGTGACAAGGTTACACAGTTGTCTTATCCA
CTATTGACAAGTTACAAGCTACCCCTGCTTCCAGTGAAAAAATGATGTTGAGGCTAA
TCGGGAAAGTGAGTCAAAAAAGAGAAAAGACAACGAAGGAAATGAGGTTGTG
CCCAAACCGCAACGTCATATGTTTTCGTTTAAACAATAGAACAGTTATGGATAATATCA
AGATGACCCTTCAACAAATCATCTCACGGTATAAAGATGCAGATATCTACGAAGAAAAG
AGAAGAAGAGAGGAGTCTGCGCAACACACAGAAACACCAATGAGCTCTTCTTCTGTT
ACTGCAGGGACTCCCACACCACATCTCGATACACCACAATTGAATAATGGGGCTCCG
TTGATTAATACAGCCAAACTAGATGATTCTCTCTCTAAAGAAAAATTGTTGACCAATT
TAAAGCTACAGCAATCTTTACTGAAAGGAAACAAAGTTCTAATGAAGGTTTTTCAGG
AAACAGTCATTAACGCCGGTTTGCCTCCATCTGAATTTTGGTCAACTAGAATTCGGTT
ATTGAGGGCTTTTGCCTTATCTACTTCTCAAAAAGTTGGGCCTTACAACGTTTTGTCA
ACTATCAAGCCGGTGGCTTCATCGGAAAACAAAGTCAATGTTAATTTGTCAAGAGAA
AAAATTTTGAATATTTTGGAGAACTATCCAATTGTAAAGAAAGCTTACACTGATAATG
TGCCCCAAAATTTCAAAGAACCAGAGTTCTGGGCAAGGTTCTTCTCTTCGAAGTTATT
CAGAAAATTAAGGGGTGAAAAGATCATGCAAAATGATAGAGGTGACGTAATCATTG
ACAGGTACTTGACATTGGATCAAGAGTTCGACAGAAAAGATGATGACATGCTATTGC
ATCCTGTGAAAAAAATTATAGATTTAGATGGTAACATACAGGACGACCCAGTTGTAC
GAGGCAACAGGCCCGACTTCACTATGCAGCCAGGTGTGGATATTAATGGTAATAGCG
ATGGTACCGTGGACATCTTAAAGGGTATGAATAGATTGAGTGAAAAAATGATTATGG
CTTTGAAGAATGAGTATTCAAGGACAAATCTACAGAACAAATCTAATATTACAAACG
ATGAGGAAGATGAAGATAATGATGAAAGAAATGAACTGAAAATCGATGACTTAAAC
GAAAGCTACAAGACAACTATGCAATCATACATCTGAAAAGGAACGCACATGAAAA
GACAACCGACAACGATGCGAAAAGCTCGGCAGACTCGATAAAGAATGCAGATTTGA
AGGTTTCTAATCAACAAATGTTACAACAGTTGTGATTGGTCATGGATAATTTAATTAA
TAAGCTAGACTTGAACCAAGTAGTTCCTAACAACGAAGTCAGCAACAAGATCAATAA
AAGAGTCATAACTGCAATCAAGATTAACGCCAAACAGGCTAAGCATAACAATGTTAAT
TCAGCACTCGGCTCTTTTGTGCAACACTTCTCAAGCAAATGAATTAGAGGTGAAAAGT
ACCCTACCAATAGACCTATTAGAAAGTTGTAGAATGCTACACACAACGTGCTGTGAATTT
CTAAAGCACTTTTATATTCAATTTTCAAGAGCGGTGAACAAAAGCAAGCCAGTACCGTCAA
AACTTTATAATCATTTGAAGGACTGTATTGAAAAGCTGAATGAGCTATTTCAAGACGTC
CTTAATGGTGATGGTGAATCTATGTCAAACACATGTACCGCCTATTTGAAGCCAGTTTTG
AACTCCATTACTTTGGCTACTCATAAGTACGATGAGTACTTCAACGAATATAACAACAAT
TCGAACTAGATGGAAGTACAGCCCACTCTTTTTGGTATAATAGAGGCATTGGCTCCTC
AATTATTGTGCGCAGAGTCATTTGCAGACATTTGTATCTGATGTAGTCAATTTACTGCG
ATCATCCACCAAATCGGCAACTCAATTAGGCCCTTTAATTGATTTTTACAAATTACAA
TCACTAGATTCGCCTGAAACAACAATTATGTGGCATAAAAATTGAGAAATTTCTCGAT
GCTTTATTTGGAATCCAGAACACCGATGATATGGTAAAGTACCTCTCTGTCTTTCAAT
CTTTGCTTCCATCAAATTACAGAGCAAAAATTGTCCAAAATCATCTGGGCTCAATAT
GGAGAACCTTGCTAACCATGAACATTTACTTAGCCCAAGTGCAGGCTCCAAGTATATA
TACAGAAGCTTCATTTGAAAACATGGACCGATTTTCTGAAAGAAGGTCCATGGTATC
TTCGCCTAATCGTTACGTTCCCTCTTCAACCTACAGTTCTGTTACTTTGAGACAGTTGT

FIGURE 80 (CONT'D)

CAAATCCTTATTATGTGAACACTATACCCGAGGAAGATATCCTAAAATACGTATCATA
TACATTATTAGCTACGACATCGGCACTATTTCCGTTTGATCATGAGCAAATACAAATT
CCGTCTAAGATACCCAATTTTGAGAGTGGACTTTTACATTTAATATTTGAAGCGGGTT
TATTATATCAAAGTTTGGGTTATAAAGTGGAGAAGTTTAGGATGTTGAATATATCTCC
AATGAAAAAAGCATTGATTATAGAAATTTTACAGAAGAATTACAAAACACTACACAGCATT
TGTGAACAATCTGGTCTCTTCAGGGACAGTAGTGTCATTGAAATCGTTATATCGTGAA
ATATATGAAAATATAATAAGGCTTCGAATATACTGTAGGTTTACAGAACACCTTGAA
GAATTGAGCGGAGATACATTCTTGATTGAATTAATATTTTCAAATCCCACGGAGAT
CTTACTATAAGAAAAATAGCAACGAATTTGTTAATTCAATGATTTCTCTTTATTATG
AGTATTTAATGAATTGGTTGACTAAAGGTCTACTCCGAGCTACTTATGGAGAATTCTT
CATTGCTGAAAACACTGATACAAATGGTACAGACGATGATTTTATTTACCACATTCCT
ATAGAGTTCAACCAAGAAAGAGTTCCGGCCTTCATACCGAAAGAGTTGGCATATAAA
ATATTCATGATCGGCAAATCGTATATCTTCCTAGAAAAGTACTGTAAAGAGGTTCAAT
GGACAAACGAATTTTCTAAAAAGTATCATGTCCTGTACCAGAGCAATTCCTATCGGGGA
ATATCAACGAACCTTTTTTGAATTTATAAATGATCAATATTCTGAAATTGTTAATCATACT
AATCAAATTCCTAAATCAGAAGTTTCATTACAGAGACGTGGTATTTGCGTTAAAGAATATT
CTTCTCATGGGTAAATCTGATTTTATGGATGCTCTTATAGAAAAGGCCAATGATATTCTC
GCGACACCATCGGATTCATTGCCAAATTATAAGTTAACAAGGGTTTTACAGGAAGCC
GTGCAGCTTTCTTCCTTAAGACATTTAATGAATAGTCCCCGTAATAGTTCTGTCTATTA
ATGGATTGGATGCGAGGGTACTCGATCTTGGACATGGATCCGTGGGTTGGGATGTTT
TTACTTTAGATTACATCCTCTACCCCCCTTTGAGTTTAGTATTAACGTAAATCGTCCT
TTTGGCAGGAAAGAGTATCTACGAATTTTCAATTTTTTATGGAGATTTAAAAAGAAC
AATTATTTCTATCAAAAGGAAATGTTGAAGAGTAATGATATAATCAGATCATTCAAG
AAAATCAGAGGTTACAACCCGCTCATCCGTGATATTATCAATAAACTTTCTAGAATCA
GTATACTTAGAACTCAA

Candida albicans nucleic acid: SEQ ID NO: 105

ATGGATATAATTAGAGGTGCATGTTCAAGTTGATAAAAATTGGGGGGATGGTGTATATT
AGAGAAGATTTAGCACCGCTGATGTTGGAATGGAAACCAATTGATGAACAAGAAGA
AGATAGAGCAATTTCAATCCCATTTGAATTTCTTAACTACATTACAAAGTACCAAAGAA
ACCTCACCGAAAATGATACTAAAAATTGTATACAACTAACATCTGGTCCACCTAAT
ACAAATGCAGATGGAAGTACAAATGGTGGTGGTGGTGGTGGTGAACAAAAATCATTT
AAATTGACATTTACTAATAGACCAACCATGAACACTATTAAAGATTCTCTACAAACAA
TTGTTGCTAGATCAAGAACTAAGGGTTTGAAGGTACCAGTACTCCAACCTCCAGCTCC
AGCACCAGCTTCAACATTTGGGGTCAGCACCACAAGCTGATTCTACCAGAGATTCTGA
CATCATCATCAACACCAATACCACCTACAACATCTGGAACCTCTACTAGTTTCATCATT
ATTATCATTAGCAGCATCACAATCATTATCTGATGCAAATTTATTGAAAAATTTTCGAA
CTACAGCAAAAACCTTTTATTAGAAGATCGTCAATTACGTGATGTTTTCACTAAATCAG
TCATGCAATTTAAATTATCTCCTCAAGTATTTTGGTCATCAAGATTAAATCAATTACG
AACATTTGCTTTGACAATATCTCAACATAAAGGTCCATATAATGTATTGAGTACAATT
AAACCGGTGGCCACTTCTGATAATCAAGTGAATGTTAATGTTACGCGTGATACCATT

FIGURE 80 (CONT'D)

AATGAAATATTTACTATTTACCCCATCATAAAGAAAGCATTGATGATTTGGTTCCTA
ACAAGTTTAATGAAGGAGAATTTTGGTCGAGATTTTCAATTCTAAATTGTTTAGACG
CTTAAGAGGTGATAAAATCAGTATTAGTAATAGTCGAGGAGATGTTGTATTGGACAA
ATATTTGTATAATAGATCAAACTATCAAGAAAAATTACAAAAATCATCTACTTTGGAA
AACAACGGTTCTGGTGGTGGTGGTGGTGGCGCTGGTGGTGGTAGTGGTAATTCAGAA
CAAGGAATACAAACATTGGAATCTCCACATGTTAAAAAATTTCTTGATTTGATGGGA
AATCAACAAGATAATTCACAAAAATTGGGGAATAGACCAGATTTTACTATGAGATAT
GATGAAGACACCAATGTAGATGATGATAATAAAAAACCTACTTTAGGAAATGAAAAT
GAAATGATTATATTGATGAAAAATATGAATCGATTATCGTCGAAAATGATGAGTATG
AGTTCTACTAATGGACCAGAGAAACCTTCAGAACTACAATTGATGGATTATCTGCT
GCTGAATTGAATGAATATGAAGAAGAATTAGATTTGCATGATTTAAATGATTCAGAA
AATTTACAATATATAAAATTAAACATTAATACTGATATTGCCAAGGGAACAAAACCTT
GATTCATATGAAGGATCAAATACTAATAACAAGATTTCTCAAGATGAATTACATAAA
TATTTACAATCTCAAACCTTCCAAGGACAAATAGAATTAACAGAACTTATACTTGTA
AAAGTGAAGAAATTGAAAAAACCTCCATGGAAATAGCCATGCTTATTAAACAAAATT
TCCGAACATTTAAATTAATTAATAAAGAAAATGATATTGCGGGGACAAACATTGTTC
CTAATTCATTAATACAAGAAATCATTACTTATAATATTACGATAGTTGAATTTTTATC
TCATTTTTGGAAGATTTTTTTACATGGGAATAATCCTGGTCAATTAAAGAAAATTTTC
ACCAGTTTGAAAAATTGTCAATCTGGTTTAAATAGAATTAGAAAATAAAGCGATTGAT
CAATTCAAATCTATGGATATATTACAAAAAATCAAAAATTACAAGATAAAGTTTTA
AAAGATTTTGCATCATGTCTTCAACCCATGAAAATAGCATTAGATAAAGCATGTAAT
GAATATGTTGAAGCAGTAAAGAAAGCTAAACCTGAATTAATGAAAATGGTAAACGT
CCTCTACCAGAGGAGTGA

Human GENBANK Accession Number: W19128

Human nucleic acid sequence: SEQ ID NO: 106

NGNCACATTCTGCNNAGAGATCCTTTGACCCTGNATNCAGCCGATCCCTGTGAAAAT
AATGGGANTGGAAAAACGTGTCCAGNATTCCTTCTCTGTCATGTNGTGGGNAACAT
TTTCTGCATATTTCATTTTNACTGCTGGATAGGTCCTNAATATGGACTCAATGATANC
AGAAGTTAAATTATATCTTAGACCGTTANAGCCATCAGTTTGGGGCCGGACATCAGC
NAGAAATGCAGCAGANATGCCAANATCCTGCTTATGATTGGATNTGGAAGAACTATC
TGTTGCATTACATTTAAACCGATTGGNCCAGAATTCCTCAGCACTGATCACTTGACT
CACGAACAAGGTCTTTATAAAGCTGAAACAAAACCAGGATCTTCTTGCAGCATTCTG
TTCATNCCCTCCAGTNCCTGNATTTGCNTTCCNCTTGAATTTGGGCAGCANCTGCTGA
NGAAGGT

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YER022W

Saccharomyces cerevisiae gene name: SRB4

GENBANK Accession Number: AAB64555.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 144

```
ATGACAACGGAAGATCCAGATTCAAATCACTTAAGTTCCGAAACTGGCATTAAATTG
GCATTGGACCCGAACCTTAATTACATTGGCACTAAGTTCTAATCCAAACTCTAGCCTTC
ATTCACCAACGTCTGATGAACCCGTACCTGAATCTGCAGGAAAAGCAGATACTAGTA
TTCGACTAGAAGGTGATGAGTTAGAGAATAAACTAAGAAAAGACAATGATAAGAACT
TAAATTTTTGAAGAATAAAGATTCTCTAGTCAGTAATCCACACGAAATTTATGGCTC
CATGCCGTTGGAGCAATTGATCCCAATCATCTTAAGACAGCGTGGTCCAGGCTTTAA
ATTCGTTGATTTAAATGAAAAAGAATTGCAAAATGAGATTAAGCAGCTTGGTAGTGA
TAGTAGTGACGGTCATAACAGCGAGAAGAAGGACACTGATGGCGCTGATGAGAATG
TACAAATTGGAGAAGATTTTCATGGAAGTGGATTATGAAGATAAAGATAATCCAGTGG
ATTCACGAAATGAAACAGACCACAAAACGAATGAAAATGGCGAGACCGATGATAAT
ATTGAAACGGTAATGACACAGGAACAGTTTGTTAAAAGAAGGAGGGATATGCTAGA
GCATATAAATCTGGCCATGAACGAATCGTCTTTGGCTTTGGAATTCGTTTCTTTGCTA
CTGTCGAGTGTTAAAGAGTCTACAGGTATGTCATCAATGTCACCATTCTTAGGAAA
GTTGTTAAACCTTCTAGTTTAAACAGTGATAAAATTCATATGTTGCACCTACAAAAA
AAGAATATATCGAGTTGGATATATTGAATAAGGGATGGAAGTTACAAAGTTTAAACG
AATCTAAAGATCTCCTACGCGCAAGTTTAAATAAACTGAGTTCCATATTACAGAACGA
ACATGACTATTGGAATAAGATAATGCAGAGTATTAGCAACAAGGATGTTATTTTTAA
GATTAGGGACAGGACTAGTGGTCAAAAGCTGTTGGCAATTAAGTATGGTTACGAAGA
CTCTGGATCTACCTATAAGCATGACAGAGGTATTGCTAATATAAGGAATAATATAGA
ATCACAAAATTTGGATTTGATACCCACAGTAGTTCAGTGTTCAAAGGCACTGATTTT
GTACATTCAGTAAAGAAATTCCTTAAGGGTTCGTATCTTCACAAAAATCGAATCAGAA
GATGATTACATATTGAGTGGCGAAAAGTGTGATGGATAGGGATAGTGAAGTGAAGA
AGCTGAAACGAAAGATATCAGAAAGCAAATCCAACTTTTGAAAAAGATCATTTTTGA
AAAAGAACTGATGTACCAAATAAAGAAAGAATGCGCTTTGTTGATTTCTATGGTGT
CAGTATTGAAAACGAAAACAAGGTAATAATTGAACTACCTAACGAAAAATTTGAAAT
CGAGTTGTTGTCCCTTGACGATGACTCCATTGTCAATCATGAACAAGACTTACCAAAA
ATCAACGACAAGAGAGCAAAATTAATGCTTGTTATGTTGAGACTATTATTAGTCGTTA
TATTCAAGAAAACATTACGATCGAGAATAAGCTCACCCACGGACTGATCAATTTGA
ATGTTGACGATGATATCTTAATAATACGTCCATTCTTGGTAAAGTTTCGGTTTGCTAA
TTACAAACTGTTACTAAAAAAATCATAAAGGATTACGTGCTCGATATAGTTCCTGG
CTCAAGTATAACAGAAACGGAAGTTGAGAGAGAACAACCTCAAGAAAATAAAAAACA
TTGATGATGAAAATATAACTAAATTAATAAAGAGATCCGTGCCTTCGATAAACTAT
TGAATATACCTAGACGTGAACTCAAATAAATCTACCATTAACTGAGCACAAAAGCC
CTAATCTAAGTTTAATGCTCGAAAGTCCTAACTATTGTAACGCACTCATTCACATCAA
GTTTTAGCTGGTACGGAAGCCAACGCAGTGTCTTT
```

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 145

ATGGTGGAAAAACAGTTTAACATAGACCTAGAGTTAAATGATACTGGTCATATAGAT
CCATTCTTACAAGATGAGTATGTTTGCTTTCTAACTTTATTGGTATTTTTGGTTCTGTT
TTTTAGTTTACTAACCCTTGACCAAGAGATAAATTGAAACTTGAGGAACTAATTCCACG
AATTTTATTTGAACGTAAATCATTTTTGAATGTGACGGAGGATTCTTTGAGAAAAAGAA
ATAGACAATTCATTGAAGATTTCCGAAGAGGATGCTTTAGACACTGAAGAAAGTAGA
GAGGACACAGTTGAAGCAGATCAACAAGAAGTGTTCAATAAACACAAGTTTGAATTA
TCGAAAAATATAAACAATGCACTTAATGAAACCCAACTTTCCTTAGATTTTGTATCCT
TATTAATATCTTCAGTGAAACCAAGTTTGGCAAAATCTACCATTTACCACACTTGTC
AAAATTTGTCAAACCGACATCTTTAAATTCGGATAGATTGGGTCAAGATAGTAATGA
TAATCAAGAGAGTAAGGCTACTGATTCTTTTGGACAAGGATGGAAATTGGAGTCACT
TGGAAAGATAACCGATCTTTTCAGAGAAGCTAGTACTAATTTAAACGATCAAGTTAT
CAAAGAAAGACGATATTGGAATATGATAAATTTGGTGCTTGCCAACGACGAGGTTCT
ATTTGCAATGAGGGACCCCCAAAATAATGCTAGAGCAATAGGAGTGAAATATGGGTA
TGGAGATTCAGGATCAAATTTTCACGACCAAGGGTTGGCATTGTTACGCAAGGACAA
CCAAACAGGAGAAATCTCATTTACCCCCATATCGTCAATCAACAATGCTAAAATTGTA
GAAAAAGTTTCGAGATTTATTAGAGTGAAAATTTTGAGCCAAATAGATGGGGACTAT
ATGCTTACAGGACAGTCAATTTTTAATTTTGATTTTGAAAAAAGCAAGCAAAGCATA
ATTAATGACATCGAAAAAGGCTAGATTCTTTTTATTTGAGGAGGACTTGTTTCATCAAT
TGATACGCGAGGCCAAATTGTTGGTAAACTACAATGTGTCAATCATATCGAATAAAA
TAATAATTGAAATCAACAACATTATTATTGAAATAGAGTCTATCGTGTATGATGAGTT
GAATGAGGAGGAACTAGAAAACTATTACCAGAATGTAAATGAATATTCCACCTTACA
CAATAAAAAGTGTCAGCTTATTTTAAACTACTTGAACTTATGCTTTGTTGTTATTAC
AAATACAATCTCAAATTGAAACAGAAGGTTCCAACAGCATTGACTAAATGGAAGCAG
AGTAACTCCCATCCTTTGATTTTGCCTCCGTTAGTGGGTAAATATGAGGCATGAGTTAA
ATTTGCTAAATATGAAGAGTGTTTTAGATCGATTAATGCACGCTCATGAGAGTGAAC
TTTCTTATTCCAACTAGATGTGGAGAAGTTTATTAAGTTAGCCACAAGAAGCAAAA
AGCAAAAACCCATTCCAAAAGTCAATTGAAAAGCCAATTTCAAAGTTCCATTTAGTTTT
ATGCAACAAAACCTCTAATATGTTGGACGTCAACATAACAATTGACAATAATGAGCT
GTTTGTCAATCTAATCATCAATATGACAATTATTAGATTTGAAACAGAAGACGATTTT
AAGAACAATGTCAATGGTATTAACGTTCTACAGCTTGGGTTTCAGTGATTTCATGAA
ATCGAAGAATGCTTGGATTGGTCGATCCAAAATTTTGTATAGGACACAACATTTTCTG
ATTTTAAAGAAGTAGAGGACTTCCTACATTTTATTGTCGCTGAGTACATCCAGCAAAA
GAAGGTGTAA

Human GENBANK Accession Number: AB015617.1

Human nucleic acid sequence: SEQ ID NO: 146

ATGTATGGAAGTGCCCGCTCTGTTGGGAAGGTGGAGCCGAGCAGCCAGAGCCCTGG
GCGTTCACCCAGGCTTCCACGTTCCCTCGCTTGGGTCACCGTCGAACCAACAGTACG
GGAGGGAGTTCCGGGAAGCAGTGTTGGAGGTGGCAGTGGGAAAACCCTTTCAATGGA
AAATATACAATCTTTAAATGCTGCCTATGCCACCTCTGGCCCTATGTATCTAAGTGAC

FIGURE 80 (CONT'D)

CATGAAAATGTGGGTTTCAGAAACACCTAAAAGCACCATGACACTTGCCCGTTCTGGG
GGACGTCTGCCTTACGGTGTTTCGGATGACTGCTATGGGTAGTAGCCCCAATATAGCT
AGCAGTGGGGTTGCTAGTGACACCATAGCATTTGGAGAGCATCACCTCCCTCCTGTG
AGTATGGCATCCACTGTACCTCACTCCCTTCGTCAGGCGAGAGATAACACAATCATG
GATCTGCAGACACAGCTGAAGGAAGTATTAAGAGAAAATGATCTCTTGCGGAAGGAT
GTGGAAGTAAAGGAGAGCAAATTGAGTTCTTCAATGAATAGCATCAAGACCTTCTGG
AGCCCAGAGCTGAAGAAGGAACGAGCCCTGAGAAAAGATGAAGCTTCCAAAATCAC
CATTTGGAAGGAACAGTACAGAGTTGTACAGGAGGAAAACCAGCACATGCAGATGA
CAATCCAGGCTCTCCAGGATGAATTGCGGATCCAGAGGGACCTGAATCAGCTGTTTC
AGCAGGATAGTAGCAGCAGGACTGGCGAACCTTGTGTAGCAGAGCTGACAGAGGAG
AACTTTCAGAGGCTTCATGCTGAGCATGAGCGGCAGGCCAAAGAGCTGTTTCTTCTT
CGAAAGACATTGGAGGAAATGGAGCTGCGTATTGAGACTCAAAAGCAGACCCTAAAT
GCTCGGGATGAATCCATTAAGAAGCTTCTGGAAATGTTGCAGAGCAAAGGACTTTCT
GCCAAGGCTACCGAGGAAGACCATGAGAGAACAAGACGACTGGCAGAGGCAGAGAT
GCACGTTTCATCACCTAGAAAGCCTTTTGGAGCAGAAGGAAAAAGAGAACAGTATGTTG
AGAGAGGAGATGCATCGAAGGTTTGAAGATGCTCCTGATTCTGCCAAAACAAAAGCT
CTGCAAACTGTTATTGAGATGAAGGATTCAAAAATTTCTCTATGGAGCGTGCGGCTT
CGAGACCTGGAAGAGGAAATTCAGATGCTGAAATCGAATGGTGCTTTGAGTACTGAG
GAAAGGGAAGAAGAAATGAAGCAAATGGAAGTGTATCGGAGCCATTCTAAATTTAT
GAAAAATAAGATTGGCCAGGTGAAACAGGAGCTGTCCAGAAAGGACACAGAACTAC
TCGCCCTGCAGACAAAGCTAGAAACACTCACAAACCAGTTCTCAGATAGTAAACAGC
ACATTGAAGTGTTGAAGGAGTCCTTGACTGCTAAGGAGCAGAGGGCTGCCATCCTGC
AGACTGAGGTGGATGCTCTCCGATTGCGTTTGAAGAGAAGGAAACCATGTTGAATA
AAAAGACAAAACAAATTCAGGATATGGCTGAAGAGAAGGGGACACAAGCTGGAGAG
ATACATGACCTCAAGGACATGTTGGATGTGAAGGAGCGGAAGGTTAATGTTCTTCAG
AAGAAGATTGAAAATCTTCAAGAGCAGCTTAGAGACAAGGAAAAGCAGATGAGCAG
CTTGAAAGAACGGGTCAAATCCTTGCAAGGCTGACACCACCAACACTGACACTGCCTT
GACAACTTTGGAGGAGGCCCTTGCAAGAGAAAGAGCGGACAATTGAACGCTTAAAGG
AGCAGAGGGACAGAGATGAGCGAGAGAAGCAAGAGGAAATTGATAACTACAAAAAA
GATCTTAAAGACTTGAAGGAAAAAGTCAGCCTGTTGCAAGGCGACCTTTCAGAGAAA
GAGGCTTCACTTTTGGATCTGAAAGAGCATGCTTCTTCTTGGCATCCTCAGGACTGA
AAAAGGACTCACGGCTTAAGACACTAGAGATTGCTTTGGAGCAGAAGAAGGAGGAG
TGTCTGAAAATGGAATCACAATTGAAAAAGGCACATGAGGCAGCATTGGAAGCCAGA
GCCAGTCCAGAGATGAGTGACCGAATACAGCACTTGGAGAGAGAGATCACCAGGTA
CAAAGATGAATCTAGCAAGGCCCAGGCAGAAGTTGATCGACTCTTAGAAATCTTGAA
GGAGGTGGAATAATGAGAAGAATGACAAAGATAAGAAGATAGCTGAGTTGGAAAGTC
TCACCTCAAGGCAAGTGAAAGACCAGAATAAGAAGGTAGCAAATCTGAAGCACAAG
GAACAGGTGGAATAAAGAGAGTGACAAATGTTAGAGGAGGCGCGACGACGGGA
GGACAATCTCAACGACAGCTCTCAGCAGCTACAGGTGGAGGAGTTACTGATGGCCAT
GGAGAAGGTAAAGCAGGAAGTAAATCCATGAAAGCAAAGCTGTCCTCCACCCAGC
AGTCTCTGGCAGAAAAGGAAACTCACTTGACTAATCTTCGGGCAGAGAGAAGGAAAC
ACTTAGAGGAAGTTCTGGAGATGAAGCAAGAAGCTCTTCTGGCTGCCATTAGTGAAA

FIGURE 80 (CONT'D)

AAGACGCCAATATAGCTCTCTTGGAGCTTTCGTCCTCTAAGAAGAAGACCCAAGAGG
AAGTGGCTGCCCTGAAGCGGGAGAAGGATCGTCTGGTACAGCAGCTTAAGCAGCAG
ACGCAAAATCGAATGAAGCTAATGGCCGACAACACTACGAG

Saccharomyces cerevisiae orf name: YER127W

Saccharomyces cerevisiae gene name: LCP5

GENBANK Accession Number: AAC03225.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 125

ATGTCTGAACCTTAATGCATTATTAAGATATCAACGGCTCGCTCACTGCGACATCAGAA
TCCTTGGAGAGGTTGTCTGGGATTTATAGTAATTCTGCGACCGATGAGATTCTGAAAGT
AACCAACTACATGAGCATCTATTTTACGACGCTAAGAAGCCTGCTGAGAAAGTATCG
CTGCTATCCTTAAAAAATGGGAGCATGCTAGGGTACATAAATTCTCTATTGATGCTTA
TAGGCAATAGGCTAGACGACGAGTGCAAAGATCCTTCTGCTATGGATGCACGTGAAC
GCTCTATTCAACACCGTGTGGTATTAGAGCGTGGTGTAAACCACTAGAAAAAAGT
TGGCTTACCAATTGGACAAGCTGACTAGAGCATATGTGAAAATGGAAAAGGAATATA
AAGACGCTGAGAAGCGTGCACTGGAAAAATCTACCTTAGTGAATCATAGCGGCAACG
ACGATAGCGAAGATGATGAGTCTAGTGAGGATGAAATAGCATACAGGCCAAATACCT
CTGGAATTATCAACACAAATAAAAAATCATCAGCATACAGGGTGGAGGAAACGGCTA
AGCAAGAAAACGGGGAAGAAAACGATGACAATGAGACTGGCGTGTATAAACCACCA
AAGATTACGGCTGTTCTACCACCGCAACAAACGCATTTTGAAGATAGATTTCGATGCC
AGAGAACACAAAGATCGTAGTAACAAATCGCGTATGCAAGCCATGGAAGAATATATT
AGAGAGTCATCGGACCAACCGGACTGGAGTGCATCTATTGGTGTGCTGACATTGTGAAC
CATGGAAGAGGCGGTATCAAATCTTTGAGAGACACAGAGAAGGAACGTAGAGTCAC
TTCATTGCAAGAAGATAATTTTACCAGATTGAATATTACAAATAAAGCTGAAAAAAG
GAAGCAAAAGCAACGAGAAAGAAATGCAAGGATGAACGTTATCGGTGGTGAAGATT
TTGGTATATTAGCTCAAAGAGGAAGCTGGAAGATAGCACTTCGAGA

Candida albicans nucleic acid: SEQ ID NO: 126

ATGTCAAAGGTAGACACTGTATTAAAGGAAATCATCTCGTCTACCAAGTCAACTGAA
GCTTCAGTGAAAGAGTTGATAGCTTTTGTCAAGGACTCGTCTTCCCAACATCCAGAAT
TGGTGCGGAACCTTGTTAGCAAAATCAAACCTGCTGTTAGAAGGGGTATCGTTGTTGG
GGTTGAAAAACGAATCGTTGGTGTCTATATCAACAATATAGTGCTTGTTGTTTGTGTC
TCATCTAGAGCGTCTAGAAAGCGATCTGGAGACGGGATCCAGCGCTGTCGAACGATC
GATAATTCAAAGGGTGACATTGGAAAAAGGCGTTAAACCTCTAGAAAAGAACTCAG
TTATCAGTTGGATAAAATGATCAGGGCATATGGACGGATGGAACAAGACGAAATCAA
AGCTGAACAGAAGTTAAACGATAGAGGAAGTGGGGAGAACGATGAGAACGATGAGA
ACGATTCTGAGGAAGATTCTGAAGAAGATTCTGAAGACGACTCTGAGGACGACGAAT
TGGCTTATAGACCAGATGCATCATCGTTTGCTAAATTGACATCGGCCAAAACCAAAC
TGAAACCAACATCATCAGCAGTCTCTACATCGAATGAAAAGTATAGACCACCAAAGA
TATCAGCAATGGCACCTCCAACCTGCAGTAAAGAGCCACGACCTTGATGCCAACACCA

FIGURE 80 (CONT'D)

CGTCGTCAAAGAACCGTAAATTACAGAGCATGGAAGAGTACTTGCAAGAGCAAAGTG
ATATGCCAATGGTGGAGGCATCGGTGGGGTCTACAATTGTGGAGCATGGAAGAGGTGG
TGTTAAAACACAGCACGATCGTAAGAAAGAACGAGAGATACAAACGTATGAAGAGG
ATAATTTTGTGAGACTACCAACCAGTCAAACAAAAGAAAAGTTTCAAGGAAAAACAAC
GTGATATCCGTAATCAATTTGCTGGTGAAGACTGGTCGATGTTTAATAATAACAAGG
ATGTGACCCGTCAAGGCACATCGCGAAAGAGAAAGGCAACCACCGTTTGGGACAAA
GTCAAGAAAAAGAAGAATACTTAGATGGTAAGTAGACGCTGACATTTTGTGTCAGTA
TAG

Human GENBANK Accession Number: AL050003

Human nucleic acid sequence: SEQ ID NO: 127

GGGGGCTTTGCGAAGATGGCGGCGCTGGGGTGCTGGAGTCCGACCTGCCAAGTGC
CGTGACACTTCTGAAAAATCTCCAGGAGCAAGTGATGGCTGTAAGTGCACAAGTGAA
ATCACTGACACAAAAAGTTCAAGCTGGTGCCTATCCTACAGAAAAGGGTCTCAGCTT
CTTGGAGTGAAAGACCAGCTGCTGCTCATGTACCTTATGGATTTGACCCACCTCATT
CTGGACAAAGCCTCAGGAGGATCTCTTCAGGGACATGATGCAGTTTTGAGACTGGTG
GAGATTTCGCACGGTTTTGGAAAAGCTTCGTCCCTTGGACCAAAGCTGAAGTATCAA
ATTGACAAGCTGATCAAGACTGCAGTGACAGGCAGCCTTAGTGAGAATGACCCACTT
CGTTTTAAGCCTCATCCCAGCAATATGATGAGCAAGTTGAGCTCTGAGGATGAGGAG
GAAGATGAAGCAGAAGATGACCAGTCTGAGGCTTCAGGGAAGAAATCTGTGAAGGG
AGTGTCTAAGAAATATGTTCCCTCCACGCTTGGTTCCAGTACATTATGATGAAACAGA
AGCTGAGCGGGAGAAGAAGCGTCTAGAACGAGCCAAGAGACGGGCATTGAGCAGCT
CTGTCAATTCGTGAACTTAAGGAGCAGTACTCAGATGCTCCAGAGGAAATCCGTGATG
CTCGGCATCCCATGTTACCCGCCAGAGTCAGGAGGACCAACACAGGATTAAGTATG
AGGAGAGCATGATGGTGCGTTTGAGCGTCAGTAAGCGAGAGAAAGGACGGCGAAAA
CGAGCAAATGTCATGAGCTCACAACCTTCAATCCCTTACACACTTCAGTGACATCAGTG
CTTTGACAGGGGGAAGTGTTCATCTTGATGAGGATCAGAATCCTATTAAGAAGCGGA
AGAAGATACCTCAGAAAGGTCGGAAGAAAAAAGGCCAGTGAAGTCTGTTGGGACTTAG
GTGATCAGGTGCAAGGTGGGGAGTACAAATTGAGTCTCTTTGGATTTGCCATTCTGG
GTCTCACCAAGCCCTGTAGTATCTCTTCCATACTGGGCAATAATCTCCTTAGGTGGGC
GTGGGGCCAAGAAGACTCGTTCTGCCTGGGATAGAGCTCAAAGGAGACTGTAG

Saccharomyces cerevisiae orf name: YFR027W

Saccharomyces cerevisiae gene name: ECO1

GENBANK Accession Number: BAA09266.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 130

ATGAAAGCTAGGAAATCGCAGAGAAAAGCGGGCAGTAAACCAAATCTTATCCAGTCT
AAATTGCAAGTTAATAATGGTTCGAAATCGAATAAAATAGTCAAGTGTGATAAATGT
GAGATGTCATATTCCTCGACATCAATAGAAGATCGCGCCATCCACGAGAAATACCAC
ACTTTACAGCTGCATGGACGTAAATGGTCGCCGAATTGGGGTTCTATAGTATACACA

FIGURE 80 (CONT'D)

GAGCGAAACCATTCAAGGACGGTGCATCTATCAAGATCGACAGGGACAATAACGCCA
TTGAACTCCTCACCTTTGAAAAAAGTAGTCCGTCTATTACCCATCAGGAGGAGAAG
ATTGTATATGTGAGACCAGATAAGTCGAATGGTGAAGTCCGAGCCATGACGGAGATA
ATGACACTAGTGAATAACGAGCTGAATGCGCCACACGATGAGAATGTCATTTGGAAC
AGTACCACAGAAGAAAAAGGCAAAGCGTTTGTATACATAAGAAATGACAGGGCGGT
CGGAATAATAATTATAGAGAACCTTTATGGGGGCAATGGTAAACATCTAGTCGTGG
ACGTTGGATGGTTTATGATTCTAGAAGATTGGTACAGAATGTGTACCCCGATTTTAA
GATTGGCATATCGAGAATTTGGGTGTGCAGGACAGCAAGGAAGTTGGGTATCGCAAC
CAAATTGATTGACGTTGCAAGAGAAAAATATTGTTTACGGTGAAGTTATTCCTAGGTA
CCAGGTAGCATGGTCGCAACCCACAGACAGCGGTGGAAAACTGGCTAGCAAATACA
ACGGCATTATGCATAAATCAGGCAAGTTACTATTGCCGGTATAC

Candida albicans nucleic acid: SEQ ID NO: 131

ATGGGCTCCATTAATTCTCAAAAACCTCAAAAAATCCAATCAATTCTTGCATTACCAT
CTAATTTCAAAAAAATTACTTGTTCACATGTGATATGACATATAATCCCCATATATC
TCAAGATAAATTACTACATAACAAATACCACACAAATTTTCATCAATGGAATACCCTG
GAATTATAAACTGATAATGATGTTTTAATAATTGAGAATTTTACATTAGTTGAAACC
CCGAAATTGAATTCCACGGGGAATCATTAAAGCTGACAAAAACGCGTCAGACATTT
AAAGGTTCTATAATTTGTATAAATAAATCCAACAAACGACATATACAAAAAGTGGA
CTACTATTAAACATGGTGAATCAAGAGTTGAATGCTAGTCAAGATTCAGGACAATGG
AAGAAACCTGAATTTGATAGAAGTAAAGCATTGTGTGATAATAATAGACAGTAAGGCC
ATTGGATTATGCACAACAGATACAATTCAACCTGATCAAGGAAGGTGGATGATACAT
AAAACACAATCTATAGTACCTAATCAGATTAATAAAAAATGTTGTCATTGGAATTTCAA
GAATATGGATAAGTCGGAAATGGAGACAATATGGATTAGGTAAAAAACTTTAAATG
TTGTTTTGAAAAATTCTATTTACAGTGTGCAATTATTGAAGAATCAAGTTGCCTTTAG
TCAACCAAGTTTTAGTGGTGGAAATGTTGGCAAAATCATTCAATGGGGTGAAACATAA
AAGTGGTGAAATGTTGTTACCCGTATATATTGAATGATCCTTTCAGGTTTTTCGGAGGC
GGCGGTGATTATGGGTGTACATATTTGTATATTTTTTGT

Saccharomyces cerevisiae orf name: YGL122C

Saccharomyces cerevisiae gene name: NAB2

GENBANK Accession Number: CAA96830.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 82

ATGTCTCAAGAACAGTACACAGAAAACTGAAGGTTATCGTTGCCGAAAACTGGCT
GGTATACCAAACCTTTAACGAAGATATCAAGTATGTTGCGGAGTATATTGTCTTATTGA
TCGTTAACGGTGGTACTGTTGAATCTGTCGTAGACGAGCTGGCTAGTTTGTGTTGATAG
TGTTTCGAGAGATACGCTTGCAAATGTTGTTCAAACAGCCTTTTTTCGCATTAGAAGCT
CTGCAACAGGGAGAAAGTGCTGAAAATATTGTTTCCAAAATTAGAATGATGAATGCG
CAAAGCTTGGGACAATCGGATATCGCACAAACAGCAACAACAGCAACAACAACA
GCAACCAGACATCGCGCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCAACA

FIGURE 80 (CONT'D)

GCAACCTCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCAACAGCAACCTCA
ACAGCAACCTCAACTTCAACCACTTCAGCCACAACCTAGGGACCCAGAATGCAATGCA
GACAGATGCTCCTGCAACTCCATCCCCATATCAGCCTTTTCCGGCGTTGTTAACGCT
GCAGCTCCCCCTCAGTTTGCGCCTGTAGATAACAGCCAAAGGTTCACTCAACGTGGC
GGAGGCGCCGTTGGAAAGAATCGTAGAGGTGGTCGCGGTGGGAACCGTGGAGGACG
CAACAATAATTCCACACGTTTTAATCCGTTAGCAAAAGCACTTGGAATGGCGGGTGA
GAGTAATATGAACTTCACTCCAACCAAGAAAGAGGGGCGTTGCAGATTGTTTCCTCA
CTGTCTCTTGGTAGATCATGCCACATGCACACCCAACTAAGGTATGTAATGAATAT
CCAAATTGTCCAAAGCCTCCCGGAACCTTGTGAGTTTTTACATCCAAATGAAGATGAA
GAGTTGATGAAGGAAATGGAAAGAACTCGTGAAGAATTTCAAAAAAGAAAAGCTGA
TTTATTGGCGGCAAAAAGGAAACCGGTACAAACTGGTATCGTTCTGTGTAAATTTGG
GGCTCTGTGTTCCAATCCATCATGCCATTTGGTCATCCAACACCAGCAAATGAAGAT
GCGAAAGTCATTGATCTAATGTGGTGTGACAAGAATTTGACATGTGATAATCCTGAG
TGTAGAAAGGCCCACTCTTCATTGTCGAAGATCAAGGAAGTAAAACCAATAAGCCAG
AAGAAAGCAGCTCCACCTCCGGTTGAAAAGTCCTTAGAACAATGTAAGTTCGGTACG
CACTGCACCAATAAACGTTGCAAATATAGACATGCTCGTTCTCATATTATGTGCCGTG
AAGGAGCAAACGTACTAGAATTGATTGTTTATTTGGCCATCCAATTAATGAAGATT
GTAGATTTGGTGTCAATTGTAAGAATATTTACTGTCTATTCAGACATCCTCCAGGCAG
AGTACTTCCGGAAGAAAGGCGCTGCACCCAATTCAAACGTTCTACCAATGAAAG
GCCATTTGCATTGCCAGAAAACGCAATAATTGAAAATGCTCCTCCGCAAACCAGTTTT
ACGCACCAAGAACAA

Candida albicans nucleic acid: SEQ ID NO: 83

ATGCAATTTGCTCCAGATAACCAAATAGGCCAAAGAGTTACAGCAAAACTTGATTCAA
GAAATACAAAGGCGTTTCAATAAACCGGCTGATGATGCCGTAGATATTGCTGACTAT
ATCATCTACTTGATTGTGGCAAAAAAGAGCGAACAAGAAATAGTCGCAGAAGTCAAA
GATATTGCTGACATATCTATTGATGTTGGGTTTATTGGGGATGTTTATCTGGAAATCA
GAAAGTTGGAAGTAAAATATAATCAACCTCCTGCTGCAGTGGAGGAAGCTTCTCAAC
CTCAACAAGAACAGCAACAGCAATCTCAAGCTTCTGTAGTGGCTCCACAAATTCCTA
TTGGTCCTAAGAAACAATTAAGTGAAGGAAGAGATTGCCCTTCGAAGTCAAAGAT
TTGGAACCTACTACTAGATTGAGTGGGCGAGGTGGACGTGGTGGTATAACTAAAATA
GAACCGATTTCAGAAATGGGCACAATAATAAGAACTTCCTAGACCCTAAAAAATTAG
ACCAAATAATTTCTGGTGCCAATAATGGGGCTATTAAGTTTGTACCACTCCACCAAA
AGGTAGATGTCCAGATTTCCCATATTGTAAGAATCAGAATTGTGAAAAAGCTCATCC
AACAAAAAACTGTTTCAACTACCCGATTGCCCTAACCCACCGGGAACATGTAATTTT
TTGCATCCGGATCAAGACCAAGAGTTGATTGCTAAATTAGAAACATCTAAAAAAGAA
TTTGAAGAAAAGAAAAAGAATCAACTTATGGTCAAACAAGGCTCATGTAAATATGGT
TTGAAATGTGCTAAAGAAAATTGTCCATTTGCTCACCCAACACCAGCTAATCCTGAAT
CTGGTAAGATTGAAACTTTGGAATGGTGTCCACAAGGTAAGAATTGTCAAGATAGAA
ATTGTACTAAATCACATCCACCTCCACCTACGGCAAACCTCAGAAAAATTATTATCAGC
TGCTGACTTGGCATTGGAACAATGTAAATTTGGTTCACAATGTACTAATCTCAATGT

FIGURE 80 (CONT'D)

CCAAGAAGACATGCAACTTCGGCTGTGCCATGTCGTGCTGGTGCTGAATGTAGAAGA
GTCGATTGTACATTTTCCCATCCATTGAAAGAACCATGCCGTTTTGGAACAAAATGTA
CAAATAAAGTGTGTATGTACCAACATCCTGAAGGAAGAACTATTGCCTCTCACACTT
GGACCAAGGATGGTAGTGGCAATAATAACAGTACCTCAAATCGATCATTGCTGTTT
CTGAAGATCAGATTATGGAACAAGTTGCTCAATAG

Human GENBANK Accession Number: AF155107.1

Human nucleic acid sequence: SEQ ID NO: 84

ACCCACAGCAGTTGCACTTGCTGAGCAGGCAGCTTGAGGACCCAAATGGTAGCTTTT
CTAACGCTGAGATGAGTGAAGTGAAGTGTGGCACAGAAACCAGAAAACTTTTGGAGC
GCTGCAAGTACTGGCCTGCTTGTAATAATGGGGATGAGTGTGCCTACCATCACCCCA
TCTCACCCCTGCAAAGCCTTCCCCAATTGTAAATTTGCTGAAAAATGTTTGTGTTTCA
CCCAAATTGTAGATACGGAAATGAACTGAAATATGATGCAAAGTGTACTAAACCAGA
TTGTCCCTTCACTCATGTGAGTAGAAGAATTCCAGTACTGTCTCCAAAACCAGTTGCA
CCACCAGCACCACCTTCCAGTAGTCAGCTCTGCCGTTACTTCCCTGCTTGTAAGAAGA
TGGAATGTCCCTTCTATCATCCAAAACATTGTAGGTTTAACTCAATGTACAAGACC
GGACTGCACATTCTACCATCCCACCATTAATGTCCCACCACGACATGCCTTGAAATGG
ATTCGACCTCAAACCAGCGAATAGCACCCAGTCCTGCCTGGCAGAAGATCATGCAGT
TTGGAAGTTTTTCATGTCTGATGAAAGATCTCTACAGAACTTGTCAAATCTTTGAACT
TGGAATATATTGCTTTCATAATATGAAGGTTTATTGGCTATCTAAAA

Saccharomyces cerevisiae orf name: YGR195W

Saccharomyces cerevisiae gene name: SKI6

GENBANK Accession Number: CAA97221.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 119

ATGTCAAGACTAGAAATATACTCGCCAGAAGGGCTACGTCTCGATGGACGTCGATGG
AATGAACCTCCGCCGTTTTGAAAGTTCCATCAACACACATCCGCACGCTGCAGACGGT
TCATCCTACATGGAACAAGGTAACAACAAAATTATCACTCTTGTTAAAGGTCCAAAA
GAGCCAAGATTGAAATCTCAAATGGATACCTCAAAGGCTTTATTGAACGTATCGGTA
AACATTACAAAATTCTCCAAATTCGAAAGAAGTAAATCAAGCCACAAGAATGAAAGG
CGTGTTCTTGAGATACAAACCTCCCTGGTGAGGATGTTTGAGAAGAATGTCATGCTG
AATATCTACCCCAGAACAGTTATCGATATCGAGATCCATGTCCTTGAGCAAGATGGC
GGTATTATGGGATCTTTAATCAACGGTATTACCCTCGCTTTAATAGATGCCGGTATAT
CAATGTTTCGATTACATAAGTGGTATATCCGTCGGGCTGTACGATACTACCCATTATT
AGATACCAATTTCATTAGAAGAAAATGCTATGAGTACAGTGACACTAGGTGTGGTAGG
GAAGTCAGAAAACTTTCTCTTTTATTGGTGGAAGACAAAATTCCGTTAGATAGGTT
AGAGAACGTTCTTGCCATCGGCATCGCAGGTGCTCATAGGGTAAGAGATTTGATGGA
TGAAGAAGTGAAGAAACATGCTCAGAAAAGAGTC

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 120

ATGGAATTATATTCACCTGAGGGACTTAGAATAGACGGAAGAAGATGGAACGAATTG
CGTAGATTTGAATGCCGTATCAACACTCATCCAACTCATCGGATGGCTCCTCATATG
TCGAACAAGGTAATACCAAAGTGATGTGCACAGTACAAGGACCAA
TAGAACCAGCATTAAAGATCTCAACAACATTCAGAACGAGCAAATATAGAAGTGAATT
TGAATATTGCTAGTTTTTCAACTTTTGAAAGGAAAAACGAAGTAGAAATGAAAGAA
GATTAGTTGAACTTAAACTACTTTAGAAAAAACATTTGAAGAAAGTGTTATGATAA
ATTTATATCCAAGAACAAATATTGTTATAAATGTTCAAGTATTATGCCAGGATGGTGG
GATGTTAGCTGCAGTTATCAACTCTATTACATTAGCACTCATTGACGCTGGTATATCA
ATGTATGATTATGTGAGTGGTGTATCTTGTGGATTATATGATCAAACACCATTATTAG
ATGTAAATAACTTAGAAGAACACGATATGAGTTGTTTAACAGTTGGTGTATTGGTA
AAAGTGAGAAATTGGCATTAAATGTTGTTAGAAGATAAAATGCCATTGGATAGATTGG
AATCAGTATTGTCAATTGGTATTGCTGGAAGTCATAAAATAAGAGAATTAATGGATC
AAGAAGTGAGGAAGCATGGAATTATTAGGGCTTCTAAAATGCAATAA

Human GENBANK Accession Number: AK000598.1

Human nucleic acid sequence: SEQ ID NO: 121

AGAGAGCGGACCTGGCGGCCGGGCAGCATGGCGGGGCTGGAGCTCTTGTCGGACCA
GGGCTACCGGTGGACGGCGGCGCGCCGGGGAGCTGCGCAAGATCCAGGCGCGGA
TGGGCGTGTTGCGCAGGCTGACGGCTCGGCCCTACATTGAGCAGGGCAACACCAAGG
CACTGGCTGTGGTCTACGGCCCGCACGAGATCCGGGGCTCCCGGGCTCGAGCCCTGC
CGGACAGGGCCCTAGTGAAGTGTCAATATAGTTCAGCGACCTTCAGCACAGGTGAGC
GCAAGCGACGGCCACATGGGGACCGTAAGTCCTGTGAGATGGGCCTGCAGCTCCGCC
AGACTTTCGAAGCAGCCATCCTCACACAGCTGCACCCACGCTCCAGATTGATATCTA
TGTGCAGGTGCTACAGGCAGATGGTGGGACCTATGCAGCTTGTGTGAATGCAGCCAC
GCTGGCAGTGCTGGATGCCGGGATACCCATGAGAGACTTTGTGTGTGCGTGCTCAGC
TGGCTTCGTGGACGGCACAGCCCTGGCGGACCTCAGCCATGTGGAGGAAGCAGCTGG
TGGCCCCAGCTGGCCCTGGCCCTGCTGCCAGCCTCAGGACAGATTGCGCTGCTTGA
GATGGATGCCCGGCTGCACGAGGACCACCTGGAGCGGGTGTGGAGGCTGCTGCCCA
GGCTGCCCGAGATGTGCACACCCTCTTAGATCGAGTGGTCCGGCAGCATGTGCGTGA
GGCCTCTATCTTGCTGGGGGACTGACCACCCAGCCACCCATGTCCAGAATAAAACCC
TCCTCTGCCACACAAAAA

Saccharomyces cerevisiae orf name: YHR005C-A

Saccharomyces cerevisiae gene name: TIM10

GENBANK Accession Number: AAB68435.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 141

ATGTCCTTCTTAGGTTTCGGTGGTGGTCAGCCTCAATTATCATCTCAACAAAAGATTCAA
GCTGCGGAAGCTGAACTAGATTTGGTCACAGACATGTTCAATAAATTGGTTAATAACTGT
TATAAAAAATGTATCAATACTTCTATTCCGAGGGTGAGCTGAATAAGAATGAATCTTCG

FIGURE 80 (CONT'D)

TGCCTAGACAGATGTGTGGCCAAATATTTTGAGACCAATGTTCAAGTCGGTGAAAAC
ATGCAGAAAATGGGCCAATCATTTAACGCAGCCGGTAAGTTTTAG

Candida albicans nucleic acid: SEQ ID NO: 142

ATGTTTGGCTTAGGTGGTACTACTCCTCAAATTTTCATCTCAACAAAACTTCAAGCTG
CTGAAGCTGAATTAGATATGGTTACTGGCATGTTCAATGCTTTAGTTTCCCAATGTCA
CACCAAATGTATCAACAAATCATATAATGAAGCTGATATTTCAAAGCAAGAATCTTT
ATGTCTTGATAGATGTGTTGCCAAATATTTTGAAACCAATGTTCAAGTTGGTGAAAAT,
ATGCAAAAATTAGGTCAATCTGGTCAATTTATGGGTAGAAGATAAAT

Human GENBANK Accession Number: NM_012456.1

Human nucleic acid sequence: SEQ ID NO: 143

GGAGCCTCACGRGAGCGKGGTAACGTTATAGTATTTGTCAGAAGTTGGGGTCTCCGT
GGGCATTGTGATCCGTCCCAGGCAGTGGATTAGGAGGCCAGAAGGAGATCCCTTCCA
CGGTGCTAGGCTGAGATGGATCCTCTCAGGGCCCAACAGCTGGCTGCGGAGCTGGAG
GTGGAGATGATGGCCGATATGTACAACAGAATGACCAGTGCCTGCCACCGGAAGTGT
GTGCCTCCTCACTACAAGGAAGCAGAGCTCTCCAAGGGCGAGTCTGTGTGCCTGGAC
CGATGTGTCTCTAAGTACCTGGACATCCATGAGCGGATGGGCAAAAAGTTGACAGAG
TTGTCTATGCAGGATGAAGAGCTGATGAAGAGGGTGCAGCAGAGCTCTGGGCCTGCA
TGAGGTCCTGTGAGTATACACCTGGGGTGTACCCACCCCTTCCCACTTTAATAAA
CGTGCTCCCTGTTGGGTGTCATCTGTGAAGACTGCCAGGCCTAGGCTCTCTGTAGAG
AGTCTTCAAGATCCCGGAGTGGTAGCGCTGTCTCCTGGTGAAGGAGTATTTGTCACA
CTGGAATGTGACTGTGTGTGTATGTATGTATATATATATATATATATATATAAAA
CAAGTTTGTGACACCTACAAAAA

Saccharomyces cerevisiae orf name: YKL186C

Saccharomyces cerevisiae gene name: MTR2

GENBANK Accession Number: CAA82029.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 88

ATGAACACCAATAGTAATACTATGGTAATGAATGACGCAAATCAAGCACAAATAACG
GCCACATTTACGAAGAAGATATTAGCGCATTTGGATGATCCGGACTCCAACAAATTG
GCCCAATTCGTACAGCTTTTAAATCCAAACAACCTGCAGAATAATATTTAATGCTACCC
CCTTCGCGCAAGCAACAGTTTTTCTGCAAATGTGGCAAAACCAGGTCGTACAAACAC
AACATGCCCTAACAGGAGTAGACTATCACGCTATTCGGGATCCGGCACGTTGATAT
GCAACGTCAATTGCAAAGTCAGATTCGACGAAAGCGGCAGAGACAAGATGGGGCAA
GACGCGACTGTTCCCATTCACCAATAAACAACCTGGGAACAGAAATCGACCCAACGAT
ATGAACAAGCCAAGACCTCTATGGGGTCCATATTTTGGCATTTCCTGCAGCTGATCA
TCGACGACCGCATATTTAGAAATGATTTTAAATGGTGTAATATCGGGGTTTAACTATAA
CATGGTTTACAAACCCGAGGATTCTCTGCTAAAAATTTAG

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 89

CATCCTATAGCACACAACACTAGAGCCGTTTCTCAAACGATTTCTTGCATCGTTAGATT
TACTGTACACACAGCCAACATCACAACCATTCCCCAACGTTGAATCGTATGCCACTCA
GTTAGGATCAAACCTTAAAGCGGTCAAGTGCAATTATAGTGAACGGCCAGCCTATTAT
ACCGAGCCCACAAGAAGACTGTAAATTACAATTCCAAAAGAAATGGTTACAAACTCC
GTTATCGTCACACCAATTGACAAGTTACGATGGGCATTTAATTCCAGGCACGGGGAC
CTTTGTCGTTCAATTTTCAGCAAAAGTAAGATTTGATCAAAGTGGAAGGAACCGGTT
AGGTGAATCTGCCGACTTGTTTCAGGAAAATAATTCAATTGTTTCCAAAACCAATCAA
AGACCTATTTGGGGTTCGTGGTTTGGAGTCGACGTCAATTTGGTTGTTGACGAAAAC
GTTATGCAAGATGGAGAGATTATAAATAGTATGGATTATAGATTTACCTATGTACCT
AACGATAGCATTATAAAAGTATAA

Saccharomyces cerevisiae orf name: YKR062W

Saccharomyces cerevisiae gene name: TFA2

GENBANK Accession Number: CAA82141.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 79

ATGAGTAAAAACAGGGACCCCTCTACTGGCTAATTTGAACGCTTTCAAAAGCAAAGTG
AAGTCTGCCCCGGTGATCGCACCCGCTAAAGTTGGACAGAAGAAGACCAATGACACA
GTGATTACTATAGATGGAACACTAGGAAGAGGACGGCCTCCGAACGTGCGCAAGA
AAACACTTTGAACTCTGCGAAAAATCCTGTGTAGTGGATATCAAGAAAGAAGCTGG
GAGCAATAGCTCTAATGCTATTTTCATTAGATGACGACGATGACGACGAAGATTTTGG
TAGCTCTCCTTCAAAAAAAGTAAGGCCTGGCTCTATTGCTGCAGCCGCTTTACAAGCA
AATCAAACAGATATTTCCAAGAGTCACGATTCTTCAAAGTTGCTTTGGGCGACTGAA
TACATTCAAAGAAAGGTAAGCCCGTTTTGGTGAATGAGTTATTGGACTACTTGTCA
ATGAAAAAAGATGACAAGGTTATTGAGCTTTTAAAAAATTAGATAGAATAGAGTTT
GACCCCAAGAAGGGGACTTTCAAATACCTTTCCACCTACGATGTCCATTCCCCTTCGG
AACTGCTGAAGTTGTTACGTTTACAAGTAACATTCAAAGGTATTTCTGCAAAGACTT
GAAAGACGGTTGGCCACAATGCGATGAAACGATTAACCAACTGGAGGAAGACAGCA
AAATTTTGGTGTTAAGAACTAAAAAGGATAAACTCCAAGATACGTTTGGTATAACA
GCGGTGGTAACTTGAAATGTATTGACGAGGAGTTTGTAAAAATGTGGGAAAATGTGC
AATTACCGCAATTTGCAGAATTGCCAAGAAAGCTGCAAGATTTAGGTCTAAAGCCTG
CTAGTGTGATCCTGCTACTATCAAAAAGACAAACAAAGAGAGTTGAAGTTAAAAAGA
AGAGACAAAGAAAGGGTAAGATTACTAACAACCTCATATGACCGGTATC

Candida albicans nucleic acid: SEQ ID NO: 80

ATGTCGGACTTATCAGCTCAACTTTTCAAGATAAGATCAAAAGTGGACCAT
CGGTGATTGTTCTAGAAAGGCAACTTTTACTCAATCTCCATCATCACCATTATCATC
ATCAACCACAACAACAACACTGAAGAATGACGCCAATGTGAAGAAGAGATCAACGA
CGGATTCAGTAACCCGAGTATTGAAGAAACAAAAGGCAATATGGGAGAAATGACG
GGATCACATTTATCGACACAATTACACCTTGCTGTTGAATATATCAAGGAACATGACC

FIGURE 80 (CONT'D)

AACCAATATCGGTGGAGAAGTTGCAGAATTATTTATCATTGATATATCACATACTTT
ATTGCCATTATTGAATGAAATTGATCGAGTGAAATACGACGAATCTAAGGGTACAT
TGGAATATGTTTCATTGCATAATATTCGTAGTAGTGATGATTTATTGGAATTTTGGAG
ACGTCAAACCAACATTCAAGGGCACTTCCGTAAAAGAATTAAAAGATGGTTGGGCTGG
TTGTGTTGCCGCTATAGACGAATTAGAATCACAAGGCAAAATTTTGGTGTTCGTAA
CAAGAAGGAAAATGCTCCAAGATTAGTATGGGCTAATAATGGTGGTGAGTTGGGTTA
TATTGACACAGAATTCAAGGATATGTGGGATCAAGTGAAATTGCCGGAACCAGATGT
ATTGTATCAGAAATTATTGGATCAAGGATTGAAACCTACGGGAGCTGATCCTAATTT
GATCAAAAAGCAACCACAACAAAAGGAAAAGAAACAAAAGAAAGCAAGAAGAGGAAA
GATTACAAATACACATATGAAAGGTATTTGAAGGATTATTCTCAATTAGTTTGA

Human GENBANK Accession Number: NM_002095.1

Human nucleic acid sequence: SEQ ID NO: 81

CTTAAATTACCCACTACGTTGTCCAGTCGCCGCTCAGCTACCGCCGCTGCCGCCGCCGC
CGCCGCCACCGCCAGTGGTGAGACCCCGACCTGGCGGGTTCAGCGCTGGGCGTGCGTG
CGGGCAGGCGGGGGCGCTGACGAGAAGCAGGAAGAGGGTGCAGTGCCGGCGTGGGC
GGCCGGCCGAGGCGGAGGCGCAGGAAGGGGGCGGCGAGTCGTGCGAGGCTGCCCTT
CTCACTCAGCATTATGGATCCAAGCCTGTTGAGAGAAAAGGGAGCTGTTCAAAAAACG
AGCTCTTTCTACTCCTGTAGTAGAAAAACGTTTCAGCATCTTCTGAGTCATCATCATCA
TCGTCAAAGAAGAAGAAAACAAAGGTAGAACATGGAGGATCGTCAGGCTCTAAACA
AAATTCTGATCATAGCAATGGATCATTAACTTGAAAGCTTTGTCAGGAAGCTCTGG
ATATAAGTTTGGTGTCTTGCTAAGATTGTGAATTACATGAAGACACGGCATCAGCG
AGGAGATACGCATCCTCTAACCTTAGATGAAATTTGGATGAAACACAACATTTAGA
TATTGGACTCAAGCAGAAACAATGGCTAATGACTGAGGCTTTAGTCAACAATCCCAA
AATTGAAGTAATAGATGGGAAGTATGCTTCAAGCCCAAGTACAACGTGAGAGATAA
GAAGGCCCTACTTAGGCTCTTAGATCAGCATGACCAGCGAGGATTAGGAGGAATTCT
TTTAGAAGACATAGAAGAAGCACTGCCCAATTCCCAGAAAGCTGTCAAGGCTTTGGG
GGACCAGATACTATTTGTAAATCGTCCCGATAAGAAGAAAATACTTTTCTTCAATGAT
AAGAGCTGTCAGTTTTCTGTGGATGAAGAATTCAGAAACTGTGGAGGAGTGTCACT
GTAGATTCCATGGACGAGGAGAAAATTGAAGAATATCTGAAGCGACAGGGTATTTCT
TCCATGCAGGAATCTGGACCAAAGAAAGTGGCCCTATTTCAGAGAAGGAAAAAGCCT
GCTTCACAGAAAAAGCGACGCTTTAAGACTCATAACGAACACTTGGCTGGAGTGCTG
AAGGATTACTCTGACATTACTTCCAGCAAATAGGGAACAGTTTTGCCCTGGAACAGA
GTTACAGATACACAATCAAGAGTGTTCTTGCTGATGCTCGGGGTCTGAAGACTGTCTT
CCTATCTGCTTCTTGCGGCTGAGGAGAGGAGCAGTTCAGTTTACAAAACAAGTGCAA
ATTACCAAACCTCAAAGCTTATTTGAGTAGAATGGGCTCATGGGCAATGTGATGTTCC
CTGTTAACCTTCTGTTACTCCCTGGGAGAAAGGCGCTGAGCGTGGCATGCAGGTGTC
TTTGCTGTGTTTTCTCCACTTCTAAATGGTTCCTGGTTCCTTTCTTCCTCGTTTGTTA
CTTTAGAGCAAGTTTGCCCATAGTCTTGAATGCAATATTTGTTTATTCCAAAAGAACA
TATTTATAATAA

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YLR078C

Saccharomyces cerevisiae gene name: BOS1

GENBANK Accession Number: CAA97636.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 90

ATGAACGCTCTTTACAACCATGCTGTGAAGCAAAAAATCAACTACAACAAGAGTTG
GCCAGGTTTGAAAAGAATTCTGTGACCGCCCTATTTCTTTACAAGGGTCCATCTCTG
CAACTCTGGTCTCACTGGAGAAAACAGTTAAGCAATATGCAGAACATTTAAACAGAT
ATAAGAAGATACTAATGCAGAGGAAATTGATCCTAAGTTCGCTAATCGACTAGCAA
CTTTAACACAGGATCTGCACGACTTTACTGCCAAGTTTAAGGATTTAAAACAATCCTA
CAACGAAAATAATTCCAGAACTCAGTTGTTTGGCTCAGGAGCATCGCATGTTATGGA
CTCCGATAACCCCTTTAGTACATCAGAGACCATCATGAATAAAAGGAACGTTGGTGG
TGCGAGTGCAAATGGTAAAGAGGGCTCTAGCAACGGTGGGGGACTACCGTTGTACCA
AGGGCTACAAAAGGAACAGTCTGTTTTCGAAAGGGGTAACGCTCAATTAGATTACAT
TCTAGAAATGGGCCAACAATCATTGCGAAATATAGTGGAACAAAACAAAATTTTATC
CAAGGTACAAGATAGAATGTCAAATGGCCTAAGAACATTGGGTGTTTCGGAACAAAC
TATCACCTCTATCAATAAACGGGTGTTCAAAGATAAACTAGTCTTTTGGATCGCGTTA
ATTCTCTTGATCATAGGTATTTATTATGTGTTG

Candida albicans nucleic acid: SEQ ID NO: 91

ATGAATTCAATATATAATCATGGTTTAAACAAACCCAAACTATAACTAAAGATTTAA
CTCAATTCGAGAAAACTTATCCACATCACCATTATCATTACAAGTGCAATCACAACA
TCATTAAGTGCATTTCAGGAAAACTATCGAAGAATATGATGATTTATTGGAAGTAAAT
GTCTATGATACATCTGATACCATAGATGAGGGTAGATTAGATATATTCAATCCAGATT
TAAATGAATACACTCTGAAATATGATACTTTAAATAAGCTACGTGAGTTTCTTCTCCA
TCAAGCTAATAAACAAGAATTATTAGGAGAAGGACACTTATCACCAACAGCAACAGC
AGCATTGGATCGACATCATCAGATAATCCGTATGAATCTAGCTCAAATCCATCTCAAC
AACAAACAGCAATTACAAGATGAACAAAACACCATGTCTTATAGAGAAGGATTAT
ATCATGAAAAGAATTCTCTAGA

Human GENBANK Accession Number: NM_003569.1

Human nucleic acid sequence: SEQ ID NO: 92

GAGGGAGCCGTGGAGGTCCAGGTGACTGCTTAGAAAACTGCACAGCATCTGATGAA
ATTAGCGAATAAGAACATCAACCATGTCTTACACTCCAGGAGTTGGTGGTGACCCCA
CCCAGTTGGCCCAGAGGATCTCTTCTAACATCCAGAAGATCACACAGTGTTCTGTGG
AAATACAAAGAACTCTGAATCAACTTGGAACACCTCAAGATTCACCTGAATTGAGGC
AACAGTTGCAACAGAAGCAGCAGTATACTAACCAGCTTGCCAAAGAAACAGATAAGT
ACATTAAAGAGTTTGGATCTCTGCCCACCACCCCAAGTGAACAGCGTCAAAGGAAAA
TACAGAAGGATCGCTTAGTGGCAGAGTTCACAACATCACTGACAACTTCCAGAAGG
TCCAGAGGCAGGCTGCTGAGCGAGAGAAAGAGTTTGTGCTCGAGTAAGAGCCAGTT
CCAGAGTGTCTGCCAGTTTTCCTGAGGACAGCTCAAAGAAAGGAATCTTGTATCCT

FIGURE 80 (CONT'D)

GGGAAAGCCAACTCAACCTCAAGTGCAGGTGCAGGATGAAGAAATTACAGAGGAT
GACCTCCGTCTTATTCATGAGAGAGAATCTTCTATCAGGCAACTTGAAGCTGATATTA
TGGATATTAATGAAATATTTAAAGATTTGGGAATGATGATTCATGAACAAGGAGATG
TAATAGATAGCATAGAAGCCAATGTGGAAAATGCAGAGGTGCACGTTTCAGCAAGCA
AATCAGCAGCTGTCAAGGGCAGCAGATTATCAGCGCAAATCCAGAAAAACCTGTGC
ATCATCATTCTTATCCTTGTATTGGAGTTGCGATTATCAGTCTCATCATATGGGGAT
TGAACCACTGAAGTTATAAAGGAGCACACTGTCGCACTACATTGTCTAAATTATGTA
GGAAGATTCCCTGTAATCATGTTTTTTTAAATTATTATTTTAAAGCTATTGTATAAAGGA
TGGTTCCCATACTTTGTTATTTTTATTGGGGGGGTTGGGCGGGTTCCTTTGGATTAAA
TCTGATATTTTCTAATACTGAAAGATTTTCTAAATGTCAGTCTGACATAACTCCCTT
GGTCTTCAATTTAATAGTTGTTAAGTTTTGGGCCACATTGCATATGCCTTTCATTTAT
AATTTATTTACCCTGCTTGACTTAGTTTGGGAATTCGGAAATTTAAGGTGTGTGTAT
TCTGTTGGGATCTCCCTGCCACGTGAACACACCAAGATGTGTGTTACTTCAAGTTAAAA
CTCCCCAAAATTTAATTTTTGATTTGCTTCCACCAGGGGAAAATATTCTCCAATAATGTA
AAATAATTAAGGTCCAATACATGGGTTGTATTTTTCTGGTTCACAACAGCACAAAGTGTG
TTTCATTTTTTTGTTGGATTTCCTTTAAGATCTTTTTTACCCTGAAGTCGGTGAACACTT
TTCTAGTTAATTTGATACTCTTCTGTGTATATAATAAGCTTTTGCTGTAGATTGCCTAG
TAAATTACTAAGGATAGGTTGTTTTTACATATGGTCTATTTAAGTCTGATGTTTACGGG

Saccharomyces cerevisiae orf name: YLR291C

Saccharomyces cerevisiae gene name: GCD7

GENBANK Accession Number: AAB67337.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 116

ATGTCCTCTCAAGCATTCACTTCAGTACATCCGAATGCGGCAACATCTGATGTGAATGTT
ACCATTGACACTTTCGTTGCTAAGTTAAAAAGAAGACAAGTGCAAGGTTTCATACGCCATC
GCCTTGGAACCTTTACAACCTGTTAATGCGATTTATCTCTGCAGCTCGTTGGAACCATGTT
AATGACCTTATTGAACAAATCAGAGATTTAGGTAATAGTCTAGAAAAAGCTCATCCTACT
GCTTTCAGTTGCGGTAACGTAATTAGAAGAATACTGGCTGTTTTGAGGGATGAAGTA
GAAGAAGACACTATGAGCACAACTGTCACATCCACATCCGTTGCTGAACCTTTGATTT
CCTCTATGTTTAATTTATTACAGAAACCGGAGCAACCTCATCAGAATAGAAAAAATA
GTTCAGGGAGCTCTAGTATGAAAACCAAGACTGATTACCGTCAAGTAGCCATTACAGG
GTATCAAGGATCTTATAGATGAGATAAAAAACATTGATGAAGGTATTCAGCAAATTG
CTATTGATTTGATTACGATCATGAGATTTTATTAACCTCCACACCTGATTCAAAAAC
CGTATTAATAATTTCTGATTACTGCTCGCGAACGTAGTAATAGAACATTTACGGTTTTA
GTTACAGAGGGGTTCCCTAATAACACCAAGAATGCACATGAGTTTGCCAAAAAATTA
GCACAGCACAAACATAGAAACCCTAGTAGTCCCAGACTCAGCTGTTTTTGTCTTTAATGT
CCCGTGTGGGTAAGGTTATTATCGGCACTAAAGCCGTTTTTGTCAATGGGGGGACTA
TCTCGTCAAATTCAGGTGTATCATCCGTTTGTGAATGCGCCCGAGAATTTAGAACCCC
TGTATTTGCTGTTGCAGGTTTGATAAGCTTTCTCTCTATATCCGTTTCGACGTAGAG
AAGTTTGTGCAATTTGGTGGGTCCCAACGTATATTACCTAGAATGGATCCAAGAAAA
AGATTAGATACAGTTAATCAAAATACCGATTATGTTCCGCCTGAAAATATTGATATCT

FIGURE 80 (CONT'D)

ACATTACAAACGTCGGTGGGTTCAATCCAAGTTTTATATATCGTATTGCGTGGGATAA
TTACAAGCAAATTGATGTGCATTTGGATAAAAATAAG

Candida albicans nucleic acid: SEQ ID NO: 117

ATGTCGAAATTGCTTACTCCTGAAATTCTAGCGCTCATAGACCCAGTGGTGTCTAGTT
TGAAACGTCATCAGCTTGTGGATGATAAGGAGATAGCATTAAACAATTGCCAGTTGT
TGATGAAAGTCATATCAGCAGCAAGATGGTCTAATACATATGATTTAATTGAATTGA
TAAGACAAGTTGGTGTATATTTACCGAAGCATATCCTAGAAAAGTCATTCCAGGAA
ATATTGTGAGAAGAGTGTTAGCTTTAATACGTGATGAAACCGAAACTGAAACTGAGA
CAGAGACTGAACAAACAGATAACATCCCAATGATGAGCTCTATGTTTAGTTTATTGG
CAACACATAACAAAAATGAACTATAAAGGAACAAACACAATTACAACCTGAAGAAAC
AAACAAGCGATATGAGAGCCATAATTATACAAGGGATTAGAGATTTAGTTGATGAAA
TTTCCAATGTTAATGATGGGATTGAACTATGGCGGTTGATTTGATTCATGACGATGA
AATATTATTAACCTCAACCCCTAATTTCGGAACAGTGCAACATTTTTTAATCAAAGCA
AGATTGAAAAGAAAATTACAGTAGTTGTTACTGAAAACCTATCCAAACGACATCAAG
GCAGCCCAACAAGTTTGTAAGACACTAGCTGAACACAACATCGAAACAATTTAATT
CCAGACACAACAATTTATGCAGTGATGTCAAGAGTTGGGAAAGTTATAATAGGTACT
AATGCTGTATTTGCCAATGGTGGCTGTTTGTGAGATTCAGGTGTTGCCAATGTAGTTG
AATGTGCCAAAGAACACAGAACACCTGTGTTTGTGCTGTGGCAGGGTTATTCAAATTAT
CTCCATTGTATCCATTTACAAGAAACGATTTGATTGAAGTAGGAAACTCCGGGAAGG
TTTTGAACTACGACGATTTTGAATTGGTACAAAATGTTGATGTTGTGACTAATCCTTT
GGAAGATTATATACCTCCTCAACATATCGACATTTTATGACCAATATTGGAGGGTTT
TCTCCTTCATTTATTATAGAATTGTTTTGGATAATTATAAAGCTGAAGACAACAAAC
TTGAATAA

Human GENBANK Accession Number: L40395.1

Human nucleic acid sequence: SEQ ID NO: 118

AAAAAGGGTTCGGAGTTGTCAGAGAGGATCGAGAGCTTCGTGGAGACCCTGACGCG
GGGTGGTGGGCCGCGCAGGTCCGAGGAAATGGTTCGGGAGACCCTAGGGTTGCTGCG
CCAGATCATCACGGACCACCGATGGAGAAACGCGGGGGAGCTGATGGAGCTGATCC
GCAGAGAGGGCAGGAGGATGACGGCCGCTCAGCCCTCCGAGACCACCGTGGGCAAC
ATGGTGCAGAGAGTGCTCAAGATTATCCGGGAGGAGTATGGAGACTCCATGGACGC
AGCGACGGAGAGTGATCAGCAGGAGTCCCTGGACAACTGTTGACAYCCGGAGGCC
TAAACGAGGATTTGAGCTTCCATTATGSCCAACTCCAGTCCAACATCATTGAGGCGAT
TAATGAGCTGCTAGTGGAGCTGGAAGGGACAATGGAGAACATTGCAGCCCAGGCTCT
GGAGCACATTCACCTCAATGAGGTGATCATGACCATTGGCTTCTCCCGAACAGTAGA
GGCCTTCCTCAAAGAGGGCTGCCCGAAAAGAGGAAATTCATGTGATTGTAGCAGAGTG
TGCTCCTTTCTGCCAGGGTCATGAAATGGCTGTGAATTTGTCCAAAGCAGGTATTGA
GACAACTGTCATGACTGATGCTGCCATTTTTGCCGTTATGTCAAGAGTCAACAAGGT
GATCATTGGCACCGAAGACCATCCTGGCCAATGGGGCCCTGAGAGCTGTGACAGGAA

FIGURE 80 (CONT'D)

CTCACACTCTGGCACTGGCAGCAAAACACCATTCCACCCCACTCATCGTCTTGTGCAC
CTATGTTCAAACCTTTCTCCACAGTTCCCCAATGAAGRRGMCYCATWWMATAAGTTTG
GTGGCTCCTGAAGAAGTCCTGCCATTACAGAAGGGGAMATYCTGGAGAAGGTCAG
CGTGCATTGYCCTGTGTTTGACTACGYTCCCCCAGAGCTCAWTACCCTCTTTAGCGTGA
TCTCCAACATTGGTGGGAATGCACCTTCTTACATCTACCGCCTGATGAGTGAACCTCTACC
ATCCTGATGAWCATGTTTTATGACCGACCACACGTGTCCTAAGCAGATTGCTTAGGC
AGATACAGAWTGAAGAGGAGACTTGAGTGTTGCTGCTGAAGCACATCCTTGCAATGT
GGGAGTGCACAGGAGTCCACCWAAAAAAAAAATCCTTGATACTGTTGCCTGCCTTTT
TAGTACCCCCGTAACAAGGGCACACATMCAGCAYTGTGTCTTGCCTTTCAGATCTTA
ACAGAGCAGCAGGGCTTAACTTGTTGATTTKGGAGSCTCTTAGTGACCTGGTTGCGTC
TGTGTCAGGAACCTTAACTTTCTGGTTCAGTAGTGTGKTAACATAACRCTGWANAC
CTTACTGGGATACAGATTTTTGCTCAGAAATGGCTATGACACTTTTTCTAGGCTCTAC
CAATAAAARCCACTTGAAGGTTT

Saccharomyces cerevisiae orf name: YMR005W

Saccharomyces cerevisiae gene name: MPT1

GENBANK Accession Number: CAA88520.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 85

ATGGCAAATTCGCCGAAAAAGCCATCTGATGGCACTGGAGTATCAGCGTCAGACACG
CCTAAATATCAACATACCGTCCCAGAAACGAAACCAGCATTTAATTTGTCACCAGGT
AAAGCTAGTGAGCTATCACATAGCCTTCCGTCGCCTAGCCAGATAAAATCAACCGCA
CATGTATCTTCAACTCACAATGATGCGGCAGGTAATACGGATGATTCTGTTCTTCCTA
AAAATGTATCACCCACAATAATTTGAGAGTTGAAAGTAATGGAGATACAAACAATA
TGTTCTCTAGCCCTGCTGGACTAGCTCTACCAAAAAAGGATGATAAAAAAAAAAACA
AGGGTACGAGTAAAGCAGATTCTAAAGATGGCAAAGCATCCAACCTCAGGACAGA
ATGCACAACAACAATCAGACCCAAATAAAATGCAAGATGTCCTTTTTTCCGCAGGTA
TCGATGTTAGGGAGGAGGAGGCTCTTCTAAATTCATCTATTAATGCCTCAAATCCCA
AGTTCAAACAATAACGTTAAGATCCCCAACCATTACCATTCCTTCACCCGGAACAA
GTTTCCAATTATATGAGGAAAGTCGGAAAAGAGCAAAACTTCAACCTGACCCCTACA
AAGAATCCTGAAATTTTGGACATGATGTCAAGTGCCTGCGAAAACTATATGAGAGAT
ATCCTAACAAATGCCATTGTCATCTCCCGACATAGAAGAAAAGCAGTCAAGATAAAT
TCTGGTAGAAGAAGTGAAGTTTCTGCGGCTTTAAGAGCCATTGCACTAATTCAAAAA
AAAGAAGAAGAAAGGCGTGTGAAAAAAGAATTGCGTTGGGACTCGAGAAGGAAGA
TTATGAAAATAAGATTGATTCCGAAGAGACGTTACACAGAGCATCGAACGTTACGGC
TGGCCTTAGAGCAGGTAGTAAAAACAGTATGGTTGGCTAACTTCATCAGTAAATAA
GCCGACGTCCTTGGGAGCAAAATCTTCAGGCAAAGTCGCCTCCGACATCACGGCTAG
AGGAGAAAGTGGGCTAAAGTTTAGAGAAGCTAGAGAGGAGCCTGGTATAGTAATGA
GGGATTTACTCTTTGCTCTCGAAAATAGGCGCAACAGCGTTCAGACTATTATTCA

FIGURE 80 (CONT'D)

Candida albicans nucleic acid: SEQ ID NO: 86

AATCACCGAATTATATCACATAAAATCCATGACAAGTACACCTCAAGAATCCTCTAATT
TAAAGAGACAATTAGAAAACAGTGAGGACTCCAGCTCACCAAATAAGGAATCTAAAA
CAGAGACTACCACGGAACAGAGCTCATGGGAGTCTGACTTTAATAGTTTACCAG
TGGAATTACTACAACTGAAACAAATGGTACATCACCAGCACCAGCACCAGCAACAC
CGATCGATACCACCAATGCATCAAGCACAAAGGAACGTGATCAGGATACTTCTAAAT
TAAATGACGCGATTGCTGCTGCAGGAGTTGATATTCAACAAGAAGAAGAGATATTAT
TACAACAACAATTAAATAGAAAATCTGCAGAGGGTATGGCAAGCAATCTAAAAAGTG
TGATCAGGTCCAGCAAACCTGCCTCCATTTCTACACAATTACCATTTAGCTGCCTTTAT
TGATAAAGTGCTAAACAAAATGGAATTCAACAGAATTTCTTAATGGATGGTGAGAT
GTTGGAATTAATTTAGCTGCTTGTGAGACTTGGTTAAGTAATCTAGCAACAAAAAC
GATAATCTTGTACGCCACAGGAGAAGGGGAATACCTGTTATTAATAAGAAGTCAGG
AAGTAGTTCAGTTCCAAGATCAGAAATTTCAAAAGAATTGAGAAGCTTGGCCTTAAA
ACAAAAGGAAATGGAAGAGAAACGAGTGAATAAAAGAGTGATGTTGGGGTTGGAAA
AAAGCACCAAAGACGCATCCAAAAATGACGAAAATGGTGAATCAAAGCTGGTGCTGA
AGAAACATTACATCGTGCAGCAAATGCTACAGCTGCAATGATGACTATGAATCCCGG
GAGAAAGAAATATAGTTGGATGACTTCAAGTGCTACAGCAGGCGGTGGGTGAGACTT
TGGTAAATCAAGTGGTGGCTCATCAAAGGACTCGGGAAAACACCAAAGTCCTATTAT
TTCAGTACGTGGTGATAATGGCCTTAGGTTTAGAGAAATAAGGTCAGGTAATTCCAT
TATTATGAAAGATTTGTTAGGCGCAATTGAAGATGAAAAAATGGGTACGAGAAATGC
TGTAATAAAAGGATATGCAAAATTGAAAGATTAA

Human GENBANK Accession Number: Y11354.1

Human nucleic acid sequence: SEQ ID NO: 87

ATGGCGGCGGGCTCGGATCTGCTGGACGAGGTCTTCTTCAACAGCGAGGTGGACGAG
AAAGTGGTGAGCGACCTGGTGGGCTCGCTGGAGTCGCAGCTGGCGGCCAGCGCGGC
CCACCACCACCCTCGCGCCGCGCACGCCCCGAGGTGCGGGCCGCGGCCCGCGCGC
GCTCGGGAACCATGTTGTGAGCGGCAGCCCGGCCGGAGCCGCGGGCGCAGGGCCGG
CCGCCCCCGCGAGGGCGCGCCCCGAGCGCGCGCGGAGCCGCCCCCGCAGGTAGA
GCGCGGCCGGGGGGCGGGGGGCGCGAGCGCCCGGGCCCCCCCCCTACCGCGCCGCC
CCTTGTCCTCGCAGGGCCCCGCGCCCGCCCGCGCAAGCTGAGGCCGCGCCCGAGGG
CAGCGCGGGGGCCTGCGCCCCGGTGCCCCCGCGCCCGCGCGCTGCGCGCGGGGCCG
AGCCCCCCCCCGCGGCCCGCCCAAGCCCCGCGCGCCCCGCGCGCTGGCCGCCCCGCG
CCGGCCCCCGGCCCGGGCCCCGCCCCGCCCCGCCCCGGCCCTGGCAAGCCCCGCG
GCCCCGCGCGCGCAAACCTTTGAATGGGAGCGCCGCGCTGCTGAACTCGACACAG
CCGCCGCACCTGCTGTCAGCCTGGTCAACAACGGGCCCGCCGCGCTGCTGCCGCTGC
CAAAGCCCCGCGCCCCCGGCACTGTCATCCAGACGCCCCCTTCGTGGGCGCCGCCG
CGCCCCCGCGCCCCCGCGCGCCCTCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCG
CCGCCGCCCCGCCCCCGCCACCCCCCGCGCCCGCCACCCTGGCCCGGCCGCCCGGCC
ACCCCGCCGGACCCCCGACCGCCGCGCCCGCGCTGCCGCCCCCGCGCGCCAAGGGTT
ATGCCAAGATCAGAGATTAAGCCAGAACGGGGGCAGCGCCGGGGCAGCCCCCGCC

FIGURE 80 (CONT'D)

CCCCCCCCGGCCGCCGGGGGCCCCGCTGGGGTCAGCGGCCAGCCCCGGGCCCCGGCGC
GGCGGCTGCGGCGCCGGCGCCGGGGGTCAAGGCCGAGTCGCCCAAGAGGGTGGTGC
AGGCGGCGCCCCCGGCGGGCGCAGACCCTGGCGGCCAGCGGCCCGGCCAGCACGGCG
GCCAGCATGGTCATCGGGCCAATATGCAAGGGGCGCTGCCAGCCCCGGCCGCCGTC
CCGCCGCCCGCCCCGGGACCCCCACCGGGCTGCCCAAAGGCGCGGCCGGCGCAGTG
ACCCAGAGCCTGTCCCGGACGCCACGGCCACCACCAGCGGGATTTCGGGCCACCCTG
ACGCCCCACCGTGCTGGCCCCCGCTTGCCGCAGCCGCCTCAGAACCCGACCAACATC
CAGAACTTCCAGCTGCCCCCAGGAATGGTCCTCGTCCGAAGTGAGAATGGGCAGTTG
TTAATGATTCTCAGCAGGCCTTGCCCCAGATGCAGGCGCAGGCCCATGCCAGCCT
CAGACCACCATGGCGCCTCGCCCTGCCACCCCCACAAGTGCCCTCCCGTCCAGATCT
CCACCGTACAGGCACCTGGAACACCTATCATTGCACGGCAGGTGACCCCAACTACCA
TAATTAAGCAAGTGCTCAGGCCCAGACAACGGTGCAGCCAGTGCAACCCTGCAGCGC
TCGCCCGGCGTCCAGCCTCAGCTCGTTCTGGGTGGCGCTGCCAGACGGCTTCACTTGGG
ACGGCGACGGCTGTTACAGACGGGGACTCCTCAGCGCACGGTACCAGGGGCGACCAC
CACTTCCTCAGCTGCCACGGAACCTATGGAAAACGTGAAGAAATGTAAAAATTTCT
ATCTACGTTAATAAACTGGCTTCATCTGGCAAGCAGTCTACAGAGACAGCAGCTAA
TGTGAAAGAGCTCGTGCAGAATTTACTGGATGGAAAAATAGAAGCAGAAGATTTAC
AAGCAGGTTATACCGAGAACTTAATTCTTCACTCAACCTTACCTTGTGCTTTCTCTG
AAGAGGAGCTTACCCGCTTGAGACAGCTGACCCCCGACTCCGCGGCCTTCATCCAG
CAGAGCCAGCAGCAGCCGCCACCGCCACCTCGCAGGCCACCACTGCGCTCACGGCC
GTGGTGCTGAGTAGCTCGGTCCAGCGCACGGCCGGGAAGACGGCGGCCACCGTGAC
CAGTGCCCTCCAGCCCCCTGTGCTCAGCCTCACGCAGCCACGCAGGTTCGGCGTCGG
CAAGCAGGGGCAACCCACACCGCTGGTCATCCAGCAGCCTCCGAAGCCAGGAGCCCT
GATCCGGCCCCCGCAGGTGACGTTGACGCAG

Saccharomyces cerevisiae orf name: YMR131C

Saccharomyces cerevisiae gene name: RSA2

GENBANK Accession Number: CAA88556.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 96

ATGTCGAAAAGGTCTATCGAGGTCAACGAGGAACAAGATAGAGTGGTCTCTGCTAAA
ACAGAATCTCACTCTGTTCCTGCTATTCCCGCCTCTGAAGAGCAAGATGCTCCCAAGA
ATGACCTAGAAGAACAATTGAGTGATGAATTTGATAGTGATGGTGAAATTATTGAAA
TTGATGGCGATGATGAGATTAATGACGAAGATGACCTTAGGAAAAAGCAAGAAGAA
GCTGAAACTTTAGTACAAAAGGACCAATCCGAAGGCAACAAAGAAAAGATCCAGGA
GCTTTACTTACCCCATATGTCTCGTCCATTAGGGCCAGATGAAGTCCTTGAGGCTGAT
CCCCTGTTTATGAAATGCTACATAATGTCAATATGCCATGGCCATGCTTGACATTAG
ATGTCATTCCAGATACACTAGGTTCTGAACGTAGAACTATCCACAGTCTATTTTGT
GACCACGGCTACTCAATCTTCCAGGAAAAAGGAGAATGAACTAATGGTTCTAGCACT
TTCTAATTTAGCGAAAACACTTTTGAAAGACGATAATGAAGGTGAAGATGATGAAGA
GGATGATGAAGATGATGTGGATCCAGTCATTGAGAATGAAAATATACCATGAGAGA
TACAACCAATAGATTAAAGGTTTCTCTTTTGGCATTCTAATCAAGAGGTGTTAACC

FIGURE 80 (CONT'D)

GCTACAATGAGCGAAAATGGTGATGTTTATATATACAATCTAGCTCCACAAAGCAAA
GCTTTTTCCACACCAGGTTATCAGATTCCGAAGTCTGCTAAGCGTCCTATTCACACTG
TAAAAAATCATGGGAATGTTGAAGGCTACGGGTTGGATTGGTCACCATTGATCAAGA
CTGGTGCGTTACTATCAGGTGATTGCTCAGGACAAATATATTTTACCCAAAGGCACA
CATCGAGATGGGTGACTGATAAACAACCATTACTGTTTCAAACAATAAATCCATAG
AAGATATCCAGTGGTCTCGCACTGAATCCACCGTTTTTGC AACCGCAGGATGTGATG
GATATATAAGGATTTGGGACACAAGATCAAAAAACATAAACCTGCTATCTCTGTTA
AAGCTTCTAATACTGACGTAAATGTCATAAGTTGGAGTGATAAAATTGGTTACTTGCT
AGCAAGCGGTGACGATAACGGTACATGGGGAGTATGGGATTTAAGACAGTTTACGCC
AAGTAATGCTGACGCCGTCCAACCGGTTGCTCAATATGACTTCCATAAGGGAGCCATT
ACTTCCATTGCATTCAACCCATTAGATGAGTCTATCGTTGCGGTAGGCTCAGAAGATAAT
ACTGTGACTTTGTGGGATTTGTCTGTAGAAGCTGACGATGAGGAAATTAACAACAG
GCCGCCGAAACAAAAGAGCTACAAGAAATCCACCACAATTATTGTTTGTTCACTGG
CAAAAGGAAGTTAAAGATGTCAAATGGCATAAGCAAATCCCAGGTTGTTTAGTAAGT
ACCGGTACT

Candida albicans nucleic acid: SEQ ID NO: 97

ATGTCAAAAAGATCAGCTGAAGATGATTTAAGTGGCAATAGATCCACCAGTCATACT
GCCATTA AAACTAATAAAGATTCTCTTCCA ACTACTACAAATGGAAAGGAAGAAGAA
CCAGACAATATGGATATTGGGGAATTTGAAGATCCATACGGTGATGAATTTGAAAGT
GATGAAGAAATTATAGAATTAGACGATAACAATGATGAAGAAGATGATGAAATGATT
GATGAAAATTCAACACAAGCCAAAATTGAAGAATTAGAAGCCAAAGAACAAGAACA
AGAACAACAATCATCAATATATTTACCTCATAAATCAAAACCATTAGGACCAGATGA
AGTCTTAGAAGCCGATCCAACAGTCTATGAAATGTTGCATAATATCAATTTACCATGGC
CATGTTTGACTGTTGATATTTTACCAGATTCTTTAGGTAATGAAAGAAGATCATATCC
AGCAACAGTTTATTTAGCTACTGCGACTCAAGCTGCTAAAGCCAAAGATAATGAATT
GTTAGCTATGAAAGCATCTTCATTGGCCAAAACATTAGTTAAAGATGAAAATGAAGA
AGATGAGGAAGATGAAGACGATGACGATGATGTTGATAGTGATCCAATATTAGATT
AGAATCTATTCCATTAAGACATACTACAAATAGAATAAGAGTAAGTCCTCATGCTCA
ACAACTGGGGAATACTTAACTGCTTCAATGTCAGAAAATGGTGAAGTTTATATATT
TGATTTACTGGCACAATATAAGGCATTTGACACACCAGGTTATATGATTCCTAAATCA
TCGAAAAGACCAATTCATACTATTCGTGCCCATGGGAATGTTGAAGGTTATGGATTA
GATTGGTCTCCATTAGTAAATACAGGGGCTTTATTATCTGGAGATATGTCAGGGAGA
ATTTATTTAACTAATAGAACGACATCAAGTTGGACCACTGATAAACTCCATTTTTG
CATCACAATCTTCAATTGAAGATATTCAATGGTCAACTGGTGAACTACAGTGTTTGC
CACGGGTGGATGTGATGGATATATTTGTATTTGGGATACAAGATCGAAAAACATAA
ACCTGCATTATCAGTAATTGCTTCTAAATCTGATGTTAATGTGATATCTTGGAGTTCT
AAAATCAATCATTTATTGGCATCAGGACATGACGATGGTAGTTGGGGTGTATGGGAT
TTAAGAAATTTACAAACAATACCACCAGTAATCCTTCACCTGTGGCTAATTATGATT
TCCATAAATCGCCAATCACATCAATTTCAATCCATTAGATGAATCAATCATTCG
TGTTTCATCAGAAGATAATACTGTTACATTATGGGATCTTGCTGTTGAAGCTGATGAT

FIGURE 80 (CONT'D)

GAAGAAATTTCTCAACAAAGAAAAGAAGCTCAAGAATTACATGATATTCCACCACAA
TTATTATTTGTCCATTGGCAAAGAGATGTTAAAGATGTTAGATGGCATCCACAAATTC
CTGGTTGTTGGTATCTACTGGTGGTGGTATTAACATTTGGAAAATATATCTGT
GTAA

Human GENBANK Accession Number: NM_005610.1

Human nucleic acid sequence: SEQ ID NO: 98

CGCGCGCACAGAGCGAGCTCTTGACGCTCCCCGCCCCCTCCCGCAACGCTCGACCCC
AGGATTCCCCCGGCTCGCTGCCCGCCATGGCCGACAAGGAAGCAGCCTTCGACGAC
GCAGTGAAGAACGAGTGATCAACGAGGAATACAAAATATGGAAAAAGAACACCCC
TTTTCTTTATGATTTGGTGGTGGTATGACCCATGCTCTGGAGTGGCCCAGCCTAACTGCCAG
TGGCTTCCAGATGTAACCAGACCAGAAGGGAAAGATTTAGCATTTCATCGACTTGTC
CTGGGGACACACACATCGGATGAACAAAACCATCTTGTTATAGCCAGTGTGCAGCTC
CCTAATGATGATGCTCAGTTTGATGCGTCACACTACGACAGTGAGAAAGGAGAATTT
GGAGGTTTTGGTTCAGTTAGTGGAAAAATTGAAATAGAAATCAAGATCAACCATGAA
GGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGATCATCGCAACAAAG
ACTCCTTCCAGTGATGTTCTTGTCTTTGACTATACAAAACATCCTTCTAAACCAGATC
CTTCTGGAGAGTGCAACCCAGACTTGCGTCTCCGTGGACATCAGAAGGAAGGCTATG
GGCTTTCTTGAACCCAAATCTCAGTGGGCACTTACTTAGTGCTTCAGATGACCATAC
CATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAA
GACCATCTTTACAGGGCATAACGGCAGTAGTAGAAGATGTTTCCTGGCATCTACTCCA
TGAGTCTCTGTTTGGGTGAGTTGCTGATGATCAGAACTTATGATTTGGGATACTCGT
TCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGCTCACACTGCTGAAGTGAAC
TGCCTTTCTTTCAATCCTTATAGTGAGTTCACTTCTGCCACAGGATCAGCTGACAAGA
CTGTTGCCTTGTGGGATCTGAGAAATCTGAAACTTAAGTTGCATTCTTTGAGTCACA
TAAGGATGAAATATTCCAGGTTCAAGTGGTACCTCACAAATGAGACTATTTTAGCTTCC
AGTGGTACTGATCGCAGACTGAATGTCTGGGATTTAAGTAAAATTGGAGAGGAACAA
TCCCCAGAAGATGCAGAAGACGGGCCACCAGAGTTGTTGTTTATTCATGGTGGTTCAT
ACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTG
TATCAGAAGACAATATCATGCAAGTGTTGGCAATGGCAGAGAACATTTATAATGATGAA
GACCCTGAAGGAAGCGTGGATCCAGAAGGACAAGGGTCCTAGATATGTCTTTACTTG
TTGTGATTTTAGACTCCCCCTTTTCTTCTCAACCCTGAGAGTGATTTAACACTGGTTT
TGAGACAGACTTTATTCAGCTATCCCTCTATATAATAGGTACCACCGATAATGCTATT
AGCCCCAACCGTGGGTTTTTCTAAATATTAATAGGGGGGCTTGATTCAACAAAGCCA
CAGACTTAACGTTGAAATTTTCTTCAGGAATTTTCTAGTAACCCAGGTCTAAAGTAGC
TACAGAAAGGGGAATATTATGTGTGATTATTTTCTTCTTATGCTATATCCCCAAGTT
TTTCAGACTCATTTAAGTAAAGGCTAGAGTGAGTAAGGAATAGAGCCAAATGAGGTA
GGTGTCTGAGCCATGAAGTATAAATACTGAAAGATGTCACTTTTATTCAGGAAATAG
GGGGAGTTCAAGTCGTATAGATTCTACTCGAAAATCTTGACACCTGACTTTCCAGG
ATGCACATTTTCATACGTAGACCAGTTTCTCTTGGTTTCTTCAGTTAAGTCAAAACA
ACACGTTCTCTTTCCCATATATTCATATATTTTGGCTCGTTAGTGTATTTCTTGAGC

FIGURE 80 (CONT'D)

TGTTTTTCATGTTGTTTATTTCCTGTCTGTGAAATGGTGTTTTTTTTTTTGTTGTTGGTT
TTTTTTTTTTTTTTTTTAACTTGGGACCACCAAGTTGTAAAGATGTATGTTTTTACCTGA
CAGTTATACCACAGGTAGACTGTCAAGTTGAGAAGAGTGAATCAATAACTTGTATTT
GTTTTAAAAATTAAATTAATCCTTGATAAGAGTTGCTTTTTTTTTTTAGGAGTTAGTC
CTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCTGTTTACCAGCAGGCCT
GTTACTCTCCATGACTAACTGTGTAAGTGCTTAA

Saccharomyces cerevisiae orf name: YMR235C

Saccharomyces cerevisiae gene name: RNA1

GENBANK Accession Number: CAA90206.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 113

ATGGCTACCTTGCACTTCGTTCCCTCAGCACGAGGAAGAACAAGTTTACTCCATCTCTGGG
AAGGCACTCAAGTTAACAACCAGTGACGATATCAAACCATACCTGGAAGAATTGGCA
GCTTTGAAAACCTGTACCAAATTAGACCTTTCAGGGAATACAATCGGTACTGAAGCT
TCGGAAGCATTAGCTAAATGCATCGCTGAAAATACACAGGTCAGGGAATCTTTGGTT
GAAGTAAATTTTGCTGACTTATACACTTCGAGGTTGGTTGACGAAGTCGTTGATTCGT
TGAAGTTTTTATTGCCTGTTCTGTTGAAATGTCCTCACTTGGAGATTGTGAACCTTTC
TGATAATGCGTTTGGGCTAAGAACAATCGAGTTACTAGAAGATTACATTGCACATGC
CGTGAATATCAAACATTTGATCTTAAGTAACAATGGTATGGGCCCTTTTGCTGGTGAA
AGGATTGGTAAGGCCCTATTTTCATCTCGCTCAAAAATAAGAAAGCTGCTTCCAAACCA
TTTTTGAAAACCTTTTATCTGTGGTAGAAATAGATTAGAGAATGGATCCGCAGTCTACT
TAGCTCTGGGTTTGAAAAGCCACTCCGAAGGTTTGAAAGTCGTAAAGCTGTACCAAA
ATGGTATTAGGCCTAAAGGTGTCGCCACGCTAATTCATTACGGTTTACAGTACTTGAA
AACTTGGAATCTTGGATCTTCAAGACAATACTTTCACGAAACATGCTTCTTTGATC
CTTGCTAAGGCCTTGCCTACATGGAAGGATAGTTTATTTGAATTGAATTTGAACGACT
GTCTTTTGAAAACCTGCTGGTTCAGATGAAGTCTTTAAAGTATTCACCGAAGTTAAATT
CCCCAATTTGCATGTCTTGAAATTCGAATATAATGAAATGGCTCAAGAAACCATTGA
AGTATCCTTCTTACCGGCTATGGAAAAGGGAAATTTACCTGAATTGGAAAAGCTAGA
AATAAATGGTAACAGATTAGATGAAGATTCTGATGCTTTAGATTTGCTCCAAAGCAA
ATTTGATGATTTAGAGGTTGACGATTTTGAAGAGGTCGATAGTGAAGATGAGGAAGG
CGAGGACGAGGAAGACGAGGACGAGGATGAAAACTCGAAGAAATTGAAACGGAAA
GGCTTGAAAAGGAACTGCTAGAAGTACAAGTAGATGATCTTGCTGAACGT

Candida albicans nucleic acid: SEQ ID NO: 114

ATGGCATCAGTAGAAGTTGAATTAGGAGTTACTCCAGAAACCACTTATTCAATTTCA
GGAAAACAACTAAAATTTGATTCTGAATCGGATATTGCTCCATATATCAAGGAATTG
ACGAAAAAAGAAAATGTCAAAAAAGTTGATTTTTCAGGAAATACTATTGGTATTGAAG
CATCAAAAGCATTAAGTGAAGCATTATTAACATAAAGACACTATCGTTGAAATCA
ACTTTTCTGATTTATACACTGGTAGATTGAATACTGAAATTCCTCAATCTTTAGAGTA
TTTGTACCAGCATTGTCGAAATTGCCAAATTTGAAATTGATCAACTGAGTGACAA

FIGURE 80 (CONT'D)

TGCTTTTGGATTGCAAACTATTGATCCAATTGAAGCTTACTTGGCCAAAGCTGTTTCC
ATCGAGCATTTGATTTTGTCAAACAATGGTATGGGTCCATTTGCTGGGTCAAGAATTG
GAGGATCTTTGTTTAAAGTTAGCTAAGGCTAAGAAAGCAGAAGGAAAGGAGTCTTTGA
AAACATTTATTTGTGGTAGAAACAGATTGGAAAATGGTTCTGTAACTATTTATCTGT
TGGGTAAAGAAATCACAAGGATTTGGAAGTGGTTAGATTGTATCAAAATGGTATTAG
ACCTGCTGGTATTTCTAAATTGGTTGAGCAAGGTTTATCTAACAACAAAAAATTAAA
AGTGCTTGATTTGCAAGACAATACCATCACTACCAGAGGAGCTATTCACATTGCAGA
ATCATTATCTAACTGGCCACTTTTGGTTGAGTTGAATCTTAACGATTCTTATTGAAG
AACAAAGGTTCTTTGAAATTAGTCGAAGCCTTCCATGCTGGAGATGAAAAACCGCAA
TTAATTACCTTGAAATTACAATATAATGAGTTAGAAACAGATAGTTTAAAGAGTTTGG
CTGATGCAATTGCCAGTAAATTACCACAATTGAAGTTCTTGGAATTGAACGGTAATA
GATTTGAAGAGGATTCGGAACATATCGATAAAATCAATGGAATCTTCGAAGAAAGAG
GCTATGGCGAAATAGATGAATTGGATGAATTAGAAGAGCTTGATAGTGAAGAAGAA
GAAGATGACGAGGATGACGAAGGAGAAGACGACACATTAGAGGAAGACCTTGATTT
GACACAATTAGAAGAAGAATTGGCTGGAGTTTCTTTGGAAGACAAAGATGGTAACGTGG
ATGAAATTGCCGAAGAATTATCCAAAACTCATATTAAATAG

Human GENBANK Accession Number: X82260.1

Human nucleic acid sequence: SEQ ID NO: 115

ATGGCCTCGGAAGACATTGCCAAGCTGGCAGAGACACTTGCCAAGACTCAGGTGGCC
GGGGGACAGCTGAGTTTCAAAGGCAAGAGCCTCAAACCTCAACACTGCAGAAAGATGCT
AAAGATGTGATTAAAGAGATTGAAGACTTTGACAGCTTGGAGGCTCTGCGTCTGGAA
GGCAACACAGTGGGCGTGGAAGCAGCCAGGGTCATCGCCAAGGCCTTAGAGAAGAA
GTCGGAGTTGAAGCGCTGCCACTGGAGTGACATGTTACGGGAAGGCTGCGGACCG
AGATCCCACCAGCCCTGATCTCACTAGGGGAAGGACTCATCACAGCTGGGGCTCAGC
TGGTGGAGCTGGACTTAAGCGACAACGCATTGCGGGCCGACGGTGTGCAAGGCTTCG
AGGCCCTGCTCAAGAGCTCAGCCTGCTTCACCCTGCAGGAACTCAAGCTCAACAAC
GTGGCATGGGCATTGGCGGCGGCAAGATCCTGGCTGCAGCTCTGACCGAATGTCACC
GGAAATCCAGTGCCCAAGGCAAGCCTCTGGCCCTGAAGGTCTTTGTGGCTGGCAGAA
ACCGTCTGGAGAATGATGGCGCCACTGCCTTGGCAGAAGCTTTAGGGTCATCGGGA
CCCTGGAGGAGGTCCACATGCCACAGAATGGGATCAACCACCCTGGCATCACTGCCC
TGGCCCAGGCTTTCGCTGTCAACCCCCTGCTGCGGGTCATCAACCTGAATGACAACA
CCTTCACTGAGAAGGGCGCCGTGGCCATGGCCGAGACCTTGAAGACCTTGCGGCAGG
TGGAGGTGATTAATTTTGGGGACTGCCTGGTGCCTCCAAGGGTGCAGTTGCCATTG
CAGATGCCATCCGCGGCGGCTGCCCAAGCTAAAGGAGCTGAACCTGTCTATTCTGTG
AAATCAAGAGGGATGCTGCCCTGGCTGTTGCTGAGGCCATGGCAGACAAAGCTGAGC
TGGAGAAGCTGGACCTGAATGGCAACACCCTGGGAGAAGAAGGCTGTGAACAGCTT
CAGGAGGTGCTGGAGGGCTTCAACATGGCCAAGGTGCTGGCGTCCCTCAGTGATGAC
GAGGACGAGGAGGAGGAGGAAGGAGAAGAGGAAGAAGAGGAAGCAGAAGAAG
AGGAGGAGGAAGATGAGGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAAGA
GCCTCAGCAGCGAGGGCAGGGAGAGAAGTCAGCCACGCCCTCACGGAAGATTCTGG

FIGURE 80 (CONT'D)

ACCCTAACACTGGGGAGCCAGCTCCCGTGCTGTCCTCCCCACCTCCTGCAGACGTCTC
CACCTTCCTGGCTTTTCCCTCTCCAGAGAAGCTCCTGCGCCTAGGGCCCAAGAGCTCC
GTGCTGATAGCCAGCAGACTGACACGTCTGACCCCGAGAAGGTGGTCTCTGCCTTC
CTAAAGGTGTCATCTGTGTTCTTAGCTGAAACTGAAATCAAATAGAAGGACGAAGCT
ACTGTGAGGATGGCAGTGCAGGATGCAGTAGATGCCCTGATGCAGAAGGCTTTCAAC
TCCTCGTCCTTCAACTCCAACACCTTCCTCACCAGGCTCCTCGTGCACATGGGTCTGC
TCAAGAGTGAAGACAAGGTCAAGGCCATTGCCAACCTGTACGGCCCCCTGATGGCGC
TGAACCACATGGTGCAGCAGGACTATTTCCCCAAGGCCCTTGACCCCTGCTGCTGG
CGTTCGTGACCAAGCCCAACAGCGCCCTGGAATCCTGCTCCTTCGCCCGCCACAGTCTG
CTGCAGACGCTGTACAAGGTCTAG

Saccharomyces cerevisiae orf name: YMR309C

Saccharomyces cerevisiae gene name: NIP1

GENBANK Accession Number: A46417

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 122

ATGTCCCGTTTCTTTTCGTCTAATTACGAATACGATGTAGCCAGTTCTTCATCCGAAGAA
GATCTTTTATCTTCGTCTGAAGAAGATTTGTTAAGCTCTTCCTCCTCTGAGTCTGAATTG
GACCAAGAATCTGACGACTCCTTTTTCAATGAAAGTGAAAGTGAAAGTGAAAGCTGAT
GTAGACTCTGATGATTCTGATGCAAAGCCTTATGGTCCTGACTGGTTCAAGAAATCTG
AGTTCAGAAAACAAGGTGGAGGTTCAAATAAATTTTGAAGGCTCTAACTATGATT
CCAGTGATGAAGAATCCGATGAAGAAGATGGCAAGAAGGTAGTCAAGTCTGCCAAA
GAAAAACTATTGGATGAAATGCAAGACGTTTATAATAAGATCTCTCAAGCTGAGAAC
TCTGATGACTGGTTGACTATTTCTAATGAGTTTGATTTGATCTCGCGTCTCTTAGTTA
GGGCTCAACAACAAAACCTGGGGGACTCCAAATATTTTCATCAAGGTTGTTGCCCAAG
TGGAGGACGCTGTGAATAATACACAACAAGCTGATTTGAAGAATAAAGCTGTTGCAA
GAGCTTATAACACTACAAAGCAAAGAGTCAAGAAAGTTTCTAGAGAAAATGAAGACT
CAATGGCTAAATTCAGAAATGATCCTGAATCATTGATAAGGAACCAACCGCAGATT
TGGATATTTCTGCTAATGGATTCACAATTTCTTCGTCTCAAGGCAATGACCAAGCGGT
ACAAGAAGATTTCTTCACTAGATTACAAACAATAATTGACTCAAGAGGTAAGAAGAC
TGTCATCAACAATCCTTGATTTCTACTTTGGAGGAGTTATTAAGTGTAGCTGAAAAA
CCATATGAATTCATAATGGCTTATTTGACTTTGATTCCATCAAGATTCCGATGCCTCAG
CTAACCTATCTTACCAACCAATTGATCAATGGAAATCTTCATTCAACGATATTAGTAA
ATTATTGTCTATTTTAGACCAGACAATTGACACCTACCAAGTTAATGAATTTGCTGAT
CCAATCGATTTCAATTGAAGATGAACCTAAAGAAGATTCTGATGGTGTCAAGAGGATT
CTGGGTTCCATTTTCTCATTTGTTGAAAGATTAGATGACGAATTCATGAAATCCCTGT
TAAACATCGATCCTCATTCCAGTGATTATTTGATCCGTTTAAGGGATGAACAATCAAT
CTATAATTTGATCCTAAGAACTCAATTGTACTTTGAAGCGACTTTGAAAGATGAACAC
GACCTAGAAAGAGCATTGACACGTCCATTCGTCAAGAGATTGGATCATATCTACTAT
AAATCCGAAAATTTGATAAAAAATTATGGAAACTGCTGCTTGGAATATCATACCTGCT
CAATTCAAATCTAAATTTACTTCAAAGACCAGCTCGATTCTGCTGATTATGTCGACA
ATTTAATAGACGATTATCGACAATCTTATCCAAGCAAAACAACATTGCTGTTCAAAAA

FIGURE 80 (CONT'D)

CGTGCTATTTTATACAACATTTACTACACTGCATTAAACAAAGATTTCCAAACTGCTAAA
GATATGTTACTAACTTCCCAAGTTCAAACAAATATCAACCAATTCGATTCATCCCTACAA
ATTTTATTCAACAGGGTGTGTTGTTCAATTGGGTCTATCCGCCTTTAAATTATGTTTGATT
GAAGAATGTCATCAAAATTTGAATGATCTTCTGTCAAGTTCTCACTTAAGAGAAATTTTG
GGCCAACAATCCCTACACAGAATATCTCTCAATTCTAGTAACAATGCTTCAGCTGATGAG
CGTGCTAGACAATGTTTGCCATATCACCAACACATCAATCTCGATTTAATCGATGTCGTC
TTCTTAACATGTTTCCTTATTGATCGAAATTCCAAGAATGACTGCCTTCTATTCCGGTATT
AAGGTCAAGAGAATTCCTTACTCTCCAAAATCCATTTCGTCGTTCCCTAGAACATTACGAC
AAGTTAAGTTTCCAAGGTCCACCAGAACTTTAAGAGATTATGTCTTGTTGCTGCCAAA
TCAATGCAAAAAGGTAAGTGGAGAGACTCTGTTAAATACTTAAGAGAAATAAAATCT
TGGGCTTTATTACCAAACATGGAAACGGTGTGTAATAGTTTAACGGAAAGAGTACAA
GTTGAATCTTTGAAGACTTATTTCTTTTCTTTCAAGAGGTTCTATTCAAGTTTTTCTGT
TGCTAAACTAGCCGAATTATTTGATCTTCCAGAAAATAAGGTGGTTGAAGTTTTGCAA
TCTGTTATCGCAGAATTGGAAATCCCAGCCAAATTAAACGACGAGAAGACCATCTTT
GTTGTCGAAAAG

Candida albicans nucleic acid: SEQ ID NO: 123

ATGTCTCGTTTTTTTTGTTTCAGGATACACTTCTGACTCTTCTTCTGAAGAGGAGGATT
TATTGAGTACTTCTGAAGAAGAGTTATTATCTTCTTCTGATGAAGGAGAAGACAACG
AATCAGATAGTTCATTTTTTGGTGAAGATGATGATGAATCAGAAGAATCTAGTTCTG
ATGATGAAGATGGTCGACCATCTGGTCCAGCATATTTTTTAAAGAAATCATTTTTAAA
AGGAGCTGGAGGAGATGATTCTGACAGTGATAGTGATGAAGGTCGTAAAGTTGT
TAAATCAGCTAAAGATAAATTATTAGATGATATGAAATCTTCAATTGAAATTATAAAT
TCCAACAAATATAATAACAATTGGAGTATAGTTTTAGGTGAATTTGATAAGTTTGGTA
GATTTTTGATTAGATGTAATCAAACCAATTTGGGTACACCAAATTTTATATTAAATT
GTTGACTAGTTTAGATAACTCCATAACTGAACTAGTAATAATGAAAGAGATGATAA
AACATTAAGCTGATGAAGCCAGAGCTTTCAATACTTTGAGACAAAGAATTAAAAA
ACAAATAAGAGAATTCCAAGTTTATTATGATTTGTATAAGGAAAATCCAGAAGAATT
TGATGAAAATGAAGATGAACCATTAGAATCTGTTCAAGCTGGTCTTAACGATAATGT
TAAAAATGAAGCTGATAATTCTAATGTTGGTGCTCTTGCGTCAAACAGAGTATTGAG
TCCTATTTTCCATACTTTGAAAATTTTCCGAAAGTCGTGGTAAAAAGAATATTGAT
AAATTGGAACAAATTGCTACTTTGGAAAAATTATTAGAAGCAATGTTTCTAAAAGT
TCACCATTTGAATTGATTTCTATTTATCAGATGTTATTATCAGTTAGATTTGATGCTTC
ATCTAATCAAGCTTTTATGCCTTTGGAACAATGGCAAAAGAATGAACACGATTTAGG
TAAATTATTGGATTTGTTGGAAGCTAATGTTGATACTTATCAAGTTTCTGAATTGGGT
TCAACTACTGATGATATTGATATTGAACCAGTTGCTAATGCCCAAGGTGTTAAAGTTA
TTTTCGGATCAATCACTTCTTCTATTGATAGATTGGACGATGAATTGACCAAATCTTT
ACAACATACTGACCACATTCTATTGAATATGTTGAAAGATTGAAGGATGAAAGTAC
TATTTACAATTTGATTGTTAGAGGTCAAGCATATGTTGAATCCATAACTCCAGAAGAT
GTCAAGTATAATTCTGAACAATTGGCAAGAATTGTTTTGAGAAGATTGGAACACATT

FIGURE 80 (CONT'D)

TATTATAAACCAAAACAATTGATTAAAGCTAATGAAGAAGAAGCTTGGCGTAATATT
GAATACAATTCATCTATTGTCAGTAAAGGTTCTTCAGTTGATGAAGTTATTGATCAATTG
ACGGAATTTTACAAAAGCAACAAAAAACAACCTTATGGGAAACATGCTATACTA
TTCTCCATTTATTATTATGCTGTCAATAGTCAATATGAAAAGGCTAAAGAATTATTTT
TGAGATCTCAATTTTATAGTAACATCAATTCTGCTGAATCTTCTTTACAAGTTCAATA
TAATCGTGCTTTAGTTCAATTAGGTTTAAAGTGCTTTTAGAGCAGGTAGTATTGAAGAA
TCTCATAAAATTTTGAATGAAATTGTCAATTCTCAAAGATCTAAAGAATTATTGGGTC
AAGGTTTCAATTCTAAATTCCCCAATCAAGCTACTGTTTTGGAAAGACAAAAATTATT
ACCATTCCATCAACATATTAATTTGGAATTATTGGAATGTGTATTTATGACTTGTCT
TTATTAATTGAAATTCCAACCTTTGGCTGCTATTGCTAATAATCATAAGGATTCAAAC
GTA AAAATGCTTCATTGAAATCTTTCAAAGTAAATTGGATTTCCATGATAGACAATT
TTTCACTGGTCCACCAGAAAGTATTAAGATCATATTGTGGTGATGAAATTACTAAAT
TGGAAGAAGCAATGGTAAAATTGAACAAAGAATATAAAATCGCTAAAGAACGTCTTA
ACCCACCATCAAATCGTCGTTGA

Human GENBANK Accession Number: U46025.1

Human nucleic acid sequence: SEQ ID NO: 124

TGACTCGCGGGCTCAGCTGGTCCGGCCGTAGCACCTCCGCGCCGTCGCCATGTCGCGGTT
TTTACCACCGGTTTCGGACAGCGAGTCCGAGTCGTCCTTGTCGGGGAGGAGCTCGT
CACCAAACCTGTTCGGAGGCAACTATGGCAAACAGCCATTGTTGCTGAGCGAGGATGA
AGAAGATACCAAGAGAGTTGTCCGCAGTGCCAAGGACAAGAGGTTTGAGGAGCTGA
CCAACCTTATCCGGACCATCCGTAATGCCATGAAGATTCGTGATGTCACCAAGTGCCT
GGAAGAGTTTGAGCTCCTGGGAAAAGCATATGGGAAGGCCAAAAGCATTGTGGACA
AAGAAGGTGTCCCCCGGTTCTATATCCGCATCCTGGCTGACCTAGAGGACTATCTTA
ATGAGCTTTGGGAAGATAAGGAAGGGAAGAAGAAGATGAACAAGAACAATGCCAAG
GCTCTGAGCACCTTGCGTCAGAAGATCCGAAAATACAACCGTGATTTTCGAGTCCCAT
ATCACAAGCTACAAGCAGAACCCCGAGCAGTCTGCGGATGAAGATGCTGAGAAAAA
TGAGGAGGATTCAGAAGGCTCTTCAGATGAGGATGAGGATGAGGACGGAGTCAGTG
CTGCAACTTTCTTGAAGAAGAAATCAGAAGCTCCTTCTGGGGAGAGTCGCAAGTTCC
TAAAAAAGATGGATGATGAAGATGAGGACTCAGAAGATTCCGAAGATGATGAAGAC
TGGGACACAGGTTCCACATCTTCCGATTCCGACTCAGAGGAGGAAGAAGGGAAACAA
ACCGCGCTGGCCTCAAGATTTCTTAAAAAGGCACCCACCACAGATGAGGACAAGAAG
GCAGCCGAGAAGAAACGGGAGGACAAAGCTAAGAAGAAGCACGACAGGAAATCCAA
GCGCCTGGATGAGGAGGAGGAGGACAATGAAGGCGGGGAGTGGGAAAGGGTCCGG
GGCGGAGTGCCGTTGGTTAAGGAGAAGCCAAAAATGTTTGCCAAGGGAACTGAGAT
CACCCATGCTGTTGTTATCAAGAACTGAATGAGATCCTACAGGCACGAGGCAAGAA
GGGAACTGATCGTGCTGCCAGATTGAGCTGCTGCAACTGCTGGTTCAGATTGCAGC
GGAAAACAACCTGGGAGAGGGCGTCATTGTCAAGATCAAGTTCAATATCATCGCCTC
TCTCTATGACTACAACCCCAACCTGGCAACCTACATGAAGCCAGAGATGTGGGGGAA
GTGCTTGGACTGCATCAATGAGCTGATGGATATCCTGTTTGCAAATCCCAACATTTTT
GTTGGAGAGAATATTCTGGAAGAGAGTGAGAACCTGCACAACGCTGACCAGCCACTG

FIGURE 80 (CONT'D)

CGTGTCGGTGGCTGCATCCTAACTCTGGTGGGAACGAATGGATGAAGAATTTACCAA
ATAATGCAAAATACTGACCCTCACTCCCAAGAGTACGTGGAGCACTTGAAGGATGAG
GCCCAGGTGTGTGCCATCATCGAGCGTGTGCAGCGCTACCTGGAGGAGAAGGGCACT
ACCGAGGAGGTCTGCCGCATCTACCTGCTGCGCATCCTGCACACCTACTACAAGTTT
GATTACAAGGCCCATCAGCGACAGCTGACCCCGCCTGAGGGCTCCTCAAAGTCTGAG
CAAGACCAGGCAGAAAATGAGGGCGAGGACTCGGCTGTGTTGATGGAGAGACTGTG
CAAGTACATCTACGCCAAGGACCGCACAGACCGGATCCGCACATGTGCCATCCTCTG
CCACATCTACCACCATGCTCTGCACTCGCGCTGGTACCAGGCCCGCGACCTCATGCTC
ATGAGCCACTTGCAGGACAACATTCAGCATGCAGACCCGCCAGTGCAGATCCTTTAC
AACCGCACCATGGTGCAGCTGGGCATCTGTGCCTTCCGCCAAGGCCTGACCAAGGAC
GCACACAACGCCCTGCTGGACATCCAGTCGAGTGGCCGAGCCAAGGAGCTTCTGGGC
CAGGGCCTGCTGCTGCGCAGCCTGCAGGAGCGCAACCAGGAGCAGGAGAAGGTGGA
GCGGCGCCGTCAGGTCCCCTTCCACCTGCACATCAACCTGGAGCTGCTGGAGTGTGT
CTACCTGGTGTCTGCCATGCTCCTGGAGATCCCCCTACATGGCCGCCCATGAGAGCGA
TGCCCCGCCGACGCATGATCAGCAAGCAGTTCCACCACCAGCTGCGCGTGGGCGAGCG
ACAGCCCCTGCTGGGTCCCCCTGAGTCCATGCGGGAACATGTGGTCGCTGCCTCCAA
GGCCATGAAGATGGGTGACTGGAAGACCTGTCACAGTTTTATCATCAATGAGAAGAT
GAATGGGAAAGTGTGGGACCTTTTCCCCGAGGCTGACAAAGTCCGCACCATGCTGGT
TAGGAAGATCCAGGAAGAGTCACTGAGGACCTACCTCTTACCTACAGCAGTGTCTA
TGACTCCATCAGCATGGAGACGCTGTCAGACATGTTTGAGCTGGATCTGCCACTGT
GCACTCCATCATCAGCAAAATGATCATTAAATGAGGAGCTGATGGCCTCCCTGGACCA
GCCAACACAGACAGTGGTGTATGCACCGCACTGAGCCCACTGCCAGCAGAACCTGGC
TCTGCAGCTGGCCGAGAAGCTGGGCAGCCTGGTGGAGAACAACGAACGGGTGTTTG
ACCACAAGCAGGGCACCTACGGGGGCTACTTCCGAGACCAGAAGGACGGCTACCGC
AAAAACGAGGGGCTACATGCGCCGCGGTGGCTACCGCCAGCAGCAGTCTCAGACGGC
CTACTGAGCTCTCCACTCTGTTTCCCGCCTGGGCCATCCAACCTTGAAGTCCTAAACC
ACACCTCAGTCACTAAAGGTCTGTTTAAAGTTGTTCTGGTTGATTGCTTGTGCA

Saccharomyces cerevisiae orf name: YNL036W

Saccharomyces cerevisiae gene name: NCE103

GENBANK Accession Number: CAA95901.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 128

ATGAGCGTACCGAATCTTCATCTATATTACATTGAGTCACAACTCAAACCTACAAGAT
ATCTTGGCCGCCAATGCCAAATGGGCCTCCAGATGAACAACATACAGCCAACCTTTGTTT
CCAGATCACAATGCGAAGGGCCAGTCCCCTCACACTCTTTTCATCGGCTGCTCCGATTG
CGTTACAACGAAAACCTGTTTAGGTGTCTTGGCCGCGAAGTGTTCACTTGGAAAAATGTT
GCTAACATATGTCACTCAGAGGATTTAACTTTGAAGGCCACTTTAGAGTTTGCCATTATT
TGTCTAAAAGTTAACAAAGTTATTATTTGTGGCCACACTGATTGTGGTGGTATAAAGACA
TGTTTAACTAACCAAGGGAAGCCTTACCAAAAGTTAACTGTTCTCATCTGTACAAGTAC
TTAGACGATATTGACACCATGTACCATGAAGAGTCACAAAATTTGATCCATTTGAAAACG
CAACGTGAAAAATCTCATTACCTGTGCACTGTAACGTCAAAAGGCAGTTTAAATAGGATT

FIGURE 80 (CONT'D)

ATTGAAAACCCTACTGTGCAAACCTGCTGTACAAAATGGAGAATTACAGGTATACGGT
CTGCTTTACAACGTAGAGGACGGTCTACTGCAAACAGTTAGCACTTACACAAAAGTT
ACCCCAAAATAG

Candida albicans nucleic acid: SEQ ID NO: 129

ATGGGTAGAGAAAATATTTTGAAATATCAATTGGAACATGATCATGAATCTGATCTT
GTTACTGAAAAAGATCAATCATTATTACTTGATAATAATAACAACCTAAACGGGATG
AATAATACCATTAAAACTCATCCGGTACGTGTTAGTTCAGGAAATCATAATAATTTTC
CTTTCACTTTATCTTCAGAATCTACATTACAAGATTTTTTAAATAATAATAAATTTTTT
GTTGATTCCATAAAACATAATCATGGTAATCAAATATTTGATTTGAATGGTCAAGGTC
AATCTCCTCATACATTATGGATAGGGTGTAGTGATTCAAGAGCAGGTGATCAATGTT
TAGCTACATTACCAGGAGAAATATTTGTTTCATAGAAACATTGCTAATATAGTCAATGC
CAATGATATAAGTAGTCAAGGGGTTATACAATTTGCTATTGATGTATTAAGTGA
AAAAATCATTGTTTGTGGTCATACTGATTGTGGTGGTATTTGGGCATCATTATCAAAG
AAAAAAATTGGTGGTGTCTTAGATTTATGGTTAAATCCAGTTAGACATATTCGTGCTG
CTAATTTAAATTTATTAGAAGAATATAATCAAGATCCTAAATTAAGGCCAAAAAAT
TGGCTGAATTAATGTCAATTTCTTCTGTAACAGCATTGAAAAGACATCCTAGTGCTAG
TGTTGCATTAAAGAAGAATGAAATTGAAGTTTGGGGGATGTTATATGATGTGGCAAC
TGGTTATTTATCTCAAGTAGAGATTCCTCAAGATGAATTTGAGGATTTATCCATGTT
CATGATGAACATGATGAAGAAGAATATAACCCCTCATTGA

Saccharomyces cerevisiae orf name: YNL126W

Saccharomyces cerevisiae gene name: SPC98

GENBANK Accession Number: CAA96007.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 107

ATGGAAGTAGAGCCCACTCTTTTGGTATAATAGAGGCATTGGCTCCTCAATTATTGTCTG
CAGAGTCATTTGCAGACATTTGTATCTGATGTAGTCAATTTACTGCGATCATCCACAAA
TCGGCAACTCAATTAGGCCCTTTAATTGATTTTTACAAATTACAATCACTAGATTCGCCT
GAAACAACAATTATGTGGCATAAAATTGAGAAATTTCTCGATGCTTTATTTGGAATCCAG
AACACCGATGATATGGTAAAGTACCTCTCTGTCTTTCAATCTTTGCTTCCATCAAATTAC
AGAGCAAAAATTGTCCAAAAATCATCTGGGCTCAATATGGAGAACCTTGCTAACCAT
GAACATTTACTTAGCCCAAGTGCGGGCTCCAAGTATATATACAGAAGCTTCATTTGAA
AACATGGACCGATTTTCTGAAAGAAGGTCCATGGTATCTTCGCCTAATCGTTACGTTT
CCTCTTCAACCTACAGTTCTGTTACTTTGAGACAGTTGTCAAATCCTTATTATGTGAA
CACTATACCCGAGGAAGATATCCTAAAATACGTATCATATACATTATTAGCTACGAC
ATCGGCACTATTTCCGTTTGATCATGAGCAAATACAAATTCGTCTAAGATACCCAAT
TTTGAAGTGGACTTTTACATTTAATATTTGAAGCGGGTTTATTATATCAAAGTTTGG
GTTATAAAGTGGAGAAGTTTAGGATGTTGAATATATCTCCAATGAAAAAAGCATTGA
TTATAGAAATTTCAGAAGAATTACAAAACCTACACAGCATTGTGAACAATCTGGTCTC
TTCAGGGACAGTAGTGTCATTGAAATCGTTATATCGTGAAATATATGAAAATATAAT

FIGURE 80 (CONT'D)

AAGGCTTCGAATATACTGTAGGTTTACAGAACACCTTGAAGAATTGAGCGGAGATAC
ATTCTTGATTGAATTAAATATTTTCAAATCCCACGGAGATCTTACTATAAGAAAAATA
GCAACGAATTTGTTTAATTCAATGATTTCTCTTTATTATGAGTATTTAATGAATTGGT
TGACTAAAGGTCTACTCCGAGCTACTTATGGAGAATTCTTCATTGCTGAAAACACTGA
TACAAATGGTACAGACGATGATTTTATTTACCACATTCCTATAGAGTTCAACCAAGAA
AGAGTTCCGGCCTTCATACCGAAAAGAGTTGGCATATAAAATATTCATGATCGGCAAA
TCGTATATCTTCCTAGAAAAGTACTGTAAAGAGGTTCAATGGACAAACGAATTTTCTA
AAAAGTATCATGTCCTGTACCAGAGCAATTCCTATCGGGGAATATCAACGAACCTTTT
TGAAATTATAAATGATCAATATTCTGAAATTGTTAATCATACTAATCAAATTTCTAAAT
CAGAAGTTTCATTACAGAGACGTGGTATTTGCGTTAAAGAATATTCTTCTCATGGGTAA
AATCTGATTTTATGGATGCTCTTATAGAAAAGGCCAATGATATTCTCGCGACACCATC
GGATTCATTGCCAAATTATAAGTTAACAAGGGTTTTACAGGAAGCCGTGCAGCTTTC
TTCCTTAAGACATTTAATGAATAGTCCCGTAATAGTTCTGTCATTAATGGATTGGAT
GCGAGGGTACTCGATCTTGGACATGGATCCGTGGGTTGGGATGTTTTTACTTTAGATT
ACATCCTCTACCCCCCTTTGAGTTTAGTATTAAACGTAAATCGTCCTTTTGGCAGGAA
AGAGTATCTACGAATTTTCAATTTTTTATGGAGATTTAAAAAGAACAATTATTTCTAT
CAAAAGGAAATGTTGAAGAGTAATGATATAATCAGATCATTCAAGAAAATCAGAGGT
TACAACCCGCTCATCCGTGATATTATCAATAAACTTTCTAGAATCAGTATACTTAGAA
CTCAATTCCAGCAATTCAACTCGAAGATGGAATCTTATTATTTGAACTGCATTATAGA
GGAATTTTAAAGAAATGACCCGGAACTGCAACGCACAGAGAATAAAAGCCAAA
ACCAATTCGACTTAATTAGATTAAATAATGGCACCATAGAATTAAATGGGATTTTAAAC
CCCCAAAAGCTGAAGTACTAACAAGTCTTCAAGCAGTAAACCCCAAAAACACGCAAT
CGAAAAGACGCTGAATATTGATGAATTAGAAAAGTGTACATAACACGTTCTTGACGAA
TATTCTTTCTCATAAGCTTTTTGCAACTAACACAAGTGAAATAAGCGTTGGTGATTAT
TCTGGGCAACCATAACCAACTTCATTGGTTTTACTTTTAAATTCGGTTTACGAGTTTCG
TCAAAGTTTATTGTAATTTGAACGACATTGGATACGAAATCTTCATTAATAATGAATCT
CAATGATCACGAAGCATCTAACGGATTATTGGGAAAATTTAATACGAATTTAAAGGA
AATTGTTAGCCAGTATAAAAATTTTAAA

Candida albicans nucleic acid: SEQ ID NO: 108

ATGGCGTTAAACAAGGTACAACATAAATAATTATATTCCAATCGATTAGTGAAATCA
TTGGTTCCTGTGGAATTCGGTGAGGCATTATCCAAAGTATAATCAATGACTTGCAA
ACCACTTTACTAAATACTTCTTCTGAAGAACAAAATTTGTCAATAATTATAAACAAGC
TTAAAATGCAATTTTTAAGTAACAATTTAAAAAATGAATGGGTCGAATTTCAAAACA
TTGTTAATTCATTAAGCAAATTCAGTCGTTGGATCAGATTTGTAATTATCTCGCATT
TCTTGATGCTTTAAGAGATGAGAAACCAGAAGATATATTATCAACATCAACAGCGAG
CTTGTCTCCCGGTAAGCAAAATGTAATGATCAATACGGTAAACACAGCATTGACGTT
ATCACAGTTAATCGAGCCTTACTATGATACTTTATCGGAACAAACCATTTTAACTTAC
TTACCCTACACGATGTTAGGTCTGGATTCCAAAATATTACCTTCAGCAATAATTATA
CACGATTGGAGATACCGAAAAGATATAAACAACAGTTTCAGCTCATTGCTACGCGAAG
TTTTTGAGTTTGCAATACTATATAAACAATTGGCAATTGTTGTTGATAGGTATAAAGG

FIGURE 80 (CONT'D)

AAC TTTAGTACTGGCCATAAAGACAGCTTACATAGCAATACTAGAGGCTCAATTGAA
CAAATATGTGAATGATATTAACAATATCTTCAATAATAAACCGAATTCCATATTAGTT
GTTTACAATTCCATTTTCCCCTGGATATCTATACTACGATTTTATATCGAGTCTCAAA
CAGACTAAACAGATTAGATGGTTATGAATTTCTCACATTTATTTATAGTTTCACCAAC
CATGGAGATCCCAAAATACGGGGCATTGCTGTGACTGCATTCACCGAGGTTGTCAAA
CCGTATTATAATATTGTGGAACATTGGATAGTGAAAGGGGAGTTGATTGATAATAAT
AACGAGTTTTTCATTATCTTTGATCAAGAGCAGAATGAATTC AATAGTATAATTAAT
TATTGCCCAAAAAAATACCAGCCTTTATTAATCGAGTGATAAAATATTT CAGATTGG
GAAAACATTAATTTTTCTAAATAAATATTGTCGTGAAC TAAATGGGTAAATCAGTAT
AACGTGAAATATTCTGCTATATTGTTCAATAACCATCAAGGCTTGGCATCCATGACAA
CAAATGAAATGATCAAATTGATTGATCTGCAATATAATGAGATATTAACGTTTCTCAC
CCAAATAATCCAAGGAAACAATAAATTGTTTACTCATGTTTATAATTTCAAGAGGTTT
TATTTTATGGAGACCAATGATTTTATTGATGCGATTATGGTGAAAGGGAAGGACGTT
TTTAATGAGTCTTCTGTTAATATTTTCATCAACCTATCTTAGGAAAGTCTTACAAGACG
CTATACAAATTTCTGTCGGTGAAAAATTTTGAGTATGTTGACAGACTCGATTTCGAGAG
TGTTGAATCCCCAACACGGGAATTTGGGCTGGGAATCGTTCACCATTGAATACAAAA
TTGATGATCTTCCCATGAGTTATTTATTTGAAGGTCACCAACATTTACAATATTTAAA
AATGTTTTCATTTTCTATGGAAATTAAGACAATTGAATAATTTATTAAATTGGCATTTT
GAGATGTTTAATGAGTTGAATCATAATGTGGTGACGAAGTTGTCAAGCAGAAATAGA
AGACCTTTGGCGAAATCATTGAGCATAATCACCAGTATAAGATTCCATTTTACCCAGT
TTCTTAACGAACTAATAGCTTATTTGTCTTATGATGTTATTGAAGAAAATTTTCGACA
GACTGTATATTTTTAGGGCAGATTTAAAGAACGATGGCGATGAAGAGCTTTTCTTATT
GAGCAAAATCGCTCCGTTAA

Human GENBANK Accession Number: AF042378.1

Human nucleic acid sequence: SEQ ID NO: 109

CAGGAAGGGCGCGGGCCGCGGTCCCTGCGCGTGCGGCGGCAGTGGCGGGCTCTGCCC
GGACCACCGTGCACGGCTCCGGGCGAGGATGGCGACCCCGGACCAGAAGTCGCCGA
ACGTTCTGCTGCAGAACCTGTGCTGCAGGATCCTGGGCAGGAGCGAAGCTGATGTAG
CCCAGCAGTTCCAGTATGCTGTGCGGGTGATTGGCAGCAACTTCGCCCCAACTGTTG
AAAGAGATGAATTTTTAGTAGCTGAAAAAATCAAGAAAGAGCTTATTCGACAACGAA
GAGAAGCAGATGCTGCATTATTTTCAGAACTCCACAGAAACTTCATTCACAGGGAG
TTTTGAAAAATAAATGGTCAATACTCTACCTCTTGCTGAGCCTCAGTGAGGACCCACG
CAGGCAGCCAAGCAAGGTTTCTAGCTATGCTACGTTATTTGCTCAGGCCTTACCAAG
AGATGCCCACTCAACCCCTTACTACTATGCCAGGCCTCAGACCCTTCCCCTGAGCTAC
CAAGATCGGAGTGCCAGTCAGCCCAGAGCTCCGGCAGCGTGGGCAGCAGTGGCAT
CAGCAGCATTGGCCTGTGTGCCCTCAGTGGCCCCGCGCCTGCGCCACAATCTCTCCTC
CCAGGACAGTCTAATCAAGCTCCAGGAGTAGGAGATTGCCTTCGACAGCAGTTGGGG
TCACGACTCGCATGGACTTTAACTGCAATCAGCCTTCTTCACAAGCCACTACCTCAA
AAGGTGTCCCAAGTGCTGTGTCTCGCAACATGACAAGGTCCAGGAGAGAAGGGGATA
CGGGTGGTACTATGGAAATTACAGAAGCAGCTCTGGTAAGGGACATTTTGTACGTCT

FIGURE 80 (CONT'D)

TTCAGGGCATAGATGGCAAAAACATCAAAATGAACAACACTGAAAATTGTTACAAAG
TAGAAGGAAAGGCAAATCTAAGTAGGTCTTTGAGAGACACAGCAGTCAGGCTTTCTG
AGTTGGGATGGTTGCATAATAAAATCAGAAGATACACGGACCAGAGGAGCCTGGAC
CGCTCATTTCGGA CTGTCGGGCAGAGCTTTTGTGCTGCCTTGCACCAGGAAC TCAGA
GAATACTATCGATTGCTCTCTGTTTTACATTCTCAGCTACAAC TAGAGGATGACCAGG
GTGTGAATTTGGGACTTGAGAGTAGTTTAACTTCGGCGCCTCCTGGTTTGGACCTAT
GATCCCAAAATACGACTGAAGACCCTTGCGGCCCTAGTGGACCACTGCCAAGGAAGG
AAAGGAGGTGAGCTGGCCTCAGCTGTCCACGCCTACACAAAAACAGGAGACCCGTAC
ATGCGGTCTCTGGTGCAGCACATCCTCAGCCTCGTGTCTCATCCTGTTTTGAGCTTCC
TGTACCGCTGGATATATGATGGGGAGCTTGAGGACACTTACCACGAATTTTTTGTAG
CATCAGATCCAACAGTTAAAACAGATCGACTGTGGCACGACAAGTATACTTTGAGGA
AATCGATGATTCTTCGTTTATGACGATGGATCAGTCTAGGAAGGTCCTTTTGATAGG
AAAATCAATAAAATTTCTTGACCAAGTTTGT CATGATCAGACTCCCACTACAAAGATG
ATAGCTGTGACCAAGTCTGCAGAGTCACCCACAGGACGCTGCAGACCTATTCACAGAC
TTGGAAAATGCATTT CAGGGGAAGATTGATGCTGCTTATTTTGAGACCAGCAAATAC
CTGTTGGATGTTCTCAATAAAAAAGTACAGCTTGCTGGACCACATGCAGGCAATGAGG
CGGTACCTGCTTCTTGGTCAAGGAGACTTTATAAGGCACCTAATGGACTTGCTAAAA
CCAGA ACTTGTCCTCCAGCTACGACTTTGTATCAGCATAACTTGACTGGAATTCTAG
AAACCGCTGTCAGAGCCACCAACGCACAGTTTGACAGTCCTGAGATCCTGCGAAGGC
TGGACGTGCGGCTGCTGGAGGTCTCTCCAGGTGACACTGGATGGGATGTCTTCAGCC
TCGATTATCATGTTGACGGACCAATTGCAACTGTGTTTACTCGAGAATGTATGAGCCA
CTACCTAAGAGTATTTAACTTCCTCTGGAGGGCGAAGCGGATGGAATACATCCTCAC
TGACATACGGAAGGGACACATGTGCAATGCAAAGCTCCTGAGAAACATGCCAGAGTT
CTCCGGGGTGCTGCACCAAGTGTACATTTTGGCCTCTGAGATGGTCCATTTTCATTCAT
CAGATGCAGTATTACATCACATTTGAGGTGCTTGAATGTTCTTGGGATGAGCTTTGGA
ACAAAGTCCAGCAGGCCAGGATTTGGATCACATCATTGCTGCACACGAGGTGTTCT
TAGACACCATCATCTCCCGCTGCCTGCTGGACAGTGACTCCAGGGCACTTTTAAATCA
ACTTAGAGCTGTGTTTGATCAAATTATTGAACTTCAGAATGCTCAAGATGCAATATAC
AGAGCTGCTCTGGAAGAATTGCAGAGACGATTACAGTTTGAAGAGAAAAAGAAACAG
CGTGAAATTGAGGGCCAGTGGGGAGTGACGGCAGCAGAGGAAGAGGAGGAAAAATAA
GAGGATTGGAGAATTTAAAGAATCTATACCAAAAAATGTGCTCACAGTTGCGAATATT
GACCCATTTCTACCAGGGTATCGTGCAGCAGTTTTTGGTGTTACTGACGACCAGCTCT
GACGAGAGTCTTCGGTTTCTTAGCTTCAGGCTGGACTTCAACGAGCATTACAAAGCC
AGGGAGCCCAGGCTCCGTGTGTCTCTGGGTACCAGGGGGCGGCGCAGCTCCCACACG
TGAAGCTCGCGGTCTCCAGGGAGCTGCGGGTGATGTTTCGTTGCACTGCTAGACAC
GAAATTTCCATTGACGTCTGCAGGA ACTGCATGCTGCAGGTGTCCTGCCCTTCCGCC
CACGAGTGCGCCATGTTTCAGCGGAGCGGCGTGTGGGAGAAGCCACGTCGTGTTTCA
CATGTCGGAGTCGAATGCATTTGTAAATCCCTAAGTCAAGTAGGCTGGCTGCACTGT
TCACATTTGTCTCTAAAAGTCTTCATCGCTAAAAGATACCATAATTTGCTGAGGCTTC
TTAAGCTTTCTATGTTATAATTTATATTTGTCACCTTAAAAAATCCATTTCTTTTAGAA
AAAATTAGGGTGATAGGATATTCATTAGTTAAGATGGTAACGTCATTGCTATTTTTTT
AACATCCTCTTTAGAGGTAATTTTTGTTAACATAACCAAAAATTAATTTGAAACAAA

FIGURE 80 (CONT'D)

TGTCCTCAACTAAGAAAATATATAGAGCATTTTATTTTTTTTTAGTGTTGTAAAATATT
AACCTCTGTGAGATCCTTTGTATCTTAATGCATTACCTTTACACATATTTATTCTTATT
TTCTCTCCTTTCAGAGTTTACATTTTATATTTAATTTACTATTTTCAGATTTTAAAAAT
AGTATAGAAAAAAGTAGGAGTGATAGAGAACAAAAATACTCTTATACAGTGCAACCC
AAATACCGCGAATGCATCAGCTAAAGCAGCGTGTAATAGGAGTGATGAGAAAGTTA
ATGGAGTATTTTATTTTCAAAGTTCCTGATAAGCATTGGAAAGAAATCGACATGGAT
AATGAAGATTTCTTTTTCCTTGCCTATTTTTTCATTGTAAATATTTATATACTACTGA
CCAAGATGTTGGGGTGGGGGGGATTGTTTTTGTAAAAATGTCATTATCAGGTCACA
TAAATCTGCCTTTATGTTGCATAAGTGAAAATTTAGAAAATTTAAAGCAATTATCTTT
CAAAAAAATGGAATAAATTGCTTTTCTACATAAAAAA

Saccharomyces cerevisiae orf name: YNL282W

Saccharomyces cerevisiae gene name: POP3

GENBANK Accession Number: CAA96194.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 77

ATGTCCGGGTCGTTAAAATCTCTAGACAAGAAAATAGCTAAAAGAAGGCAGGTGTAT
AAGCCCGTGCTAGACAATCCGTTCAACAACGAAGCACATATGTGGCCGCGCGTGAT
GATCAGCCATTGATTTGGCAGCTGCTGCAATCCTCTATCATAAATAAGTTGATTCACA
TTCAATCGAAGGAGAACTACCTTGGGAGCTGTATACAGATTTCAATGAAATTGTGC
AGTATTTGAGCGGCGCTCACGGAAACAGCGACCCAGTATGTCTATTTGTGTGCAATA
AGGACCCTGATGTACCGCTTGTGCTCTTGCAAGCAATCCCGCTATTATGCTATATGGC
GCCCATGACGGTTAAACTGGTGCAGTTGCCCAAGAGTGCCATGGATACCTTCAAGTC
GGTTTCTAAATATGGAATGCTGCTGCTGCGGTGCGACGATAGGGTCGACAAGAAATT
CGTATCGCAGATCCAGAAGAACGTTGATCTGCTTCAGTTTCCCTGGTTAAATGCTATC
AAGTATCGGCCACATCTGTCAAGCTGTTGAAAACCTACAGTGCCAATTGTCTCGAAG
AAGAGGCAAAAGTAG

Candida albicans nucleic acid: SEQ ID NO: 78

ATGAATAAATCAAATAAAGTCAAGAAACCTTCGGTGGCCAAAGTCTCAACTAAAGCT
GTTTCATCATCACTCAAGTCTCAGGAAGCAAAGAGAAAACAAGTTTCCGTCCAATT
CTCGATAACTCATTTACACAATCAAACCAATGGCCATTTATAGAACCAACTATTGCAA
ACGATATTGTTGATCTACTAGAAGTATTGCTAAAAATGCAAGACTCTACATTTAAATA
CCGTGGGTTTAAATCCAAGTGTGCTGCTCTTGAAAAACAAGCAGCTGCTAATCGTGGT
ATACATAAAAAATGCTTGTGTACAAATAAAGTATGTATTTGTGTGCAAGTACGATATAT
CCCCAGCAACGCTCACAAATGTGTTTCTACGTTGTGTTTACGGCGTCAAAAAGTGC
TGAAGATCGGGTTAAGCTAATCCAGTTACCAAGAGGAAGTCTAGAACGGTTATCGAA
AGCACTTGGGGTAGATAGAGTTGGTATATTTGGTCTAACTAAAGATACTGAAGGGGC
ACAACCGTTATTTGATCTTATAAATGAAAATGTCAAAGATATTGAAGCTCCTTGGCTA
GACTGTATTTCCGTGAGGAGATGGTATTTAATCAACCTAACACAAAGCATGTGGCAAGT
ACTGTAGGTAGAAAGAAAAACAAGTAG

FIGURE 80 (CONT'D)

Saccharomyces cerevisiae orf name: YNR003C

Saccharomyces cerevisiae gene name: RPC34

GENBANK Accession Number: CAA96279.1

Saccharomyces cerevisiae nucleic acid: SEQ ID NO: 74

ATGAGTGGAATGATAGAAAATGGGTACAGCTATCGGACAATGCTAAAACCTTACAT
AGCCAGATGATGTCGAAAGGAATAGGCGCATTATTTACACAGCAAGAACTCCAAAAA
CAAATGGGAATCGGGTCGTTAACAGACTTGATGTCCATTGTACAGGAATTGCTAGAC
AAGAACTTGATCAAATTAGTAAAACAAAACGACGAATTTAAATTTCAAGGTGTCTTA
GAATCTGAGGCGCAAAAGAAAGCCACCATGTCTGGCTGAAGAGGCACTGGTATATTCT
TATATCGAGGCTAGCGGTAGAGAAGGGATATGGTCCAAGACTATCAAGGCAAGAAC
CAATCTCCATCAGCATGTAGTTCTTAAATGCTTGAAGAGTTTAGAATCCCAAAGATAC
GTGAAGAGTGTAAAGAGTGTAAAGTTTCCCACAAGGAAAATCTACATGTTGTACAGC
TTACAACCCTCTGTGGACATCACAGGAGGTCCATGGTTCACAGATGGAGAGCTGGAT
ATAGAATTTATCAATAGTTTATTGACTATTGTTTGGAGGTTTCATATCAGAGAACACCT
TCCCTAATGGCTTCAAGAATTTGAAAATGGACCCAAAAAAAACGTCTTTTATGCTCC
AAACGTAAAAAATTACTCTACCACACAAGAAATTTTGAATTTATTACAGCGGCACA
AGTGGCCAATGTGAGTTAACCCTTCAAATATCAGATCTTTGTGTGAAGTCTTAGTG
TACGACGACAAGCTGGAAGAAAGTCACGCATGACTGCTATAGAGTGACCTTAGAGAGC
ATTCTACAAATGAACCAAGGTGAGGGCGAGCCGGAGGCAGGTAATAAGGCTTTGGA
GGATGAAGAAGAATTTTCCATCTTTAACTACTTCAAGATGTTT

Candida albicans nucleic acid: SEQ ID NO: 75

ATGAGTGAGATGTTAGTATCAGATAAAGCACGTCATCTTTATACAAAGATGAGGGAG
TATCCAACCTTCCAACTTTTGGATCAAGATGAATTACAAACACTATTTGATATTA
AGGGATCAGAATTAATGGAATATTTACAAGAATTAGTCAATGGTAAATATGTTAAAA
TTAGTAAAATGGGAGATCAATTAATAATTTCAAACCTGTTGCTGAAGAAGAAGCCAAAA
AAGTATCGTCAATGTCTGATGATGAAGCAATGATTATTCTTATATTGAAGCTTCAGG
TCGTGAAGGGATTTGGACTAAAACCATTAAGCTAAAACCTAATTTACATCAACATAT
TGTTCAAAAATGTTTAAAAAATTTAGAAAATAATCGATACATTAAAAGTATTAAATC
AGTGAAACATCCAACAAGAAAAATTTATATGTTGTATAATTTACAACCTAGTATTGAT
GTTACTGGTGGTCCTTGGTTTACTGATTGAGAATTAGATACTGAATTTATAGAACTT
TATTGGAAGTGTGTTGGAGATTTATTGTTGGGAAAACCATGTATATAAAGGATGAAG
AAGCTGATAATGAAGATATAAATCCACTTCAAACAACATATCACAATCATCATCCAG
GGGTGAATTTGGATCAACTTGTGAATTTATAACAATAGTAATATCACCAGTGTTGA
GTTGGGTATTAATGATATTAGATCATTATGTGATGTGCTAATCTATGACGATAGAATA
GAAGAAGTTGGTGGGAATCAAGAAAATAGTGGGATTTTAAAGCTACTTGGCAAAGT
ATAATAGATAAAGGTAACACTATTTTGCAAAAATAATTATCAGGATTTGAAAAATGTT
GTTTCTGAAGATTGTTTAAATTATTTACAACAAAATCAATCAGATTTTAGTGTTTTTC
AATATAAATCTACTATTCAAGATCTTCAAGATGAATCGGATCTAGTGTATTTAGATAG
CTGGATAAATGAATAA

- 51 -

FIGURE 80 (CONT'D)

\\ODMA\WORLD\OXM\0342\0G548\LWJ4450.WPD

SEQUENCE LISTING

<110> ANADYS PHARMACEUTICALS, INC.

THOMPSON, Craig
MOORE, Jeffrey
BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
MOORE, Daniel
MCCOY, Melissa
SANDERSON, Karen
HAQ, Tariq
ZHU, Shuhao
LONG, Fan
DAVIDOV, Eugene

<120> ANTIFUNGAL COMPOUNDS AND METHODS OF USE

<130> 0342/1G548-US1

<150> US 60/215,164

<151> 2000-06-29

<150> US 60/224,457

<151> 2000-08-10

<160> 146

<170> PatentIn version 3.1

<210> 1

<211> 316

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 74

<400> 1

Met Gly Glu Val Lys Val Lys Val Gln Pro Pro Asp Ala Asp Pro Val

1 5 10 15

Glu Ile Glu Asn Arg Ile Ile Glu Leu Cys His Gln Phe Pro His Gly
20 25 30

Ile Thr Asp Gln Val Ile Gln Asn Glu Met Pro His Ile Glu Ala Gln
35 40 45

Gln Arg Ala Val Ala Ile Asn Arg Leu Leu Ser Met Gly Gln Leu Asp
50 55 60

Leu Leu Arg Ser Asn Thr Gly Leu Leu Tyr Arg Ile Lys Asp Ser Gln
65 70 75 80

Asn Ala Gly Lys Met Lys Gly Ser Asp Asn Gln Glu Lys Leu Val Tyr
85 90 95

Gln Ile Ile Glu Asp Ala Gly Asn Lys Gly Ile Trp Ser Arg Asp Ile
100 105 110

Arg Tyr Lys Ser Asn Leu Pro Leu Thr Glu Ile Asn Lys Ile Leu Lys
115 120 125

Asn Leu Glu Ser Lys Lys Leu Ile Lys Ala Val Lys Ser Val Ala Ala
130 135 140

Ser Lys Lys Lys Val Tyr Met Leu Tyr Asn Leu Gln Pro Asp Arg Ser
145 150 155 160

Val Thr Gly Gly Ala Trp Tyr Ser Asp Gln Asp Phe Glu Ser Glu Phe
165 170 175

Val Glu Val Leu Asn Gln Gln Cys Phe Lys Phe Leu Gln Ser Lys Ala
180 185 190

Glu Thr Ala Arg Glu Ser Lys Gln Asn Pro Met Ile Gln Arg Asn Ser
195 200 205

Ser Phe Ala Ser Ser His Glu Val Trp Lys Tyr Ile Cys Glu Leu Gly

210 215 220

Ile Ser Lys Val Glu Leu Ser Met Glu Asp Ile Glu Thr Ile Leu Asn
225 230 235 240

Thr Leu Ile Tyr Asp Gly Lys Val Glu Met Thr Ile Ile Ala Ala Lys
 245 250 255

Glu Gly Thr Val Gly Ser Val Asp Gly His Met Lys Leu Tyr Arg Ala
 260 265 270

Val Asn Pro Ile Ile Pro Pro Thr Gly Leu Val Arg Ala Pro Cys Gly
 275 280 285

Leu Cys Pro Val Phe Asp Asp Cys His Glu Gly Gly Glu Ile Ser Pro
 290 295 300

Ser Asn Cys Ile Tyr Met Thr Glu Trp Leu Glu Phe
305 310 315

<210> 2

<211> 330

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 75

<400> 2

Met Ser Glu Met Leu Val Ser Asp Lys Ala Arg His Leu Tyr Thr Lys
1 5 10 15

Met Arg Glu Tyr Pro Thr Ser Lys Leu Phe Asp Gln Asp Glu Leu Gln
 20 25 30

Thr Leu Phe Asp Ile Lys Lys Gly Ser Glu Leu Met Glu Tyr Leu Gln
 35 40 45

Glu Leu Val Asn Gly Lys Tyr Val Lys Ile Ser Lys Met Gly Asp Gln
50 55 60

Leu Lys Phe Gln Thr Val Ala Glu Glu Glu Ala Lys Lys Val Ser Ser
65 70 75 80

Met Ser Asp Asp Glu Ala Met Ile Tyr Ser Tyr Ile Glu Ala Ser Gly
85 90 95

Arg Glu Gly Ile Trp Thr Lys Thr Ile Lys Ala Lys Thr Asn Leu His
100 105 110

Gln His Ile Val Gln Lys Cys Leu Lys Asn Leu Glu Asn Asn Arg Tyr
115 120 125

Ile Lys Ser Ile Lys Ser Val Lys His Pro Thr Arg Lys Ile Tyr Met
130 135 140

Leu Tyr Asn Leu Gln Pro Ser Ile Asp Val Thr Gly Gly Pro Trp Phe
145 150 155 160

Thr Asp Ser Glu Leu Asp Thr Glu Phe Ile Glu Thr Leu Leu Glu Val
165 170 175

Cys Trp Arg Phe Ile Val Gly Lys Thr Met Tyr Ile Lys Asp Glu Glu
180 185 190

Ala Asp Asn Glu Asp Ile Asn Pro Leu Gln Thr Thr Tyr His Asn His
195 200 205

His Pro Gly Val Asn Leu Asp Gln Leu Val Glu Phe Ile Asn Asn Ser
210 215 220

Asn Ile Thr Ser Val Glu Leu Gly Ile Asn Asp Ile Arg Ser Leu Cys
225 230 235 240

Asp Val Leu Ile Tyr Asp Asp Arg Ile Glu Glu Val Gly Gly Asn Gln
245 250 255

Glu Asn Ser Gly Ile Phe Lys Ala Thr Trp Gln Ser Ile Ile Asp Lys
260 265 270

Gly Asn Thr Ile Leu Gln Asn Asn Tyr Gln Asp Leu Lys Asn Val Val
275 280 285

Ser Glu Asp Cys Phe Asn Tyr Leu Gln Gln Asn Gln Ser Asp Phe Ser
290 295 300

Val Phe Gln Tyr Lys Ser Thr Ile Gln Asp Leu Gln Asp Glu Ser Asp
305 310 315 320

Leu Val Tyr Leu Asp Ser Trp Met Asn Glu
325 330

<210> 3

<211> 317

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human Genbank Accession No: U93869

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 76

<400> 3

Met Ser Gly Met Ile Glu Asn Gly Leu Gln Leu Ser Asp Asn Ala Lys
1 5 10 15

Thr Leu His Ser Gln Met Met Ser Lys Gly Ile Gly Ala Leu Phe Thr
20 25 30

Gln Gln Glu Leu Gln Lys Gln Met Gly Ile Gly Ser Leu Thr Asp Leu
 35 40 45

Met Ser Ile Val Gln Glu Leu Leu Asp Lys Asn Leu Ile Lys Leu Val
 50 55 60

Lys Gln Asn Asp Glu Leu Lys Phe Gln Gly Val Leu Glu Ser Glu Ala
 65 70 75 80

Gln Lys Lys Ala Thr Met Ser Ala Glu Glu Ala Leu Val Tyr Ser Tyr
 85 90 95

Ile Glu Ala Ser Gly Arg Glu Gly Ile Trp Ser Lys Thr Ile Lys Ala
 100 105 110

Arg Thr Asn Leu His Gln His Val Val Leu Lys Cys Leu Lys Ser Leu
 115 120 125

Glu Ser Gln Arg Tyr Val Lys Ser Val Lys Ser Val Lys Phe Pro Thr
 130 135 140

Arg Lys Ile Tyr Met Leu Tyr Ser Leu Gln Pro Ser Val Asp Ile Thr
 145 150 155 160

Gly Gly Pro Trp Phe Thr Asp Gly Glu Leu Asp Ile Glu Phe Ile Asn
 165 170 175

Leu Leu Thr Ile Val Trp Arg Phe Ile Ser Glu Asn Thr Phe Pro
 180 185 190

Asn Gly Phe Lys Asn Phe Glu Asn Gly Pro Lys Lys Asn Val Phe Tyr
 195 200 205

Ala Pro Asn Val Lys Asn Tyr Ser Thr Thr Gln Glu Ile Leu Glu Phe
 210 215 220

Ile Thr Ala Ala Gln Val Ala Asn Val Glu Leu Thr Pro Ser Asn Ile
 225 230 235 240

Arg Ser Leu Cys Glu Val Leu Val Tyr Asp Asp Lys Leu Glu Lys Val
245 250 255

Thr His Asp Cys Tyr Arg Val Thr Leu Glu Ser Ile Leu Gln Met Asn
260 265 270

Gln Gly Glu Gly Glu Pro Glu Ala Gly Asn Lys Ala Leu Glu Asp Glu
275 280 285

Glu Glu Phe Ser Ile Phe Asn Tyr Phe Lys Met Phe Pro Ala Ser Lys
290 295 300

His Asp Lys Glu Val Val Tyr Phe Asp Glu Trp Thr Ile
305 310 315

<210> 4

<211> 195

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 77

<400> 4

Met Ser Gly Ser Leu Lys Ser Leu Asp Lys Lys Ile Ala Lys Arg Arg
1 5 10 15

Gln Val Tyr Lys Pro Val Leu Asp Asn Pro Phe Thr Asn Glu Ala His
20 25 30

Met Trp Pro Arg Val His Asp Gln Pro Leu Ile Trp Gln Leu Leu Gln
35 40 45

Ser Ser Ile Ile Asn Lys Leu Ile His Ile Gln Ser Lys Glu Asn Tyr
50 55 60

Pro Trp Glu Leu Tyr Thr Asp Phe Asn Glu Ile Val Gln Tyr Leu Ser
 65 70 75 80

Gly Ala His Gly Asn Ser Asp Pro Val Cys Leu Phe Val Cys Asn Lys
 85 90 95

Asp Pro Asp Val Pro Leu Val Leu Leu Gln Gln Ile Pro Leu Leu Cys
 100 105 110

Tyr Met Ala Pro Met Thr Val Lys Leu Val Gln Leu Pro Lys Ser Ala
 115 120 125

Met Asp Thr Phe Lys Ser Val Ser Lys Tyr Gly Met Leu Leu Leu Arg
 130 135 140

Cys Asp Asp Arg Val Asp Lys Lys Phe Val Ser Gln Ile Gln Lys Asn
 145 150 155 160

Val Asp Leu Leu Gln Phe Pro Trp Leu Asn Ala Ile Lys Tyr Arg Pro
 165 170 175

Thr Ser Val Lys Leu Leu Lys Thr Thr Val Pro Ile Val Ser Lys Lys
 180 185 190

Arg Gln Lys
 195

<210> 5

<211> 220

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 78

<400> 5

Met Asn Lys Ser Asn Lys Val Lys Lys Pro Ser Val Ala Lys Val Ser

1 5 10 15

Thr Lys Ala Ala Ser Ser Ser Leu Lys Ser Gln Glu Ala Lys Arg Gln
20 25 30

Val Phe Arg Pro Ile Leu Asp Asn Ser Phe Thr Gln Ser Asn Gln Trp
35 40 45

Pro Phe Ile Glu Pro Thr Ile Ala Asn Asp Ile Val Asp Leu Leu Glu
50 55 60

Val Leu Leu Lys Met Gln Asp Ser Thr Phe Lys Tyr Arg Gly Phe Asn
65 70 75 80

Pro Thr Val Ser Ala Leu Glu Lys Gln Ala Ala Ala Asn Arg Gly Ile
85 90 95

His Lys Asn Ala Cys Val Gln Ile Lys Tyr Val Phe Val Cys Lys Tyr
100 105 110

Asp Ile Ser Pro Ala Thr Leu Thr Asn Val Phe Pro Thr Leu Cys Phe
115 120 125

Thr Ala Ser Lys Ser Ala Glu Asp Arg Val Lys Leu Ile Gln Leu Pro
130 135 140

Arg Gly Ser Leu Glu Arg Leu Ser Lys Ala Leu Gly Val Asp Arg Val
145 150 155 160

Gly Ile Phe Gly Leu Thr Lys Asp Thr Glu Gly Ala Gln Pro Leu Phe
165 170 175

Asp Leu Ile Asn Glu Asn Val Lys Asp Ile Glu Ala Pro Trp Leu Asp
180 185 190

Cys Ile Phe Arg Glu Glu Met Val Phe Asn Gln Pro Asn Thr Lys His
195 200 205

Val Ala Ser Thr Val Gly Arg Lys Lys Asn Lys Lys
 210 215 220

<210> 6

<211> 328

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 79

<400> 6

Met Ser Lys Asn Arg Asp Pro Leu Leu Ala Asn Leu Asn Ala Phe Lys
 1 5 10 15

Ser Lys Val Lys Ser Ala Pro Val Ile Ala Pro Ala Lys Val Gly Gln
 20 25 30

Lys Lys Thr Asn Asp Thr Val Ile Thr Ile Asp Gly Asn Thr Arg Lys
 35 40 45

Arg Thr Ala Ser Glu Arg Ala Gln Glu Asn Thr Leu Asn Ser Ala Lys
 50 55 60

Asn Pro Val Leu Val Asp Ile Lys Lys Glu Ala Gly Ser Asn Ser Ser
 65 70 75 80

Asn Ala Ile Ser Leu Asp Asp Asp Asp Asp Glu Asp Phe Gly Ser
 85 90 95

Ser Pro Ser Lys Lys Val Arg Pro Gly Ser Ile Ala Ala Ala Leu
 100 105 110

Gln Ala Asn Gln Thr Asp Ile Ser Lys Ser His Asp Ser Ser Lys Leu
 115 120 125

Leu Trp Ala Thr Glu Tyr Ile Gln Lys Lys Gly Lys Pro Val Leu Val
130 135 140

Asn Glu Leu Leu Asp Tyr Leu Ser Met Lys Lys Asp Asp Lys Val Ile
145 150 155 160

Glu Leu Leu Lys Lys Leu Asp Arg Ile Glu Phe Asp Pro Lys Lys Gly
165 170 175

Thr Phe Lys Tyr Leu Ser Thr Tyr Asp Val His Ser Pro Ser Glu Leu
180 185 190

Leu Lys Leu Leu Arg Ser Gln Val Thr Phe Lys Gly Ile Ser Cys Lys
195 200 205

Asp Leu Lys Asp Gly Trp Pro Gln Cys Asp Glu Thr Ile Asn Gln Leu
210 215 220

Glu Glu Asp Ser Lys Ile Leu Val Leu Arg Thr Lys Lys Asp Lys Thr
225 230 235 240

Pro Arg Tyr Val Trp Tyr Asn Ser Gly Gly Asn Leu Lys Cys Ile Asp
245 250 255

Glu Glu Phe Val Lys Met Trp Glu Asn Val Gln Leu Pro Gln Phe Ala
260 265 270

Glu Leu Pro Arg Lys Leu Gln Asp Leu Gly Leu Lys Pro Ala Ser Val
275 280 285

Asp Pro Ala Thr Ile Lys Arg Gln Thr Lys Arg Val Glu Val Lys Lys
290 295 300

Lys Arg Gln Arg Lys Gly Lys Ile Thr Asn Thr His Met Thr Gly Ile
305 310 315 320

Leu Lys Asp Tyr Ser His Arg Val

325

<210> 7

<211> 284

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 80

<400> 7

Met Ser Asp Leu Ser Ala Gln Leu Ser Ala Phe Lys Asn Lys Ile Lys
 1 5 10 15

Ser Gly Pro Ser Val Ile Val Pro Arg Lys Ala Thr Phe Thr Gln Ser
 20 25 30

Pro Ser Ser Pro Leu Ser Ser Ser Thr Thr Thr Thr Thr Ser Lys Asn
 35 40 45

Asp Ala Asn Val Lys Lys Arg Ser Thr Thr Asp Ser Val Thr Arg Val
 50 55 60

Leu Lys Lys Gln Lys Ala Asn Met Gly Glu Met Thr Gly Ser His Leu
 65 70 75 80

Ser Thr Gln Leu His Leu Ala Val Glu Tyr Ile Lys Glu His Asp Gln
 85 90 95

Pro Ile Ser Val Glu Lys Leu Gln Asn Tyr Leu Ser Phe Asp Ile Ser
 100 105 110

His Thr Leu Leu Pro Leu Leu Asn Glu Ile Asp Arg Val Lys Tyr Asp
 115 120 125

Glu Ser Lys Gly Thr Leu Glu Tyr Val Ser Leu His Asn Ile Arg Ser
 130 135 140

Ser Asp Asp Val Leu Glu Phe Leu Arg Arg Gln Thr Thr Phe Lys Gly
 145 150 155 160

Thr Ser Val Lys Glu Leu Lys Asp Gly Trp Ala Gly Cys Val Ala Ala
 165 170 175

Ile Asp Glu Leu Glu Ser Gln Gly Lys Ile Leu Val Leu Arg Asn Lys
 180 185 190

Lys Glu Asn Ala Pro Arg Leu Val Trp Ala Asn Asn Gly Gly Glu Leu
 195 200 205

Gly Tyr Ile Asp Thr Glu Phe Lys Asp Met Trp Asp Gln Val Lys Leu
 210 215 220

Pro Glu Pro Asp Val Leu Tyr Gln Lys Leu Leu Asp Gln Gly Leu Lys
 225 230 235 240

Pro Thr Gly Ala Asp Pro Asn Leu Ile Lys Lys Gln Pro Gln Gln Lys
 245 250 255

Glu Lys Lys Gln Lys Lys Ala Arg Arg Gly Lys Ile Thr Asn Thr His
 260 265 270

Met Lys Gly Ile Leu Lys Asp Tyr Ser Gln Leu Val
 275 280

<210> 8

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: NP_002086

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 81

<400> 8

Met Asp Pro Ser Leu Leu Arg Glu Arg Glu Leu Phe Lys Lys Arg Ala
1 5 10 15

Leu Ser Thr Pro Val Val Glu Lys Arg Ser Ala Ser Ser Glu Ser Ser
20 25 30

Ser Ser Ser Ser Lys Lys Lys Lys Thr Lys Val Glu His Gly Gly Ser
35 40 45

Ser Gly Ser Lys Gln Asn Ser Asp His Ser Asn Gly Ser Phe Asn Leu
50 55 60

Lys Ala Leu Ser Gly Ser Ser Gly Tyr Lys Phe Gly Val Leu Ala Lys
65 70 75 80

Ile Val Asn Tyr Met Lys Thr Arg His Gln Arg Gly Asp Thr His Pro
85 90 95

Leu Thr Leu Asp Glu Ile Leu Asp Glu Thr Gln His Leu Asp Ile Gly
100 105 110

Leu Lys Gln Lys Gln Trp Leu Met Thr Glu Ala Leu Val Asn Asn Pro
115 120 125

Lys Ile Glu Val Ile Asp Gly Lys Tyr Ala Phe Lys Pro Lys Tyr Asn
130 135 140

Val Arg Asp Lys Lys Ala Leu Leu Arg Leu Leu Asp Gln His Asp Gln
145 150 155 160

Arg Gly Leu Gly Gly Ile Leu Leu Glu Asp Ile Glu Glu Ala Leu Pro
165 170 175

Asn Ser Gln Lys Ala Val Lys Ala Leu Gly Asp Gln Ile Leu Phe Val
180 185 190

Asn Arg Pro Asp Lys Lys Lys Ile Leu Phe Phe Asn Asp Lys Ser Cys
195 200 205

Gln Phe Ser Val Asp Glu Glu Phe Gln Lys Leu Trp Arg Ser Val Thr
210 215 220

Val Asp Ser Met Asp Glu Glu Lys Ile Glu Glu Tyr Leu Lys Arg Gln
225 230 235 240

Gly Ile Ser Ser Met Gln Glu Ser Gly Pro Lys Lys Val Ala Pro Ile
245 250 255

Gln Arg Arg Lys Lys Pro Ala Ser Gln Lys Lys Arg Arg Phe Lys Thr
260 265 270

His Asn Glu His Leu Ala Gly Val Leu Lys Asp Tyr Ser Asp Ile Thr
275 280 285

Ser Ser Lys
290

<210> 9
<211> 480
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 82

<400> 9

Met Ser Gln Glu Gln Tyr Thr Glu Asn Leu Lys Val Ile Val Ala Glu
1 5 10 15

Lys Leu Ala Gly Ile Pro Asn Phe Asn Glu Asp Ile Lys Tyr Val Ala

20 25 30

Glu Tyr Ile Val Leu Leu Ile Val Asn Gly Gly Thr Val Glu Ser Val
35 40 45Val Asp Glu Leu Ala Ser Leu Phe Asp Ser Val Ser Arg Asp Thr Leu
50 55 60Ala Asn Val Val Gln Thr Ala Phe Phe Ala Leu Glu Ala Leu Gln Gln
65 70 75 80Gly Glu Ser Ala Glu Asn Ile Val Ser Lys Ile Arg Met Met Asn Ala
85 90 95Gln Ser Leu Gly Gln Ser Asp Ile Ala Gln Gln Gln Gln Gln Gln
100 105 110Gln Gln Gln Gln Pro Asp Ile Ala Gln Gln Gln Pro Gln Gln Gln Pro
115 120 125Gln Leu Gln Pro Leu Gln Pro Gln Leu Gly Thr Gln Asn Ala Met Gln
130 135 140Thr Asp Ala Pro Ala Thr Pro Ser Pro Ile Ser Ala Phe Ser Gly Val
145 150 155 160Val Asn Ala Ala Ala Pro Pro Gln Phe Ala Pro Val Asp Asn Ser Gln
165 170 175Arg Phe Thr Gln Arg Gly Gly Gly Ala Val Gly Lys Asn Arg Arg Gly
180 185 190Gly Arg Gly Gly Asn Arg Gly Gly Arg Asn Asn Asn Ser Thr Arg Phe
195 200 205Asn Pro Leu Ala Lys Ala Leu Gly Met Ala Gly Glu Ser Asn Met Asn
210 215 220

Phe Thr Pro Thr Lys Lys Glu Gly Arg Cys Arg Leu Phe Pro His Cys
225 230 235 240

Pro Leu Gly Arg Ser Cys Pro His Ala His Pro Thr Lys Val Cys Asn
 245 250 255

Glu Tyr Pro Asn Cys Pro Lys Pro Pro Gly Thr Cys Glu Phe Leu His
 260 265 270

Pro Asn Glu Asp Glu Glu Leu Met Lys Glu Met Glu Arg Thr Arg Glu
 275 280 285

Glu Phe Gln Lys Arg Lys Ala Asp Leu Leu Ala Ala Lys Arg Lys Pro
 290 295 300

Val Gln Thr Gly Ile Val Leu Cys Lys Phe Gly Ala Leu Cys Ser Asn
305 310 315 320

Pro Ser Cys Pro Phe Gly His Pro Thr Pro Ala Asn Glu Asp Ala Lys
 325 330 335

Val Ile Asp Leu Met Trp Cys Asp Lys Asn Leu Thr Cys Asp Asn Pro
 340 345 350

Glu Cys Arg Lys Ala His Ser Ser Leu Ser Lys Ile Lys Glu Val Lys
 355 360 365

Pro Ile Ser Gln Lys Lys Ala Ala Pro Pro Pro Val Glu Lys Ser Leu
 370 375 380

Glu Gln Cys Lys Phe Gly Thr His Cys Thr Asn Lys Arg Cys Lys Tyr
385 390 395 400

Arg His Ala Arg Ser His Ile Met Cys Arg Glu Gly Ala Asn Cys Thr
 405 410 415

Arg Ile Asp Cys Leu Phe Gly His Pro Ile Asn Glu Asp Cys Arg Phe
 420 425 430

Gly Val Asn Cys Lys Asn Ile Tyr Cys Leu Phe Arg His Pro Pro Gly
 435 440 445

Arg Val Leu Pro Glu Lys Lys Gly Ala Ala Pro Asn Ser Asn Val Pro
 450 455 460

Thr Asn Glu Arg Pro Phe Ala Leu Pro Glu Asn Ala Ile Ile Glu Asn
 465 470 475 480

<210> 10

<211> 418

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 83

<400> 10

Met Gln Phe Ala Pro Asp Asn Gln Ile Gly Lys Glu Leu Gln Gln Asn
 1 5 10 15

Leu Ile Gln Glu Ile Gln Arg Arg Phe Asn Lys Pro Ala Asp Asp Ala
 20 25 30

Val Asp Ile Ala Asp Tyr Ile Ile Tyr Leu Ile Val Ala Lys Lys Ser
 35 40 45

Glu Gln Glu Ile Val Ala Glu Val Lys Asp Ile Ala Asp Ile Ser Ile
 50 55 60

Asp Val Gly Phe Ile Gly Asp Val Tyr Leu Glu Ile Arg Lys Leu Glu
 65 70 75 80

Val Lys Tyr Asn Gln Pro Pro Ala Ala Val Glu Glu Ala Ser Gln Pro

85 90 95

Gln Gln Glu Gln Gln Gln Gln Ser Gln Ala Ser Val Val Ala Pro Gln
100 105 110

Ile Pro Ile Gly Pro Lys Lys Gln Leu Thr Glu Glu Glu Lys Ile Ala
115 120 125

Leu Arg Ser Gln Arg Phe Gly Thr Thr Thr Arg Leu Ser Gly Arg Gly
130 135 140

Gly Arg Gly Gly Ile Thr Lys Thr Arg Thr Asp Phe Arg Asn Gly His
145 150 155 160

Asn Asn Lys Asn Phe Leu Asp Pro Lys Lys Leu Asp Gln Ile Ile Ser
165 170 175

Gly Ala Asn Asn Gly Ala Ile Lys Phe Val Pro Leu Pro Pro Lys Gly
180 185 190

Arg Cys Pro Asp Phe Pro Tyr Cys Lys Asn Gln Asn Cys Glu Lys Ala
195 200 205

His Pro Thr Lys Asn Cys Phe Asn Tyr Pro Asp Cys Pro Asn Pro Pro
210 215 220

Gly Thr Cys Asn Phe Leu His Pro Asp Gln Asp Gln Glu Leu Ile Ala
225 230 235 240

Lys Leu Glu Thr Ser Lys Lys Glu Phe Glu Glu Lys Lys Lys Asn Gln
245 250 255

Leu Met Val Lys Gln Gly Ser Cys Lys Tyr Gly Leu Lys Cys Ala Lys
260 265 270

Glu Asn Cys Pro Phe Ala His Pro Thr Pro Ala Asn Pro Glu Ser Gly
275 280 285

Lys Ile Glu Thr Leu Glu Trp Cys Pro Gln Gly Lys Asn Cys Gln Asp
 290 295 300

Arg Asn Cys Thr Lys Ser His Pro Pro Pro Thr Ala Asn Ser Glu
 305 310 315 320

Lys Leu Leu Ser Ala Ala Asp Leu Ala Leu Glu Gln Cys Lys Phe Gly
 325 330 335

Ser Gln Cys Thr Asn Leu Lys Cys Pro Arg Arg His Ala Thr Ser Ala
 340 345 350

Val Pro Cys Arg Ala Gly Ala Glu Cys Arg Arg Val Asp Cys Thr Phe
 355 360 365

Ser His Pro Leu Lys Glu Pro Cys Arg Phe Gly Thr Lys Cys Thr Asn
 370 375 380

Lys Val Cys Met Tyr Gln His Pro Glu Gly Arg Thr Ile Ala Ser His
 385 390 395 400

Thr Trp Thr Arg Asp Gly Ser Gly Asn Asn Asn Ser Thr Ser Asn Arg
 405 410 415

Ser Phe

<210> 11

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: AAD42873

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 84

<400> 11

Pro Gln Gln Leu His Leu Leu Ser Arg Gln Leu Glu Asp Pro Asn Gly
1 5 10 15

Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
20 25 30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
35 40 45

Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
50 55 60

Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
65 70 75 80

Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
85 90 95

Arg Arg Ile Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met Glu
100 105 110

Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys Thr
115 120 125

Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro Arg
130 135 140

His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
145 150 155

<210> 12

<211> 360

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 85

<400> 12

Met Ala Asn Ser Pro Lys Lys Pro Ser Asp Gly Thr Gly Val Ser Ala
1 5 10 15

Ser Asp Thr Pro Lys Tyr Gln His Thr Val Pro Glu Thr Lys Pro Ala
20 25 30

Phe Asn Leu Ser Pro Gly Lys Ala Ser Glu Leu Ser His Ser Leu Pro
35 40 45

Ser Pro Ser Gln Ile Lys Ser Thr Ala His Val Ser Ser Thr His Asn
50 55 60

Asp Ala Ala Gly Asn Thr Asp Asp Ser Val Leu Pro Lys Asn Val Ser
65 70 75 80

Pro Thr Thr Asn Leu Arg Val Glu Ser Asn Gly Asp Thr Asn Asn Met
85 90 95

Phe Ser Ser Pro Ala Gly Leu Ala Leu Pro Lys Lys Asp Asp Lys Lys
100 105 110

Lys Asn Lys Gly Thr Ser Lys Ala Asp Ser Lys Asp Gly Lys Ala Ser
115 120 125

Asn Ser Ser Gly Gln Asn Ala Gln Gln Gln Ser Asp Pro Asn Lys Met
130 135 140

Gln Asp Val Leu Phe Ser Ala Gly Ile Asp Val Arg Glu Glu Glu Ala
145 150 155 160

Leu Leu Asn Ser Ser Ile Asn Ala Ser Lys Ser Gln Val Gln Thr Asn
165 170 175

Asn Val Lys Ile Pro Asn His Leu Pro Phe Leu His Pro Glu Gln Val
180 185 190

Ser Asn Tyr Met Arg Lys Val Gly Lys Glu Gln Asn Phe Asn Leu Thr
195 200 205

Pro Thr Lys Asn Pro Glu Ile Leu Asp Met Met Ser Ser Ala Cys Glu
210 215 220

Asn Tyr Met Arg Asp Ile Leu Thr Asn Ala Ile Val Ile Ser Arg His
225 230 235 240

Arg Arg Lys Ala Val Lys Ile Asn Ser Gly Arg Arg Ser Glu Val Ser
245 250 255

Ala Ala Leu Arg Ala Ile Ala Leu Ile Gln Lys Lys Glu Glu Glu Arg
260 265 270

Arg Val Lys Lys Arg Ile Ala Leu Gly Leu Glu Lys Glu Asp Tyr Glu
275 280 285

Asn Lys Ile Asp Ser Glu Glu Thr Leu His Arg Ala Ser Asn Val Thr
290 295 300

Ala Gly Leu Arg Ala Gly Ser Lys Lys Gln Tyr Gly Trp Leu Thr Ser
305 310 315 320

Ser Val Asn Lys Pro Thr Ser Leu Gly Ala Lys Ser Ser Gly Lys Val
325 330 335

Ala Ser Asp Ile Thr Ala Arg Gly Glu Ser Gly Leu Lys Phe Arg Glu
340 345 350

Ala Arg Glu Glu Pro Gly Ile Val
355 360

<210> 13

<211> 358

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 86

<400> 13

Met Ser His Lys Ser Met Thr Ser Thr Pro Gln Glu Ser Ser Asn Leu
 1 5 10 15

Lys Arg Gln Leu Glu Asn Ser Glu Asp Ser Ser Ser Pro Asn Lys Arg
 20 25 30

Ser Lys Thr Glu Thr Thr Thr Glu Asn Gln Ser Ser Trp Glu Ser Asp
 35 40 45

Phe Asn Ser Leu Pro Val Glu Leu Leu Gln Thr Glu Thr Asn Gly Thr
 50 55 60

Ser Pro Ala Pro Ala Pro Ala Thr Pro Ile Asp Thr Thr Asn Ala Ser
 65 70 75 80

Ser Thr Lys Glu Arg Asp Gln Asp Thr Ser Lys Leu Asn Asp Ala Ile
 85 90 95

Ala Ala Ala Gly Val Asp Ile Gln Gln Glu Glu Glu Ile Leu Leu Gln
 100 105 110

Gln Gln Leu Asn Arg Lys Ser Ala Glu Gly Met Ala Ser Asn Leu Lys
 115 120 125

Ser Val Ile Arg Ser Ser Lys Leu Pro Pro Phe Leu His Asn Tyr His
 130 135 140

Leu Ala Ala Phe Ile Asp Lys Val Ala Lys Gln Asn Gly Ile Gln Gln

145 150 155 160
Asn Phe Leu Met Asp Gly Glu Met Leu Glu Leu Ile Ser Ala Ala Cys
 165 170 175
Glu Thr Trp Leu Ser Asn Leu Ala Thr Lys Thr Ile Ile Leu Ser Arg
 180 185 190
His Arg Arg Arg Gly Ile Pro Val Ile Asn Lys Lys Ser Gly Ser Ser
 195 200 205
Ser Val Pro Arg Ser Glu Ile Ser Lys Glu Leu Arg Ser Leu Ala Leu
 210 215 220
Lys Gln Lys Glu Met Glu Glu Lys Arg Val Asn Lys Arg Val Met Leu
225 230 235 240
Gly Leu Glu Lys Ser Thr Lys Asp Ala Ser Lys Asn Asp Glu Asn Gly
 245 250 255
Glu Ser Lys Ala Gly Ala Glu Glu Thr Leu His Arg Ala Ala Asn Ala
 260 265 270
Thr Ala Ala Met Met Thr Met Asn Pro Gly Arg Lys Lys Tyr Ser Trp
 275 280 285
Met Thr Ser Ser Ala Thr Ala Gly Gly Gly Ser Asp Phe Gly Lys Ser
 290 295 300
Ser Gly Gly Ser Ser Lys Asp Ser Gly Lys His Gln Ser Pro Ile Ile
305 310 315 320
Ser Val Arg Gly Asp Asn Gly Leu Arg Phe Arg Glu Ile Arg Ser Gly
 325 330 335
Asn Ser Ile Ile Met Lys Asp Leu Leu Gly Ala Ile Glu Asp Glu Lys
 340 345 350

Met Gly Thr Arg Asn Ala
355

<210> 14

<211> 1023

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: CAA72189

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 87

<400> 14

Met Ala Ala Gly Ser Asp Leu Leu Asp Glu Val Phe Phe Asn Ser Glu
1 5 10 15

Val Asp Glu Lys Val Val Ser Asp Leu Val Gly Ser Leu Glu Ser Gln
20 25 30

Leu Ala Ala Ser Ala Ala His His His His Leu Ala Pro Arg Thr Pro
35 40 45

Glu Val Arg Ala Ala Ala Ala Gly Ala Leu Gly Asn His Val Val Ser
50 55 60

Gly Ser Pro Ala Gly Ala Ala Gly Ala Gly Pro Ala Ala Pro Ala Glu
65 70 75 80

Gly Ala Pro Gly Ala Ala Pro Glu Pro Pro Pro Ala Gly Arg Ala Arg
85 90 95

Pro Gly Gly Gly Gly Pro Gln Arg Pro Gly Pro Pro Ser Pro Arg Arg
100 105 110

Pro Leu Val Pro Ala Gly Pro Ala Pro Pro Ala Ala Lys Leu Arg Pro
115 120 125

Pro Pro Glu Gly Ser Ala Gly Ala Cys Ala Pro Val Pro Ala Ala Ala
130 135 140

Ala Val Ala Ala Gly Pro Glu Pro Ala Pro Ala Gly Pro Ala Lys Pro
145 150 155 160

Ala Gly Pro Ala Ala Leu Ala Ala Arg Ala Gly Pro Gly Pro Gly Pro
165 170 175

Gly Pro Gly Pro Gly Pro Gly Pro Gly Lys Pro Ala Gly Pro Gly Ala
180 185 190

Ala Gln Thr Leu Asn Gly Ser Ala Ala Leu Leu Asn Ser His His Ala
195 200 205

Ala Ala Pro Ala Val Ser Leu Val Asn Asn Gly Pro Ala Ala Leu Leu
210 215 220

Pro Leu Pro Lys Pro Ala Ala Pro Gly Thr Val Ile Gln Thr Pro Pro
225 230 235 240

Phe Val Gly Ala Ala Ala Pro Pro Ala Pro Ala Ala Pro Ser Pro Pro
245 250 255

Ala Ala Pro Ala Pro Ala Ala Pro Ala Ala Ala Pro Pro Pro Pro
260 265 270

Pro Ala Pro Ala Thr Leu Ala Arg Pro Pro Gly His Pro Ala Gly Pro
275 280 285

Pro Thr Ala Ala Pro Ala Val Pro Pro Pro Ala Ala Ala Gln Asn Gly
290 295 300

Gly Ser Ala Gly Ala Ala Pro Ala Pro Ala Pro Ala Ala Gly Gly Pro

305 310 315 320

Ala Gly Val Ser Gly Gln Pro Gly Pro Gly Ala Ala Ala Ala Pro
 325 330 335

Ala Pro Gly Val Lys Ala Glu Ser Pro Lys Arg Val Val Gln Ala Ala
 340 345 350

Pro Pro Ala Ala Gln Thr Leu Ala Ala Ser Gly Pro Ala Ser Thr Ala
 355 360 365

Ala Ser Met Val Ile Gly Pro Thr Met Gln Gly Ala Leu Pro Ser Pro
 370 375 380

Ala Ala Val Pro Pro Pro Ala Pro Gly Thr Pro Thr Gly Leu Pro Lys
385 390 395 400

Gly Ala Ala Gly Ala Val Thr Gln Ser Leu Ser Arg Thr Pro Thr Ala
 405 410 415

Thr Thr Ser Gly Ile Arg Ala Thr Leu Thr Pro Thr Val Leu Ala Pro
 420 425 430

Arg Leu Pro Gln Pro Pro Gln Asn Pro Thr Asn Ile Gln Asn Phe Gln
 435 440 445

Leu Pro Pro Gly Met Val Leu Val Arg Ser Glu Asn Gly Gln Leu Leu
 450 455 460

Met Ile Pro Gln Gln Ala Leu Ala Gln Met Gln Ala Gln Ala His Ala
465 470 475 480

Gln Pro Gln Thr Thr Met Ala Pro Arg Pro Ala Thr Pro Thr Ser Ala
 485 490 495

Pro Pro Val Gln Ile Ser Thr Val Gln Ala Pro Gly Thr Pro Ile Ile
 500 505 510

Ala Arg Gln Val Thr Pro Thr Thr Ile Ile Lys Gln Val Ser Gln Ala
515 520 525

Gln Thr Thr Val Gln Pro Ser Ala Thr Leu Gln Arg Ser Pro Gly Val
530 535 540

Gln Pro Gln Leu Val Leu Gly Gly Ala Ala Gln Thr Ala Ser Leu Gly
545 550 555 560

Thr Ala Thr Ala Val Gln Thr Gly Thr Pro Gln Arg Thr Val Pro Gly
565 570 575

Ala Thr Thr Thr Ser Ser Ala Ala Thr Glu Thr Met Glu Asn Val Lys
580 585 590

Lys Cys Lys Asn Phe Leu Ser Thr Leu Ile Lys Leu Ala Ser Ser Gly
595 600 605

Lys Gln Ser Thr Glu Thr Ala Ala Asn Val Lys Glu Leu Val Gln Asn
610 615 620

Leu Leu Asp Gly Lys Ile Glu Ala Glu Asp Phe Thr Ser Arg Leu Tyr
625 630 635 640

Arg Glu Leu Asn Ser Ser Pro Gln Pro Tyr Leu Val Pro Phe Leu Lys
645 650 655

Arg Ser Leu Pro Ala Leu Arg Gln Leu Thr Pro Asp Ser Ala Ala Phe
660 665 670

Ile Gln Gln Ser Gln Gln Gln Pro Pro Pro Thr Ser Gln Ala Thr
675 680 685

Thr Ala Leu Thr Ala Val Val Leu Ser Ser Ser Val Gln Arg Thr Ala
690 695 700

Gly Lys Thr Ala Ala Thr Val Thr Ser Ala Leu Gln Pro Pro Val Leu
705 710 715 720

Ser Leu Thr Gln Pro Thr Gln Val Gly Val Gly Lys Gln Gly Gln Pro
 725 730 735

Thr Pro Leu Val Ile Gln Gln Pro Pro Lys Pro Gly Ala Leu Ile Arg
 740 745 750

Pro Pro Gln Val Thr Leu Thr Gln Thr Pro Met Val Ala Leu Arg Gln
 755 760 765

Pro His Asn Arg Ile Met Leu Thr Thr Pro Gln Gln Val Asn Leu Ser
 770 775 780

Glu Glu Ser Ala Arg Ile Leu Ala Thr Asn Ser Glu Leu Val Gly Thr
785 790 795 800

Leu Thr Arg Ser Cys Lys Asp Glu Thr Phe Leu Leu Gln Ala Pro Leu
 805 810 815

Gln Arg Arg Ile Leu Glu Ile Gly Lys Lys His Gly Ile Thr Glu Leu
 820 825 830

His Pro Asp Val Val Ser Tyr Val Ser His Ala Thr Gln Gln Arg Leu
 835 840 845

Gln Asn Leu Val Glu Lys Ile Ser Glu Thr Ala Gln Gln Lys Asn Phe
 850 855 860

Ser Tyr Lys Asp Asp Asp Arg Tyr Glu Gln Ala Ser Asp Val Arg Ala
865 870 875 880

Gln Leu Lys Phe Phe Glu Gln Leu Asp Gln Ile Glu Lys Gln Arg Lys
 885 890 895

Asp Glu Gln Glu Arg Glu Ile Leu Met Arg Ala Ala Lys Ser Arg Ser

900 905 910

Arg Gln Glu Asp Pro Glu Gln Leu Arg Leu Lys Gln Lys Ala Lys Glu
 915 920 925

Met Gln Gln Gln Glu Leu Ala Gln Met Arg Gln Arg Asp Ala Asn Leu
 930 935 940

Thr Ala Leu Ala Ala Ile Gly Pro Arg Lys Lys Arg Lys Val Asp Cys
 945 950 955 960

Pro Gly Pro Gly Ser Gly Ala Glu Gly Ser Gly Pro Gly Ser Val Val
 965 970 975

Pro Gly Ser Ser Gly Val Gly Thr Pro Arg Gln Phe Thr Arg Gln Arg
 980 985 990

Ile Thr Arg Val Asn Leu Arg Asp Leu Ile Phe Cys Leu Glu Asn Glu
 995 1000 1005

Arg Glu Thr Ser His Ser Leu Leu Leu Tyr Lys Ala Phe Leu Lys
 1010 1015 1020

<210> 15

<211> 184

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 88

<400> 15

Met Asn Thr Asn Ser Asn Thr Met Val Met Asn Asp Ala Asn Gln Ala
 1 5 10 15

Gln Ile Thr Ala Thr Phe Thr Lys Lys Ile Leu Ala His Leu Asp Asp
 20 25 30

Pro Asp Ser Asn Lys Leu Ala Gln Phe Val Gln Leu Phe Asn Pro Asn
 35 40 45

Asn Cys Arg Ile Ile Phe Asn Ala Thr Pro Phe Ala Gln Ala Thr Val
 50 55 60

Phe Leu Gln Met Trp Gln Asn Gln Val Val Gln Thr Gln His Ala Leu
 65 70 75 80

Thr Gly Val Asp Tyr His Ala Ile Pro Gly Ser Gly Thr Leu Ile Cys
 85 90 95

Asn Val Asn Cys Lys Val Arg Phe Asp Glu Ser Gly Arg Asp Lys Met
 100 105 110

Gly Gln Asp Ala Thr Val Pro Ile Gln Pro Asn Asn Thr Gly Asn Arg
 115 120 125

Asn Arg Pro Asn Asp Met Asn Lys Pro Arg Pro Leu Trp Gly Pro Tyr
 130 135 140

Phe Gly Ile Ser Leu Gln Leu Ile Ile Asp Asp Arg Ile Phe Arg Asn
 145 150 155 160

Asp Phe Asn Gly Val Ile Ser Gly Phe Asn Tyr Asn Met Val Tyr Lys
 165 170 175

Pro Glu Asp Ser Leu Leu Lys Ile
 180

<210> 16

<211> 181

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 89

<400> 16

Met Asn Gln Asp Pro Thr Gln Gln Leu Glu Pro Phe Leu Lys Arg Phe
1 5 10 15

Leu Ala Ser Leu Asp Leu Leu Tyr Thr Gln Pro Thr Ser Gln Pro Phe
20 25 30

Pro Asn Val Glu Ser Tyr Ala Thr Gln Leu Gly Ser Asn Leu Lys Arg
35 40 45

Ser Ser Ala Ile Ile Val Asn Gly Gln Pro Ile Ile Pro Ser Pro Gln
50 55 60

Glu Asp Cys Lys Leu Gln Phe Gln Lys Lys Trp Leu Gln Thr Pro Leu
65 70 75 80

Ser Ser His Gln Leu Thr Ser Tyr Asp Gly His Leu Ile Pro Gly Thr
85 90 95

Gly Thr Phe Val Val His Phe Ser Ala Lys Val Arg Phe Asp Gln Ser
100 105 110

Gly Arg Asn Arg Leu Gly Glu Ser Ala Asp Leu Phe Gln Glu Asn Asn
115 120 125

Ser Ile Val Ser Lys Thr Asn Gln Arg Pro Ile Trp Gly Ser Trp Phe
130 135 140

Gly Val Asp Val Asn Leu Val Val Asp Glu Asn Val Met Gln Asp Gly
145 150 155 160

Glu Ile Ile Asn Ser Met Asp Tyr Arg Phe Thr Tyr Val Pro Asn Asp
165 170 175

Ser Ile Ile Lys Val
180

<210> 17
 <211> 244
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <220>
 <221> misc_feature
 <223> Corresponds to SEQ ID NO: 90

<400> 17

Met Asn Ala Leu Tyr Asn His Ala Val Lys Gln Lys Asn Gln Leu Gln
 1 5 10 15

Gln Glu Leu Ala Arg Phe Glu Lys Asn Ser Val Thr Ala Pro Ile Ser
 20 25 30

Leu Gln Gly Ser Ile Ser Ala Thr Leu Val Ser Leu Glu Lys Thr Val
 35 40 45

Lys Gln Tyr Ala Glu His Leu Asn Arg Tyr Lys Glu Asp Thr Asn Ala
 50 55 60

Glu Glu Ile Asp Pro Lys Phe Ala Asn Arg Leu Ala Thr Leu Thr Gln
 65 70 75 80

Asp Leu His Asp Phe Thr Ala Lys Phe Lys Asp Leu Lys Gln Ser Tyr
 85 90 95

Asn Glu Asn Asn Ser Arg Thr Gln Leu Phe Gly Ser Gly Ala Ser His
 100 105 110

Val Met Asp Ser Asp Asn Pro Phe Ser Thr Ser Glu Thr Ile Met Asn
 115 120 125

Lys Arg Asn Val Gly Gly Ala Ser Ala Asn Gly Lys Glu Gly Ser Ser
 130 135 140

Asn Gly Gly Gly Leu Pro Leu Tyr Gln Gly Leu Gln Lys Glu Gln Ser
145 150 155 160

Val Phe Glu Arg Gly Asn Ala Gln Leu Asp Tyr Ile Leu Glu Met Gly
 165 170 175

Gln Gln Ser Phe Glu Asn Ile Val Glu Gln Asn Lys Ile Leu Ser Lys
 180 185 190

Val Gln Asp Arg Met Ser Asn Gly Leu Arg Thr Leu Gly Val Ser Glu
 195 200 205

Gln Thr Ile Thr Ser Ile Asn Lys Arg Val Phe Lys Asp Lys Leu Val
 210 215 220

Phe Trp Ile Ala Leu Ile Leu Leu Ile Ile Gly Ile Tyr Tyr Val Leu
225 230 235 240

Lys Trp Leu Arg

<210> 18

<211> 238

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 91

<400> 18

Met Asn Ser Ile Tyr Asn His Gly Leu Lys Gln Thr Gln Thr Ile Thr
1 5 10 15

Lys Asp Leu Thr Gln Phe Glu Lys Asn Leu Ser Thr Ser Pro Leu Ser
20 25 30

Leu Gln Gly Ala Ile Thr Thr Ser Leu Thr Ala Phe Arg Lys Thr Ile

35 40 45

Lys Glu Tyr Ser Asp Leu Leu Glu Lys Asn Val Asn Asp Thr Ser Tyr
50 55 60

Thr Lys His Glu Asn Arg Leu Asn Lys Phe Asn Gln Asp Leu Asn Glu
65 70 75 80

Phe Thr Leu Lys Phe Asp Thr Leu Lys Lys Gln Arg Asp Ile Gln Val
85 90 95

Gln Glu Ala Asn Lys Gln Glu Leu Leu Gly Arg Arg His Ile Ser Thr
100 105 110

Thr Ala Thr Ala Ala Leu Gly Ser Thr Ser Ser Asp Asn Pro Tyr Glu
115 120 125

Ser Ser Ser Asn Pro Ser Gln Gln Gln Gln Gln Leu Gln Asp Glu
130 135 140

Gln Asn Thr Met Ser Tyr Arg Glu Gly Leu Tyr His Glu Lys Asn Ser
145 150 155 160

Leu Glu Arg Gly Ser Glu Gln Leu Asp Arg Ile Leu Glu Met Gly Gln
165 170 175

Gln Ala Phe Glu Asp Ile Val Glu Gln Asn Glu Ile Leu Arg Lys Val
180 185 190

Gln Thr Lys Phe Glu Glu Ser Leu Ile Thr Leu Gly Val Ser Gln Gly
195 200 205

Thr Ile Arg Ser Val Glu Arg Arg Ala Lys Gln Asp Lys Trp Leu Phe
210 215 220

Trp Phe Cys Val Val Val Met Leu Val Val Phe Tyr Tyr Ile
225 230 235

<210> 19
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> human genbank accession #: NP_003560

<220>
 <221> misc_feature
 <223> Corresponds to SEQ ID NO: 92

<400> 19

Met Ser Tyr Thr Pro Gly Val Gly Gly Asp Pro Thr Gln Leu Ala Gln
 1 5 10 15

Arg Ile Ser Ser Asn Ile Gln Lys Ile Thr Gln Cys Ser Val Glu Ile
 20 25 30

Gln Arg Thr Leu Asn Gln Leu Gly Thr Pro Gln Asp Ser Pro Glu Leu
 35 40 45

Arg Gln Gln Leu Gln Gln Lys Gln Gln Tyr Thr Asn Gln Leu Ala Lys
 50 55 60

Glu Thr Asp Lys Tyr Ile Lys Glu Phe Gly Ser Leu Pro Thr Thr Pro
 65 70 75 80

Ser Glu Gln Arg Gln Arg Lys Ile Gln Lys Asp Arg Leu Val Ala Glu
 85 90 95

Phe Thr Thr Ser Leu Thr Asn Phe Gln Lys Val Gln Arg Gln Ala Ala
 100 105 110

Glu Arg Glu Lys Glu Phe Val Ala Arg Val Arg Ala Ser Ser Arg Val
 115 120 125

Ser Gly Ser Phe Pro Glu Asp Ser Ser Lys Glu Arg Asn Leu Val Ser
 130 135 140

Trp Glu Ser Gln Thr Gln Pro Gln Val Gln Val Gln Asp Glu Glu Ile
 145 150 155 160

Thr Glu Asp Asp Leu Arg Leu Ile His Glu Arg Glu Ser Ser Ile Arg
 165 170 175

Gln Leu Glu Ala Asp Ile Met Asp Ile Asn Glu Ile Phe Lys Asp Leu
 180 185 190

Gly Met Met Ile His Glu Gln Gly Asp Val Ile Asp Ser Ile Glu Ala
 195 200 205

Asn Val Glu Asn Ala Glu Val His Val Gln Gln Ala Asn Gln Gln Leu
 210 215 220

Ser Arg Ala Ala Asp Tyr Gln Arg Lys Ser Arg Lys Thr Leu Cys Ile
 225 230 235 240

Ile Ile Leu Ile Leu Val Ile Gly Val Ala Ile Ile Ser Leu Ile Ile
 245 250 255

Trp Gly Leu Asn His
 260

<210> 20

<211> 258

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 93

<300>

<301> Bauer and Burgers

<302> Molecular cloning, structure and expression of the yeast proliferating cell nuclear

antigen gene.

<303> Nucleic Acids Research

<304> 18

<305> 2

<306> 261-265

<307> 1990

<308> X16676

<309> 1993-09-30

<400> 20

Met Leu Glu Ala Lys Phe Glu Glu Ala Ser Leu Phe Lys Arg Ile Ile
1 5 10 15

Asp Gly Phe Lys Asp Cys Val Gln Leu Val Asn Phe Gln Cys Lys Glu
20 25 30

Asp Gly Ile Ile Ala Gln Ala Val Asp Asp Ser Arg Val Leu Leu Val
35 40 45

Ser Leu Glu Ile Gly Val Glu Ala Phe Gln Glu Tyr Arg Cys Asp His
50 55 60

Pro Val Thr Leu Gly Met Asp Leu Thr Ser Leu Ser Lys Ile Leu Arg
65 70 75 80

Cys Gly Asn Asn Thr Asp Thr Leu Thr Leu Ile Ala Asp Asn Thr Pro
85 90 95

Asp Ser Ile Ile Leu Leu Phe Glu Asp Thr Lys Lys Asp Arg Ile Ala
100 105 110

Glu Tyr Ser Leu Lys Leu Met Asp Ile Asp Ala Asp Phe Leu Lys Ile
115 120 125

Glu Glu Leu Gln Tyr Asp Ser Thr Leu Ser Leu Pro Ser Ser Glu Phe
130 135 140

Ser Lys Ile Val Arg Asp Leu Ser Gln Leu Ser Asp Ser Ile Asn Ile
145 150 155 160

Met Ile Thr Lys Glu Thr Ile Lys Phe Val Ala Asp Gly Asp Ile Gly
 165 170 175

Ser Gly Ser Val Ile Ile Lys Pro Phe Val Asp Met Glu His Pro Glu
 180 185 190

Thr Ser Ile Lys Leu Glu Met Asp Gln Pro Val Asp Leu Thr Phe Gly
 195 200 205

Ala Lys Tyr Leu Leu Asp Ile Ile Lys Gly Ser Ser Leu Ser Asp Arg
 210 215 220

Val Gly Ile Arg Leu Ser Ser Glu Ala Pro Ala Leu Phe Gln Phe Asp
 225 230 235 240

Leu Lys Ser Gly Phe Leu Gln Phe Phe Leu Ala Pro Lys Phe Asn Asp
 245 250 255

Glu Glu

<210> 21

<211> 259

<212> PRT

<213> *Canidia albicans*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 94

<400> 21

Met Leu Glu Gly Lys Phe Glu Glu Ala Ala Leu Leu Lys Lys Val Val
 1 5 10 15

Glu Ala Ile Lys Asp Cys Val Lys Lys Cys Asn Phe Asn Cys Ser Glu
 20 25 30

His Gly Ile Thr Val Gln Ala Val Asp Asp Ser Arg Val Leu Leu Val
35 40 45

Ser Leu Leu Ile Gly Gln Thr Ser Phe Ser Glu Arg Cys Asp Arg Asp
50 55 60

Val Thr Leu Gly Ile Asp Leu Glu Ser Phe Ser Lys Ile Ile Lys Ser
65 70 75 80

Ala Asn Asn Glu Asp Phe Leu Thr Leu Leu Ala Glu Asp Ser Pro Asp
85 90 95

Gln Ile Met Ala Ile Leu Glu Glu Lys Gln Lys Glu Lys Ile Ser Glu
100 105 110

Tyr Ser Leu Lys Leu Met Asp Ile Asp Ser Glu Phe Leu Gln Ile Asp
115 120 125

Asp Met Glu Tyr Asp Ala Val Val Asn Met Pro Ser Ser Asp Phe Ala
130 135 140

Lys Leu Val Arg Asp Leu Lys Asn Leu Ser Glu Ser Leu Arg Val Val
145 150 155 160

Val Thr Lys Asp Ser Val Lys Phe Thr Ser Glu Gly Asp Ser Gly Ser
165 170 175

Gly Ser Val Ile Leu Lys Pro Tyr Thr Asn Leu Lys Asn Glu Arg Glu
180 185 190

Ser Val Thr Ile Ser Leu Asp Asp Pro Val Asp Leu Thr Phe Gly Leu
195 200 205

Lys Tyr Leu Asn Asp Ile Val Lys Ala Ala Thr Leu Ser Asp Val Ile
210 215 220

Thr Ile Lys Leu Ala Asp Lys Thr Pro Ala Leu Phe Glu Phe Lys Met

225 230 235 240

Gln Ser Gly Gly Tyr Leu Arg Phe Tyr Leu Ala Pro Lys Phe Asp Asp
 245 250 255

Asp Glu Tyr

<210> 22

<211> 261

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 95

<300>

<301> Almendral, Huebsch, Blundell, MacDonald-Bravo, and Bravo

<302> Cloning and sequence of the human nuclear protein cyclin: Homology with DNA-binding proteins

<303> Proc. Natl. Acad. Sci. U.S.A.

<304> 84

<305> 6

<306> 1575-1579

<307> 1987

<308> m15796

<309> 1993-04-27

<400> 22

Met Phe Glu Ala Arg Leu Val Gln Gly Ser Ile Leu Lys Lys Val Leu
 1 5 10 15

Glu Ala Leu Lys Asp Leu Ile Asn Glu Ala Cys Trp Asp Ile Ser Ser
 20 25 30

Ser Gly Val Asn Leu Gln Ser Met Asp Ser Ser His Val Ser Leu Val
 35 40 45

Gln Leu Thr Leu Arg Ser Glu Gly Phe Asp Thr Tyr Arg Cys Asp Arg
 50 55 60

Asn Leu Ala Met Gly Val Asn Leu Thr Ser Met Ser Lys Ile Leu Lys
65 70 75 80

Cys Ala Gly Asn Glu Asp Ile Ile Thr Leu Arg Ala Glu Asp Asn Ala
 85 90 95

Asp Thr Leu Ala Leu Val Phe Glu Ala Pro Asn Gln Glu Lys Val Ser
 100 105 110

Asp Tyr Glu Met Lys Leu Met Asp Leu Asp Val Glu Gln Leu Gly Ile
 115 120 125

Pro Glu Gln Glu Tyr Ser Cys Val Val Lys Met Pro Ser Gly Glu Phe
 130 135 140

Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val Val Ile
145 150 155 160

Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu Leu Gly
 165 170 175

Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys Glu Glu
 180 185 190

Glu Ala Val Thr Ile Glu Met Asn Glu Pro Val Gln Leu Thr Phe Ala
 195 200 205

Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser Ser Thr
 210 215 220

Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu Tyr Lys
225 230 235 240

Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys Ile Glu
 245 250 255

Asp Glu Glu Gly Ser
260

<210> 23

<211> 511

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 96

<400> 23

Met Ser Lys Arg Ser Ile Glu Val Asn Glu Glu Gln Asp Arg Val Val
1 5 10 15

Ser Ala Lys Thr Glu Ser His Ser Val Pro Ala Ile Pro Ala Ser Glu
20 25 30

Glu Gln Asp Ala Pro Lys Asn Asp Leu Glu Glu Gln Leu Ser Asp Glu
35 40 45

Phe Asp Ser Asp Gly Glu Ile Ile Glu Ile Asp Gly Asp Asp Glu Ile
50 55 60

Asn Asp Glu Asp Asp Leu Arg Lys Lys Gln Glu Glu Ala Glu Thr Leu
65 70 75 80

Val Gln Lys Asp Gln Ser Glu Gly Asn Lys Glu Lys Ile Gln Glu Leu
85 90 95

Tyr Leu Pro His Met Ser Arg Pro Leu Gly Pro Asp Glu Val Leu Glu
100 105 110

Ala Asp Pro Thr Val Tyr Glu Met Leu His Asn Val Asn Met Pro Trp
115 120 125

Pro Cys Leu Thr Leu Asp Val Ile Pro Asp Thr Leu Gly Ser Glu Arg

130 135 140

Arg Asn Tyr Pro Gln Ser Ile Leu Leu Thr Thr Ala Thr Gln Ser Ser
145 150 155 160

Arg Lys Lys Glu Asn Glu Leu Met Val Leu Ala Leu Ser Asn Leu Ala
165 170 175

Lys Thr Leu Leu Lys Asp Asp Asn Glu Gly Glu Asp Asp Glu Glu Asp
180 185 190

Asp Glu Asp Asp Val Asp Pro Val Ile Glu Asn Glu Asn Ile Pro Leu
195 200 205

Arg Asp Thr Thr Asn Arg Leu Lys Val Ser Pro Phe Ala Ile Ser Asn
210 215 220

Gln Glu Val Leu Thr Ala Thr Met Ser Glu Asn Gly Asp Val Tyr Ile
225 230 235 240

Tyr Asn Leu Ala Pro Gln Ser Lys Ala Phe Ser Thr Pro Gly Tyr Gln
245 250 255

Ile Pro Lys Ser Ala Lys Arg Pro Ile His Thr Val Lys Asn His Gly
260 265 270

Asn Val Glu Gly Tyr Gly Leu Asp Trp Ser Pro Leu Ile Lys Thr Gly
275 280 285

Ala Leu Leu Ser Gly Asp Cys Ser Gly Gln Ile Tyr Phe Thr Gln Arg
290 295 300

His Thr Ser Arg Trp Val Thr Asp Lys Gln Pro Phe Thr Val Ser Asn
305 310 315 320

Asn Lys Ser Ile Glu Asp Ile Gln Trp Ser Arg Thr Glu Ser Thr Val
325 330 335

Phe Ala Thr Ala Gly Cys Asp Gly Tyr Ile Arg Ile Trp Asp Thr Arg
 340 345 350

Ser Lys Lys His Lys Pro Ala Ile Ser Val Lys Ala Ser Asn Thr Asp
 355 360 365

Val Asn Val Ile Ser Trp Ser Asp Lys Ile Gly Tyr Leu Leu Ala Ser
 370 375 380

Gly Asp Asp Asn Gly Thr Trp Gly Val Trp Asp Leu Arg Gln Phe Thr
 385 390 395 400

Pro Ser Asn Ala Asp Ala Val Gln Pro Val Ala Gln Tyr Asp Phe His
 405 410 415

Lys Gly Ala Ile Thr Ser Ile Ala Phe Asn Pro Leu Asp Glu Ser Ile
 420 425 430

Val Ala Val Gly Ser Glu Asp Asn Thr Val Thr Leu Trp Asp Leu Ser
 435 440 445

Val Glu Ala Asp Asp Glu Glu Ile Lys Gln Gln Ala Ala Glu Thr Lys
 450 455 460

Glu Leu Gln Glu Ile Pro Pro Gln Leu Leu Phe Val His Trp Gln Lys
 465 470 475 480

Glu Val Lys Asp Val Lys Trp His Lys Gln Ile Pro Gly Cys Leu Val
 485 490 495

Ser Thr Gly Thr Asp Gly Leu Asn Val Trp Lys Thr Ile Ser Val
 500 505 510

<210> 24

<211> 420

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 97

<400> 24

Met Ser Lys Arg Ser Ala Glu Asp Asp Leu Ser Gly Asn Gly Ser Thr
1 5 10 15

Ser His Thr Ala Val Lys Thr Asn Lys Asp Ser Leu Pro Thr Thr Thr
20 25 30

Asn Gly Lys Glu Glu Glu Pro Asp Asn Met Asp Ile Gly Glu Phe Glu
35 40 45

Asp Pro Tyr Gly Asp Glu Phe Glu Ser Asp Glu Ile Ile Glu Leu Asp
50 55 60

Asp Asn Asn Asp Glu Glu Asp Asp Glu Met Ile Asp Glu Asn Ser Thr
65 70 75 80

Gln Ala Lys Ile Glu Glu Leu Glu Ala Lys Glu Gln Glu Gln Glu Gln
85 90 95

Gln Ser Ser Ile Tyr Leu Pro His Lys Ser Lys Pro Leu Gly Pro Asp
100 105 110

Glu Val Leu Glu Ala Asp Pro Thr Val Tyr Glu Met Leu His Asn Ile
115 120 125

Asn Leu Pro Trp Pro Cys Leu Thr Val Asp Ile Leu Pro Asp Ser Leu
130 135 140

Gly Asn Glu Arg Arg Ser Tyr Pro Ala Thr Val Tyr Leu Ala Thr Ala
145 150 155 160

Thr Gln Ala Ala Lys Ala Lys Asp Asn Glu Leu Leu Ala Met Lys Ala
165 170 175

Ser Ser Leu Ala Lys Thr Leu Val Lys Asp Glu Asn Glu Glu Asp Glu
180 185 190

Glu Asp Glu Asp Asp Asp Asp Val Asp Ser Asp Pro Ile Leu Asp
195 200 205

Ser Glu Ser Ile Pro Leu Arg His Thr Thr Asn Arg Ile Arg Val Ser
210 215 220

Pro His Ala Gln Gln Thr Gly Glu Tyr Leu Thr Ala Ser Met Ser Glu
225 230 235 240

Asn Gly Glu Val Tyr Ile Phe Asp Leu Leu Ala Gln Tyr Lys Ala Phe
245 250 255

Asp Thr Pro Gly Tyr Met Ile Pro Lys Ser Ser Lys Arg Pro Ile His
260 265 270

Thr Ile Arg Ala His Gly Asn Val Glu Gly Tyr Gly Leu Asp Trp Ser
275 280 285

Pro Leu Val Asn Thr Gly Ala Leu Leu Ser Gly Asp Met Ser Gly Arg
290 295 300

Ile Tyr Leu Thr Asn Arg Thr Thr Ser Ser Trp Thr Thr Asp Lys Thr
305 310 315 320

Pro Phe Phe Ala Ser Gln Ser Ser Ile Glu Asp Ile Gln Trp Ser Thr
325 330 335

Gly Glu Thr Thr Val Phe Ala Thr Gly Gly Cys Asp Gly Tyr Ile Cys
340 345 350

Ile Trp Asp Thr Arg Ser Lys Lys His Lys Pro Ala Leu Ser Val Ile
355 360 365

Ala Ser Lys Ser Asp Val Asn Val Ile Ser Trp Ser Ser Lys Ile Asn
 370 375 380

His Leu Leu Ala Ser Gly His Asp Asp Gly Ser Trp Gly Val Trp Asp
 385 390 395 400

Leu Arg Asn Phe Thr Asn Asn Thr Thr Ser Asn Pro Ser Pro Val Ala
 405 410 415

Asn Tyr Asp Phe
 420

<210> 25
 <211> 425
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> human genbank accession #: NP_005601

<220>
 <221> misc_feature
 <223> Corresponds to SEQ ID NO: 98

<400> 25

Met Ala Asp Lys Glu Ala Ala Phe Asp Asp Ala Val Glu Glu Arg Val
 1 5 10 15

Ile Asn Glu Glu Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr
 20 25 30

Asp Leu Val Met Thr His Ala Leu Glu Trp Pro Ser Leu Thr Ala Gln
 35 40 45

Trp Leu Pro Asp Val Thr Arg Pro Glu Gly Lys Asp Phe Ser Ile His
 50 55 60

Arg Leu Val Leu Gly Thr His Thr Ser Asp Glu Gln Asn His Leu Val
65 70 75 80

Ile Ala Ser Val Gln Leu Pro Asn Asp Asp Ala Gln Phe Asp Ala Ser
85 90 95

His Tyr Asp Ser Glu Lys Gly Glu Phe Gly Gly Phe Gly Ser Val Ser
100 105 110

Gly Lys Ile Glu Ile Glu Ile Lys Ile Asn His Glu Gly Glu Val Asn
115 120 125

Arg Ala Arg Tyr Met Pro Gln Asn Pro Cys Ile Ile Ala Thr Lys Thr
130 135 140

Pro Ser Ser Asp Val Leu Val Phe Asp Tyr Thr Lys His Pro Ser Lys
145 150 155 160

Pro Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg Leu Arg Gly His
165 170 175

Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Pro Asn Leu Ser Gly His
180 185 190

Leu Leu Ser Ala Ser Asp Asp His Thr Ile Cys Leu Trp Asp Ile Ser
195 200 205

Ala Val Pro Lys Glu Gly Lys Val Val Asp Ala Lys Thr Ile Phe Thr
210 215 220

Gly His Thr Ala Val Val Glu Asp Val Ser Trp His Leu Leu His Glu
225 230 235 240

Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp
245 250 255

Thr Arg Ser Asn Asn Thr Ser Lys Pro Ser His Ser Val Asp Ala His

260 265 270

Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile
275 280 285

Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg
290 295 300

Asn Leu Lys Leu Lys Leu His Ser Phe Glu Ser His Lys Asp Glu Ile
305 310 315 320

Phe Gln Val Gln Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser
325 330 335

Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu
340 345 350

Glu Gln Ser Pro Glu Asp Ala Glu Asp Gly Pro Pro Glu Leu Leu Phe
355 360 365

Ile His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro
370 375 380

Asn Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln
385 390 395 400

Val Trp Gln Met Ala Glu Asn Ile Tyr Asn Asp Glu Asp Pro Glu Gly
405 410 415

Ser Val Asp Pro Glu Gly Gln Gly Ser
420 425

<210> 26

<211> 431

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 99

<400> 26

Met Glu Pro Gln Glu Glu Phe Ile Thr Thr Glu Glu Val Glu Gln Glu
1 5 10 15

Ile Val Pro Thr Val Glu Val Glu Gln Asp Val Pro Val Asp Ile Glu
20 25 30

Gly Glu Asn Asp Asp Asp Asp Glu Met Met Asn Asp Asp Glu Glu Ala
35 40 45

Leu Glu Val Asp Met Ser Asn Asn Ser Leu Thr Tyr Phe Asp Lys His
50 55 60

Thr Asp Ser Val Phe Ala Ile Gly His His Pro Asn Leu Pro Leu Val
65 70 75 80

Cys Thr Gly Gly Gly Asp Asn Leu Ala His Leu Trp Thr Ser His Ser
85 90 95

Gln Pro Pro Lys Phe Ala Gly Thr Leu Thr Gly Tyr Gly Glu Ser Val
100 105 110

Ile Ser Cys Ser Phe Thr Ser Glu Gly Gly Phe Leu Val Thr Ala Asp
115 120 125

Met Ser Gly Lys Val Leu Val His Met Gly Gln Lys Gly Gly Ala Gln
130 135 140

Trp Lys Leu Ala Ser Gln Met Gln Glu Val Glu Glu Ile Val Trp Leu
145 150 155 160

Lys Thr His Pro Thr Ile Ala Arg Thr Phe Ala Phe Gly Ala Thr Asp
165 170 175

Gly Ser Val Trp Cys Tyr Gln Ile Asn Glu Gln Asp Gly Ser Leu Glu
180 185 190

Gln Leu Met Ser Gly Phe Val His Gln Gln Asp Cys Ser Met Gly Glu
195 200 205

Phe Ile Asn Thr Asp Lys Gly Glu Asn Thr Leu Glu Leu Val Thr Cys
210 215 220

Ser Leu Asp Ser Thr Ile Val Ala Trp Asn Cys Phe Thr Gly Gln Gln
225 230 235 240

Leu Phe Lys Ile Thr Gln Ala Glu Ile Lys Gly Leu Glu Ala Pro Trp
245 250 255

Ile Ser Leu Ser Leu Ala Pro Glu Thr Leu Thr Lys Gly Asn Ser Gly
260 265 270

Val Val Ala Cys Gly Ser Asn Asn Gly Leu Leu Ala Val Ile Asn Cys
275 280 285

Asn Asn Gly Gly Ala Ile Leu His Leu Ser Thr Val Ile Glu Leu Lys
290 295 300

Pro Glu Gln Asp Glu Leu Asp Ala Ser Ile Glu Ser Ile Ser Trp Ser
305 310 315 320

Ser Lys Phe Ser Leu Met Ala Ile Gly Leu Val Cys Gly Glu Ile Leu
325 330 335

Leu Tyr Asp Thr Ser Ala Trp Arg Val Arg His Lys Phe Val Leu Glu
340 345 350

Asp Ser Val Thr Lys Leu Met Phe Asp Asn Asp Asp Leu Phe Ala Ser
355 360 365

Cys Ile Asn Gly Lys Val Tyr Gln Phe Asn Ala Arg Thr Gly Gln Glu

370 375 380

Lys Phe Val Cys Val Gly His Asn Met Gly Val Leu Asp Phe Ile Leu
385 390 395 400

Leu His Pro Val Ala Asn Thr Gly Thr Glu Gln Lys Arg Lys Val Ile
 405 410 415

Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Glu Val Pro Asn
 420 425 430

<210> 27

<211> 417

<212> PRT

<213> Candida albicans

<220>

<221> MISC_FEATURE

<222> (326)..(326)

<223> X can be any amino acid

<220>

<221> MISC_FEATURE

<222> (367)..(367)

<223> X can be any amino acid

<220>

<221> MISC_FEATURE

<222> (378)..(378)

<223> X can be any amino acid

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 100

<400> 27

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr
1 5 10 15

Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala
 20 25 30

Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
 35 40 45

Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
 50 55 60

His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
 65 70 75 80

Val Leu Thr Glu Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His
 85 90 95

Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser
 100 105 110

Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala
 115 120 125

Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu
 130 135 140

Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe
 145 150 155 160

Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp
 165 170 175

Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val
 180 185 190

Gln Ile Met Ser Gly Phe Ser His Thr Leu Lys Cys Asn Gly Ala Val
 195 200 205

Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser

210 215 220

Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn
225 230 235 240

Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp
245 250 255

Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp
260 265 270

Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr
275 280 285

Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu
290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
305 310 315 320

Leu Val Ser Gly Asp Xaa Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Asn Ser Met Asp Gly Lys Xaa Tyr
355 360 365

Lys Trp Glu Pro Arg Thr Gly Glu Lys Xaa Phe Ala Gly Val Gly Thr
370 375 380

Asn Met Gly Ser Tyr Gly Leu Cys Tyr Phe Lys Ile Glu Val Lys Asn
385 390 395 400

Trp Leu Leu Leu Val Asp Glu Arg Cys Phe His Trp Ser Leu Phe Met
405 410 415

Lys

<210> 28

<211> 611

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: NP_001078

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 101

<400> 28

Met Asp Ser Gly Arg Arg Leu Gly Pro Glu Lys Trp Ile Arg Arg Leu
 1 5 10 15

Arg Arg Met Glu Ser Glu Ser Glu Ser Gly Ala Ala Ala Asp Thr Pro
 20 25 30

Pro Leu Glu Thr Leu Ser Phe His Gly Asp Glu Glu Ile Ile Glu Val
 35 40 45

Val Glu Leu Asp Pro Gly Pro Pro Asp Pro Asp Asp Leu Ala Gln Glu
 50 55 60

Met Glu Asp Val Asp Phe Glu Glu Glu Glu Glu Glu Gly Asn Glu
 65 70 75 80

Glu Gly Trp Val Leu Glu Pro Gln Glu Gly Val Val Gly Ser Met Glu
 85 90 95

Gly Pro Asp Asp Ser Glu Val Thr Phe Ala Leu His Ser Ala Ser Val
 100 105 110

Phe Cys Val Ser Leu Asp Pro Lys Thr Asn Thr Leu Ala Val Thr Gly
115 120 125

Gly Glu Asp Asp Lys Ala Phe Val Trp Arg Leu Ser Asp Gly Glu Leu
130 135 140

Leu Phe Glu Cys Ala Gly His Lys Asp Ser Val Thr Cys Ala Gly Phe
145 150 155 160

Ser His Asp Ser Thr Leu Val Ala Thr Gly Asp Met Ser Gly Leu Leu
165 170 175

Lys Val Trp Gln Val Asp Thr Lys Glu Glu Val Trp Ser Phe Glu Ala
180 185 190

Gly Asp Leu Glu Trp Met Glu Trp His Pro Arg Ala Pro Val Leu Leu
195 200 205

Ala Gly Thr Ala Asp Gly Asn Thr Trp Met Trp Lys Val Pro Asn Gly
210 215 220

Asp Cys Lys Thr Phe Gln Gly Pro Asn Cys Pro Ala Thr Cys Gly Arg
225 230 235 240

Val Leu Pro Asp Gly Lys Arg Ala Val Val Gly Tyr Glu Asp Gly Thr
245 250 255

Ile Arg Ile Trp Asp Leu Lys Gln Gly Ser Pro Ile His Val Leu Lys
260 265 270

Gly Thr Glu Gly His Gln Gly Pro Leu Thr Cys Val Ala Ala Asn Gln
275 280 285

Asp Gly Ser Leu Ile Leu Thr Gly Ser Val Asp Cys Gln Ala Lys Leu
290 295 300

Val Ser Ala Thr Thr Gly Lys Val Val Gly Val Phe Arg Pro Glu Thr

305 310 315 320
Val Ala Ser Gln Pro Ser Leu Gly Glu Gly Glu Glu Ser Glu Ser Asn
 325 330 335
Ser Val Glu Ser Leu Gly Phe Cys Ser Val Met Pro Leu Ala Ala Val
 340 345 350
Gly Tyr Leu Asp Gly Thr Leu Ala Ile Tyr Asp Leu Ala Thr Gln Thr
 355 360 365
Leu Arg His Gln Cys Gln His Gln Ser Gly Ile Val Gln Leu Leu Trp
 370 375 380
Glu Ala Gly Thr Ala Val Val Tyr Thr Cys Ser Leu Asp Gly Ile Val
385 390 395 400
Arg Leu Trp Asp Ala Arg Thr Gly Arg Leu Leu Thr Asp Tyr Arg Gly
 405 410 415
His Thr Ala Glu Ile Leu Asp Phe Ala Leu Ser Lys Asp Ala Ser Leu
 420 425 430
Val Val Thr Thr Ser Gly Asp His Lys Ala Lys Val Phe Cys Val Gln
 435 440 445
Arg Pro Asp Arg Asp Phe Ser Pro Asp Gly Ala Leu Leu Ala Thr Ala
 450 455 460
Ser Tyr Asp Thr Arg Val Tyr Ile Trp Asp Pro His Asn Gly Asp Ile
465 470 475 480
Leu Met Glu Phe Gly His Leu Phe Pro Pro Pro Thr Pro Ile Phe Ala
 485 490 495
Gly Gly Ala Asn Asp Arg Trp Val Arg Ser Val Ser Phe Ser His Asp
 500 505 510

Gly Leu His Val Ala Ser Leu Ala Asp Asp Lys Met Val Arg Phe Trp
515 520 525

Arg Ile Asp Glu Asp Tyr Pro Val Gln Val Ala Pro Leu Ser Asn Gly
530 535 540

Leu Cys Cys Ala Phe Ser Thr Asp Gly Ser Val Leu Ala Ala Gly Thr
545 550 555 560

His Asp Gly Ser Val Tyr Phe Trp Ala Thr Pro Arg Gln Val Pro Ser
565 570 575

Leu Gln His Leu Cys Arg Met Ser Ile Arg Arg Val Met Pro Thr Gln
580 585 590

Glu Val Gln Glu Leu Pro Ile Pro Ser Lys Leu Leu Glu Phe Leu Ser
595 600 605

Tyr Arg Ile
610

<210> 29

<211> 240

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 102

<400> 29

Met Ser Ala Pro Thr Met Arg Ser Thr Ser Ile Leu Thr Glu His Leu
1 5 10 15

Gly Tyr Pro Pro Ile Ser Leu Val Asp Asp Ile Ile Asn Ala Val Asn
20 25 30

Glu Ile Met Tyr Lys Cys Thr Ala Ala Met Glu Lys Tyr Leu Leu Ser
35 40 45

Lys Ser Lys Ile Gly Glu Glu Asp Tyr Gly Glu Glu Ile Lys Ser Gly
50 55 60

Val Ala Lys Leu Glu Ser Leu Leu Glu Asn Ser Val Asp Lys Asn Phe
65 70 75 80

Asp Lys Leu Glu Leu Tyr Val Leu Arg Asn Val Leu Arg Ile Pro Glu
85 90 95

Glu Tyr Leu Asp Ala Asn Val Phe Arg Leu Glu Asn Gln Lys Asp Leu
100 105 110

Val Ile Val Asp Glu Asn Glu Leu Lys Lys Ser Glu Glu Lys Leu Arg
115 120 125

Glu Lys Val Asn Asp Val Glu Leu Ala Phe Lys Lys Asn Glu Met Leu
130 135 140

Leu Lys Arg Val Thr Lys Val Lys Arg Leu Leu Phe Thr Ile Arg Gly
145 150 155 160

Phe Lys Gln Lys Leu Asn Glu Leu Leu Lys Cys Lys Asp Asp Val Gln
165 170 175

Leu Gln Lys Ile Leu Glu Ser Leu Lys Pro Ile Asp Asp Thr Met Thr
180 185 190

Leu Leu Thr Asp Ser Leu Arg Lys Leu Tyr Val Asp Ser Glu Ser Thr
195 200 205

Ser Ser Thr Glu Glu Val Glu Ala Leu Leu Gln Arg Leu Lys Thr Asn
210 215 220

Gly Lys Gln Asn Asn Lys Asp Phe Arg Thr Arg Tyr Ile Asp Ile Arg

225 230 235 240

<210> 30

<211> 314

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 103

<400> 30

Met Ser Asp Lys Thr Leu Asp Glu Arg Thr Thr Ala Ile Leu Thr Glu
1 5 10 15

His Leu Glu Phe Ala Pro Leu Thr Leu Ile Asp Asp Val Ile Asn Ala
20 25 30

Val Asn Glu Ile Met Tyr Lys Gly Thr Thr Ala Ile Glu Thr Tyr Leu
35 40 45

Lys Glu Gln Lys Gln Leu Met Lys Asn Gly Ile Thr Lys Val Thr Glu
50 55 60

Asp Glu Ile Glu Ile Gly Met Gly Lys Leu Glu Ser Leu Leu Glu Ser
65 70 75 80

Thr Ile Asp Lys Asn Phe Asp Lys Phe Glu Leu Tyr Cys Leu Arg Asn
85 90 95

Ile Phe Asn Ile Pro Lys Asp Leu Ile Pro Tyr Ile Gln Leu Ser His
100 105 110

Gln Gln Gly Ile Glu Phe Lys Ser Asp Asn Val Glu Gln Lys Arg Glu
115 120 125

Phe Asp Gln Gln Ile Lys Asn Leu Gln Leu Lys Ile Met Gln Glu Leu
130 135 140

Gln Leu Arg Lys Ile Leu Lys Leu Gln Leu Val Lys Val Gln Lys Leu
 145 150 155 160

Ile Lys Val Leu Ile Ala Ile Asp Asn Asp Phe Lys Lys Ile Asp Phe
 165 170 175

Ala Ser Gly Gly Gly Gly Asn Glu Glu Ser Ile Arg Ile Leu Lys Asn
 180 185 190

Leu Gln Pro Ile Asp Glu Thr Leu Tyr Phe Leu Ile Ser Gln Ile Lys
 195 200 205

Asn Leu Ile Asn Gln Ile Glu Gln Leu Ser Asn Lys Val Asn Thr Asn
 210 215 220

Leu Lys Thr Gln Lys Phe Ile Pro Asn Leu Arg Asp Lys Phe Ile Asp
 225 230 235 240

Gly Arg Thr Phe Arg Val Leu Gln Gln Thr Gly Ile Trp Lys Asp Leu
 245 250 255

Glu Lys Asn Asp Ile Lys Ile Leu Val Gln Gly Asn Asp Asn Asn Asn
 260 265 270

Asn Asn Asn Asn Asn Asn Asn Asn Thr Leu Thr Asp Leu Gln Asn Gln
 275 280 285

Asp Asp Ile Asp Met Ile Ile Pro Glu Gln Asp Asp Ile Asp Val Asp
 290 295 300

Ala Ile Lys Asn Ile Asn Ala Gln Ile Phe
 305 310

<210> 31

<211> 600

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 104

<400> 31

Met Ser His Ser Gly Ala Ala Ile Phe Glu Lys Val Ser Gly Ile Ile
 1 5 10 15

Ala Ile Asn Glu Asp Val Ser Pro Ala Glu Leu Thr Trp Arg Ser Thr
 20 25 30

Asp Gly Asp Lys Val His Thr Val Val Leu Ser Thr Ile Asp Lys Leu
 35 40 45

Gln Ala Thr Pro Ala Ser Ser Glu Lys Met Met Leu Arg Leu Ile Gly
 50 55 60

Lys Val Asp Glu Ser Lys Lys Arg Lys Asp Asn Glu Gly Asn Glu Val
 65 70 75 80

Val Pro Lys Pro Gln Arg His Met Phe Ser Phe Asn Asn Arg Thr Val
 85 90 95

Met Asp Asn Ile Lys Met Thr Leu Gln Gln Ile Ile Ser Arg Tyr Lys
 100 105 110

Asp Ala Asp Ile Tyr Glu Glu Lys Arg Arg Arg Glu Glu Ser Ala Gln
 115 120 125

His Thr Glu Thr Pro Met Ser Ser Ser Ser Val Thr Ala Gly Thr Pro
 130 135 140

Thr Pro His Leu Asp Thr Pro Gln Leu Asn Asn Gly Ala Pro Leu Ile
 145 150 155 160

Asn Thr Ala Lys Leu Asp Asp Ser Leu Ser Lys Glu Lys Leu Leu Thr
 165 170 175

Asn Leu Lys Leu Gln Gln Ser Leu Leu Lys Gly Asn Lys Val Leu Met
180 185 190

Lys Val Phe Gln Glu Thr Val Ile Asn Ala Gly Leu Pro Pro Ser Glu
195 200 205

Phe Trp Ser Thr Arg Ile Pro Leu Leu Arg Ala Phe Ala Leu Ser Thr
210 215 220

Ser Gln Lys Val Gly Pro Tyr Asn Val Leu Ser Thr Ile Lys Pro Val
225 230 235 240

Ala Ser Ser Glu Asn Lys Val Asn Val Asn Leu Ser Arg Glu Lys Ile
245 250 255

Leu Asn Ile Phe Glu Asn Tyr Pro Ile Val Lys Lys Ala Tyr Thr Asp
260 265 270

Asn Val Pro Lys Asn Phe Lys Glu Pro Glu Phe Trp Ala Arg Phe Phe
275 280 285

Ser Ser Lys Leu Phe Arg Lys Leu Arg Gly Glu Lys Ile Met Gln Asn
290 295 300

Asp Arg Gly Asp Val Ile Ile Asp Arg Tyr Leu Thr Leu Asp Gln Glu
305 310 315 320

Phe Asp Arg Lys Asp Asp Asp Met Leu Leu His Pro Val Lys Lys Ile
325 330 335

Ile Asp Leu Asp Gly Asn Ile Gln Asp Asp Pro Val Val Arg Gly Asn
340 345 350

Arg Pro Asp Phe Thr Met Gln Pro Gly Val Asp Ile Asn Gly Asn Ser
355 360 365

Asp Gly Thr Val Asp Ile Leu Lys Gly Met Asn Arg Leu Ser Glu Lys
370 375 380

Met Ile Met Ala Leu Lys Asn Glu Tyr Ser Arg Thr Asn Leu Gln Asn
385 390 395 400

Lys Ser Asn Ile Thr Asn Asp Glu Glu Asp Glu Asp Asn Asp Glu Arg
405 410 415

Asn Glu Leu Lys Ile Asp Asp Leu Asn Glu Ser Tyr Lys Thr Asn Tyr
420 425 430

Ala Ile Ile His Leu Lys Arg Asn Ala His Glu Lys Thr Thr Asp Asn
435 440 445

Asp Ala Lys Ser Ser Ala Asp Ser Ile Lys Asn Ala Asp Leu Lys Val
450 455 460

Ser Asn Gln Gln Met Leu Gln Gln Leu Ser Leu Val Met Asp Asn Leu
465 470 475 480

Ile Asn Lys Leu Asp Leu Asn Gln Val Val Pro Asn Asn Glu Val Ser
485 490 495

Asn Lys Ile Asn Lys Arg Val Ile Thr Ala Ile Lys Ile Asn Ala Lys
500 505 510

Gln Ala Lys His Asn Asn Val Asn Ser Ala Leu Gly Ser Phe Val Asp
515 520 525

Asn Thr Ser Gln Ala Asn Glu Leu Glu Val Lys Ser Thr Leu Pro Ile
530 535 540

Asp Leu Leu Glu Ser Cys Arg Met Leu His Thr Thr Cys Cys Glu Phe
545 550 555 560

Leu Lys His Phe Tyr Ile His Phe Gln Ser Gly Glu Gln Lys Gln Ala

565 570 575

Ser Thr Val Lys Lys Leu Tyr Asn His Leu Lys Asp Cys Ile Glu Lys
580 585 590

Leu Asn Glu Leu Phe Gln Asp Val
595 600

<210> 32

<211> 670

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 105

<400> 32

Met Asp Ile Ile Arg Gly Ala Cys Ser Val Asp Lys Ile Gly Gly Met
1 5 10 15

Val Tyr Ile Arg Glu Asp Leu Ala Pro Leu Met Leu Glu Trp Lys Pro
20 25 30

Ile Asp Glu Gln Glu Glu Asp Arg Ala Ile Ser Ile Pro Leu Asn Ser
35 40 45

Leu Thr Thr Leu Gln Ser Thr Lys Glu Thr Ser Pro Lys Met Ile Leu
50 55 60

Lys Ile Val Tyr Lys Leu Thr Ser Gly Pro Pro Asn Thr Asn Ala Asp
65 70 75 80

Gly Thr Asp Asn Gly Gly Gly Gly Gly Glu Gln Lys Ser Phe Lys
85 90 95

Leu Thr Phe Thr Asn Arg Pro Thr Met Asn Thr Ile Lys Asp Ser Leu
100 105 110

Gln Thr Ile Val Ala Arg Ser Arg Thr Lys Gly Gly Leu Lys Val Pro
115 120 125

Val Leu Gln Leu Gln Leu Gln His Gln Leu Gln His Leu Gly Ser Ala
130 135 140

Pro Gln Ala Asp Ser Thr Arg Asp Ser Thr Ser Ser Ser Thr Pro Ile
145 150 155 160

Pro Pro Thr Thr Ser Gly Thr Ser Thr Ser Ser Ser Leu Leu Ser Leu
165 170 175

Ala Ala Ser Gln Ser Leu Ser Asp Ala Asn Leu Leu Lys Asn Phe Glu
180 185 190

Leu Gln Gln Lys Leu Leu Leu Glu Asp Arg Gln Leu Arg Asp Val Phe
195 200 205

Thr Lys Ser Val Met Gln Phe Lys Leu Ser Pro Gln Val Phe Trp Ser
210 215 220

Ser Arg Leu Asn Gln Leu Arg Thr Phe Ala Leu Thr Ile Ser Gln His
225 230 235 240

Lys Gly Pro Tyr Asn Val Leu Ser Thr Ile Lys Pro Val Ala Thr Ser
245 250 255

Asp Asn Gln Val Asn Val Asn Val Thr Arg Asp Thr Ile Asn Glu Ile
260 265 270

Phe Thr Ile Tyr Pro Ile Ile Lys Lys Ala Phe Asp Asp Leu Val Pro
275 280 285

Asn Lys Phe Asn Glu Gly Glu Phe Trp Ser Arg Phe Phe Asn Ser Lys
290 295 300

Leu Phe Arg Arg Leu Arg Gly Asp Lys Ile Ser Ile Ser Asn Ser Arg
305 310 315 320

Gly Asp Val Val Leu Asp Lys Tyr Leu Tyr Ile Asp Gln Asn Tyr Gln
325 330 335

Glu Lys Leu Gln Lys Ser Ser Thr Leu Glu Asn Asn Gly Ser Gly Gly
340 345 350

Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Asn Ser Glu Gln Gly Ile
355 360 365

Gln Thr Leu Glu Ser Pro His Val Lys Lys Phe Leu Asp Leu Met Gly
370 375 380

Asn Gln Gln Asp Asn Ser Gln Lys Leu Gly Asn Arg Pro Asp Phe Thr
385 390 395 400

Met Arg Tyr Asp Glu Asp Asn Val Asp Asp Asp Asn Lys Lys Pro Thr
405 410 415

Leu Gly Asn Glu Asn Glu Met Ile Ile Leu Met Lys Asn Met Asn Arg
420 425 430

Leu Ser Ser Lys Met Met Ser Met Ser Ser Thr Asn Gly Pro Glu Lys
435 440 445

Pro Ser Glu Thr Thr Ile Asp Gly Leu Ser Ala Ala Glu Leu Asn Glu
450 455 460

Tyr Glu Glu Glu Leu Asp Leu His Asp Leu Asn Asp Ser Glu Asn Leu
465 470 475 480

Gln Tyr Ile Lys Leu Asn Ile Asn Thr Asp Ile Ala Lys Gly Thr Lys
485 490 495

Leu Asp Ser Tyr Glu Gly Ser Asn Thr Asn Asn Lys Ile Ser Gln Asp

500 505 510

Glu Leu His Lys Tyr Leu Gln Ser Gln Thr Phe Gln Gly Gln Ile Glu
515 520 525

Leu Thr Glu Thr Tyr Thr Cys Lys Ser Glu Glu Ile Glu Lys Thr Ser
530 535 540

Met Glu Ile Ala Met Leu Ile Lys Gln Asn Phe Arg Thr Phe Lys Leu
545 550 555 560

Ile Asn Lys Glu Asn Asp Ile Ala Gly Thr Asn Ile Val Pro Asn Ser
565 570 575

Leu Ile Gln Glu Ile Ile Thr Tyr Asn Ile Thr Ile Val Glu Phe Leu
580 585 590

Ser His Phe Trp Lys Ile Phe Leu His Gly Asn Asn Pro Gly Gln Leu
595 600 605

Lys Lys Ile Phe Thr Ser Leu Lys Asn Cys Gln Ser Gly Leu Ile Glu
610 615 620

Leu Glu Asn Lys Ala Ile Asp Gln Phe Lys Ser Met Asp Ile Leu Gln
625 630 635 640

Lys Asn Gln Lys Leu Gln Asp Lys Val Leu Lys Asp Phe Ala Ser Cys
645 650 655

Leu Gln Pro Met Lys Ile Ala Leu Asp Lys Ala Cys Asn Glu
660 665 670

<210> 33
<211> 498
<212> PRT
<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: W19128

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 106

<400> 33

Met Ala Thr Ser Ser Glu Glu Val Leu Leu Ile Val Lys Lys Val Arg
1 5 10 15

Gln Lys Lys Gln Asp Gly Ala Leu Tyr Leu Met Ala Glu Arg Ile Ala
20 25 30

Trp Ala Pro Glu Gly Lys Asp Arg Phe Thr Ile Ser His Met Tyr Ala
35 40 45

Asp Ile Lys Cys Gln Lys Ile Ser Pro Glu Gly Lys Ala Lys Ile Gln
50 55 60

Leu Gln Leu Val Leu His Ala Gly Asp Thr Thr Asn Phe His Phe Ser
65 70 75 80

Asn Glu Ser Thr Ala Val Lys Glu Arg Asp Ala Val Lys Asp Leu Leu
85 90 95

Gln Gln Leu Leu Pro Phe Lys Arg Ala Asn Lys Glu Leu Glu Lys Asn
100 105 110

Arg Cys Cys Lys Ile Leu Phe Cys Phe Ser Phe Ile Lys Leu Arg Thr
115 120 125

Gly Glu Glu Gln Met Leu Glu Asp Pro Val Leu Phe Gln Leu Tyr Lys
130 135 140

Asp Val Ser Gln Val Ile Ser Ala Glu Glu Phe Trp Asn Arg Leu Asn
145 150 155 160

Val Asn Ala Thr Asp Ser Ser Thr Ser Asn His Lys Gln Asp Val Gly
165 170 175

Ile Ser Ala Ala Phe Leu Ala Asp Val Arg Pro Gln Thr Asp Gly Cys
180 185 190

Asn Gly Leu Arg Tyr Asn Leu Thr Ser Asp Ile Ile Glu Ser Ile Phe
195 200 205

Arg Thr Tyr Pro Ala Val Lys Met Lys Tyr Ala Glu Asn Val Pro His
210 215 220

Asn Met Thr Glu Lys Glu Phe Trp Thr Arg Phe Phe Gln Ser His Tyr
225 230 235 240

Phe His Arg Asp Arg Leu Asn Thr Gly Ser Lys Asp Leu Phe Ala Glu
245 250 255

Cys Ala Lys Ile Asp Glu Lys Gly Leu Lys Thr Met Val Ser Leu Gly
260 265 270

Val Lys Asn Pro Leu Leu Asp Leu Thr Ala Leu Glu Asp Lys Pro Leu
275 280 285

Asp Glu Gly Tyr Gly Ile Ser Ser Val Pro Ser Ser Asn Ser Lys Ser
290 295 300

Ile Lys Glu Asn Ser Asn Ala Ala Ile Ile Lys Arg Phe Asn His His
305 310 315 320

Ser Ala Met Val Leu Ala Ala Gly Leu Arg Lys Gln Glu Ala Gln Asn
325 330 335

Glu Gln Thr Ser Glu Pro Ser Asn Met Asp Gly Asn Ser Gly Asp Ala
340 345 350

Asp Cys Phe Gln Pro Ala Val Lys Arg Ala Lys Leu Gln Glu Ser Ile
355 360 365

Glu Tyr Glu Asp Leu Gly Lys Asn Asn Ser Val Lys Thr Ile Ala Leu
370 375 380

Asn Leu Lys Lys Ser Asp Arg Tyr Tyr His Gly Pro Thr Pro Ile Gln
385 390 395 400

Ser Leu Gln Tyr Ala Thr Ser Gln Asp Ile Ile Asn Ser Phe Gln Ser
405 410 415

Ile Arg Gln Glu Met Glu Ala Tyr Thr Pro Lys Leu Thr Gln Val Leu
420 425 430

Ser Ser Ser Ala Ala Ser Ser Thr Ile Thr Ala Leu Ser Pro Gly Gly
435 440 445

Ala Leu Met Gln Gly Gly Thr Gln Gln Ala Ile Asn Gln Met Val Pro
450 455 460

Asn Asp Ile Gln Thr Asn Leu Val Ser His Ile Glu Glu Met Leu Gln
465 470 475 480

Thr Ala Tyr Asn Lys Leu His Thr Trp Gln Ser Arg Arg Leu Met Lys
485 490 495

Lys Thr

<210> 34

<211> 846

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 107

<400> 34

Met Glu Leu Glu Pro Thr Leu Phe Gly Ile Ile Glu Ala Leu Ala Pro
 1 5 10 15

Gln Leu Leu Ser Gln Ser His Leu Gln Thr Phe Val Ser Asp Val Val
 20 25 30

Asn Leu Leu Arg Ser Ser Thr Lys Ser Ala Thr Gln Leu Gly Pro Leu
 35 40 45

Ile Asp Phe Tyr Lys Leu Gln Ser Leu Asp Ser Pro Glu Thr Thr Ile
 50 55 60

Met Trp His Lys Ile Glu Lys Phe Leu Asp Ala Leu Phe Gly Ile Gln
 65 70 75 80

Asn Thr Asp Asp Met Val Lys Tyr Leu Ser Val Phe Gln Ser Leu Leu
 85 90 95

Pro Ser Asn Tyr Arg Ala Lys Ile Val Gln Lys Ser Ser Gly Leu Asn
 100 105 110

Met Glu Asn Leu Ala Asn His Glu His Leu Leu Ser Pro Val Arg Ala
 115 120 125

Pro Ser Ile Tyr Thr Glu Ala Ser Phe Glu Asn Met Asp Arg Phe Ser
 130 135 140

Glu Arg Arg Ser Met Val Ser Ser Pro Asn Arg Tyr Val Pro Ser Ser
 145 150 155 160

Thr Tyr Ser Ser Val Thr Leu Arg Gln Leu Ser Asn Pro Tyr Tyr Val
 165 170 175

Asn Thr Ile Pro Glu Glu Asp Ile Leu Lys Tyr Val Ser Tyr Thr Leu
 180 185 190

Leu Ala Thr Thr Ser Ala Leu Phe Pro Phe Asp His Glu Gln Ile Gln
195 200 205

Ile Pro Ser Lys Ile Pro Asn Phe Glu Ser Gly Leu Leu His Leu Ile
210 215 220

Phe Glu Ala Gly Leu Leu Tyr Gln Ser Leu Gly Tyr Lys Val Glu Lys
225 230 235 240

Phe Arg Met Leu Asn Ile Ser Pro Met Lys Lys Ala Leu Ile Ile Glu
245 250 255

Ile Ser Glu Glu Leu Gln Asn Tyr Thr Ala Phe Val Asn Asn Leu Val
260 265 270

Ser Ser Gly Thr Val Val Ser Leu Lys Ser Leu Tyr Arg Glu Ile Tyr
275 280 285

Glu Asn Ile Ile Arg Leu Arg Ile Tyr Cys Arg Phe Thr Glu His Leu
290 295 300

Glu Glu Leu Ser Gly Asp Thr Phe Leu Ile Glu Leu Asn Ile Phe Lys
305 310 315 320

Ser His Gly Asp Leu Thr Ile Arg Lys Ile Ala Thr Asn Leu Phe Asn
325 330 335

Ser Met Ile Ser Leu Tyr Tyr Glu Tyr Leu Met Asn Trp Leu Thr Lys
340 345 350

Gly Leu Leu Arg Ala Thr Tyr Gly Glu Phe Phe Ile Ala Glu Asn Thr
355 360 365

Asp Thr Asn Gly Thr Asp Asp Asp Phe Ile Tyr His Ile Pro Ile Glu
370 375 380

Phe Asn Gln Glu Arg Val Pro Ala Phe Ile Pro Lys Glu Leu Ala Tyr

385 390 395 400

Lys Ile Phe Met Ile Gly Lys Ser Tyr Ile Phe Leu Glu Lys Tyr Cys
 405 410 415

Lys Glu Val Gln Trp Thr Asn Glu Phe Ser Lys Lys Tyr His Val Leu
 420 425 430

Tyr Gln Ser Asn Ser Tyr Arg Gly Ile Ser Thr Asn Phe Phe Glu Ile
 435 440 445

Ile Asn Asp Gln Tyr Ser Glu Ile Val Asn His Thr Asn Gln Ile Leu
 450 455 460

Asn Gln Lys Phe His Tyr Arg Asp Val Val Phe Ala Leu Lys Asn Ile
 465 470 475 480

Leu Leu Met Gly Lys Ser Asp Phe Met Asp Ala Leu Ile Glu Lys Ala
 485 490 495

Asn Asp Ile Leu Ala Thr Pro Ser Asp Ser Leu Pro Asn Tyr Lys Leu
 500 505 510

Thr Arg Val Leu Gln Glu Ala Val Gln Leu Ser Ser Leu Arg His Leu
 515 520 525

Met Asn Ser Pro Arg Asn Ser Ser Val Ile Asn Gly Leu Asp Ala Arg
 530 535 540

Val Leu Asp Leu Gly His Gly Ser Val Gly Trp Asp Val Phe Thr Leu
 545 550 555 560

Asp Tyr Ile Leu Tyr Pro Pro Leu Ser Leu Val Leu Asn Val Asn Arg
 565 570 575

Pro Phe Gly Arg Lys Glu Tyr Leu Arg Ile Phe Asn Phe Leu Trp Arg
 580 585 590

Phe Lys Lys Asn Asn Tyr Phe Tyr Gln Lys Glu Met Leu Lys Ser Asn
595 600 605

Asp Ile Ile Arg Ser Phe Lys Lys Ile Arg Gly Tyr Asn Pro Leu Ile
610 615 620

Arg Asp Ile Ile Asn Lys Leu Ser Arg Ile Ser Ile Leu Arg Thr Gln
625 630 635 640

Phe Gln Gln Phe Asn Ser Lys Met Glu Ser Tyr Tyr Leu Asn Cys Ile
645 650 655

Ile Glu Glu Asn Phe Lys Glu Met Thr Arg Lys Leu Gln Arg Thr Glu
660 665 670

Asn Lys Ser Gln Asn Gln Phe Asp Leu Ile Arg Leu Asn Asn Gly Thr
675 680 685

Ile Glu Leu Asn Gly Ile Leu Thr Pro Lys Ala Glu Val Leu Thr Lys
690 695 700

Ser Ser Ser Ser Lys Pro Gln Lys His Ala Ile Glu Lys Thr Leu Asn
705 710 715 720

Ile Asp Glu Leu Glu Ser Val His Asn Thr Phe Leu Thr Asn Ile Leu
725 730 735

Ser His Lys Leu Phe Ala Thr Asn Thr Ser Glu Ile Ser Val Gly Asp
740 745 750

Tyr Ser Gly Gln Pro Tyr Pro Thr Ser Leu Val Leu Leu Leu Asn Ser
755 760 765

Val Tyr Glu Phe Val Lys Val Tyr Cys Asn Leu Asn Asp Ile Gly Tyr
770 775 780

Glu Ile Phe Ile Lys Met Asn Leu Asn Asp His Glu Ala Ser Asn Gly
785 790 795 800

Leu Leu Gly Lys Phe Asn Thr Asn Leu Lys Glu Ile Val Ser Gln Tyr
 805 810 815

Lys Asn Phe Lys Asp Arg Leu Tyr Ile Phe Arg Ala Asp Leu Lys Asn
 820 825 830

Asp Gly Asp Glu Glu Leu Phe Leu Leu Ser Lys Ser Leu Arg
 835 840 845

<210> 35

<211> 712

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 108

<400> 35

Met Ala Leu Asn Lys Val Gln Leu Ile Lys Leu Tyr Ser Asn Arg Leu
1 5 10 15

Val Lys Ser Leu Val Pro Val Glu Phe Gly Glu Ala Phe Ile Gln Ser
 20 25 30

Ile Ile Asn Asp Leu Gln Thr Thr Leu Leu Asn Thr Ser Ser Glu Glu
 35 40 45

Gln Asn Leu Ser Ile Ile Ile Asn Lys Leu Lys Met Gln Phe Leu Ser
 50 55 60

Asn Asn Leu Lys Asn Glu Trp Val Glu Phe Gln Asn Ile Val Asn Ser
65 70 75 80

Leu Ser Lys Phe Lys Ser Leu Asp Gln Ile Cys Asn Tyr Leu Ala Phe

85 90 95

Leu Asp Ala Leu Arg Asp Glu Lys Pro Glu Asp Ile Leu Ser Thr Ser
100 105 110

Thr Ala Ser Leu Ser Pro Gly Lys Gln Asn Val Met Ile Asn Thr Val
115 120 125

Asn Thr Ala Leu Thr Leu Ser Gln Leu Ile Glu Pro Tyr Tyr Asp Thr
130 135 140

Leu Ser Glu Gln Thr Ile Leu Thr Tyr Leu Pro Tyr Thr Met Leu Gly
145 150 155 160

Leu Asp Ser Lys Ile Phe Thr Phe Ser Asn Asn Tyr Thr Arg Leu Glu
165 170 175

Ile Pro Lys Asp Ile Asn Asn Ser Phe Ser Ser Leu Leu Arg Glu Val
180 185 190

Phe Glu Phe Ala Ile Leu Tyr Lys Gln Leu Ala Ile Val Val Asp Arg
195 200 205

Tyr Lys Gly Thr Leu Val Leu Ala Ile Lys Thr Ala Tyr Ile Ala Ile
210 215 220

Leu Glu Ala Gln Leu Asn Lys Tyr Val Asn Asp Ile Asn Asn Ile Phe
225 230 235 240

Asn Asn Lys Pro Asn Ser Ile Leu Val Val Tyr Asn Ser Ile Phe Pro
245 250 255

Trp Ile Ser Ile Leu Arg Phe Leu Tyr Arg Val Ser Asn Arg Leu Asn
260 265 270

Arg Leu Asp Gly Tyr Glu Phe Leu Thr Phe Ile Tyr Ser Phe Thr Asn
275 280 285

His Gly Asp Pro Lys Ile Arg Gly Ile Ala Val Thr Ala Phe Thr Glu
290 295 300

Val Val Lys Pro Tyr Tyr Asn Ile Val Glu His Trp Ile Val Lys Gly
305 310 315 320

Glu Leu Ile Asp Asn Asn Asn Glu Phe Phe Ile Ile Phe Asp Gln Glu
325 330 335

Gln Asn Glu Phe Asn Ser Ile Ile Lys Leu Leu Pro Lys Lys Ile Pro
340 345 350

Ala Phe Ile Lys Ser Ser Asp Lys Ile Phe Gln Ile Gly Thr Thr Leu
355 360 365

Ile Phe Leu Asn Lys Tyr Cys Arg Glu Leu Lys Trp Val Asn Gln Tyr
370 375 380

Asn Val Lys Tyr Ser Ala Ile Leu Phe Asn Asn His Gln Gly Leu Ala
385 390 395 400

Ser Met Thr Thr Asn Glu Met Ile Lys Leu Ile Asp Leu Gln Tyr Asn
405 410 415

Glu Ile Leu Thr Phe Leu Thr Gln Ile Ile Gln Gly Asn Asn Lys Leu
420 425 430

Leu Thr His Val Tyr Asn Ile Lys Arg Tyr Tyr Phe Met Glu Thr Asn
435 440 445

Asp Phe Ile Asp Ala Ile Met Val Lys Gly Lys Asp Val Phe Asn Glu
450 455 460

Ser Ser Val Asn Ile Ser Ser Thr Tyr Leu Arg Lys Val Leu Gln Asp
465 470 475 480

Ala Ile Gln Ile Ser Ser Val Lys Asn Phe Glu Tyr Val Asp Arg Leu
485 490 495

Asp Ser Arg Val Leu Asn Pro Gln His Gly Asn Leu Gly Trp Glu Ser
500 505 510

Phe Thr Ile Glu Tyr Lys Ile Asp Asp Leu Pro Met Ser Tyr Leu Phe
515 520 525

Glu Gly His Gln His Leu Gln Tyr Leu Lys Met Phe His Phe Leu Trp
530 535 540

Lys Leu Arg Gln Leu Asn Asn Leu Leu Asn Trp His Phe Glu Met Phe
545 550 555 560

Asn Glu Leu Asn His Asn Val Val Thr Lys Leu Ser Ser Arg Asn Arg
565 570 575

Arg Pro Leu Ala Lys Ser Leu Ser Ile Ile Thr Ser Ile Arg Phe His
580 585 590

Phe Thr Gln Phe Leu Asn Glu Leu Ile Ala Tyr Leu Ser Tyr Asp Val
595 600 605

Ile Glu Glu Asn Phe Gln Gln His Ile Val Arg Lys Leu Phe Tyr Asn
610 615 620

Lys Asn Asp Gln Asp Leu Leu Leu Asn Lys Leu Phe Met Asn Leu Leu
625 630 635 640

Glu Ile Asp Pro Asn Asn Asp Leu Pro Lys Phe Asn Val Asn Leu Leu
645 650 655

Thr Ile Asp Glu Leu Val Glu Leu His Gly Thr Tyr Ile Asp Ser Ile
660 665 670

Ile Asn Ser Ser Leu Leu Asn Glu Lys Leu Lys Gly Asn Glu Thr Asn

675 680 685

Ile Ser Tyr Ile Asp Gln Ile Phe Asp Ile Leu Gln Thr Ile Phe Asn
690 695 700

Phe Ile Ile Gln Val Arg Asn Ser
705 710

<210> 36

<211> 880

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: AAC39727

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 109

<400> 36

Met Ala Thr Pro Asp Gln Lys Ser Pro Asn Val Leu Leu Gln Asn Leu
1 5 10 15

Cys Cys Arg Ile Leu Gly Arg Ser Glu Ala Asp Val Ala Gln Gln Phe
20 25 30

Gln Tyr Ala Val Arg Val Ile Gly Ser Asn Phe Ala Pro Thr Val Glu
35 40 45

Arg Asp Glu Phe Leu Val Ala Glu Lys Ile Lys Lys Glu Leu Ile Arg
50 55 60

Gln Arg Arg Glu Ala Asp Ala Ala Leu Phe Ser Glu Leu His Arg Lys
65 70 75 80

Leu His Ser Gln Gly Val Leu Lys Asn Lys Trp Ser Ile Leu Tyr Leu

85 90 95

Leu Leu Ser Leu Ser Glu Asp Pro Arg Arg Gln Pro Ser Lys Val Ser
100 105 110

Ser Tyr Ala Thr Leu Phe Ala Gln Ala Leu Pro Arg Asp Ala His Ser
115 120 125

Thr Pro Tyr Tyr Tyr Ala Arg Pro Gln Thr Leu Pro Leu Ser Tyr Gln
130 135 140

Asp Arg Ser Ala Gln Ser Ala Gln Ser Ser Gly Ser Val Gly Ser Ser
145 150 155 160

Gly Ile Ser Ser Ile Gly Leu Cys Ala Leu Ser Gly Pro Ala Pro Ala
165 170 175

Pro Gln Ser Leu Leu Pro Gly Gln Ser Asn Gln Ala Pro Gly Val Gly
180 185 190

Asp Cys Leu Arg Gln Gln Leu Gly Ser Arg Leu Ala Trp Thr Leu Thr
195 200 205

Ala Asn Gln Pro Ser Ser Gln Ala Thr Thr Ser Lys Gly Val Pro Ser
210 215 220

Ala Val Ser Arg Asn Met Thr Arg Ser Arg Arg Glu Gly Asp Thr Gly
225 230 235 240

Gly Thr Met Glu Ile Thr Glu Ala Ala Leu Val Arg Asp Ile Leu Tyr
245 250 255

Val Phe Gln Gly Ile Asp Gly Lys Asn Ile Lys Met Asn Asn Thr Glu
260 265 270

Asn Cys Tyr Lys Val Glu Gly Lys Ala Asn Leu Ser Arg Ser Leu Arg
275 280 285

Asp Thr Ala Val Arg Leu Ser Glu Leu Gly Trp Leu His Asn Lys Ile
290 295 300

Arg Arg Tyr Thr Asp Gln Arg Ser Leu Asp Arg Ser Phe Gly Leu Val
305 310 315 320

Gly Gln Ser Phe Cys Ala Ala Leu His Gln Glu Leu Arg Glu Tyr Tyr
325 330 335

Arg Leu Leu Ser Val Leu His Ser Gln Leu Gln Leu Glu Asp Asp Gln
340 345 350

Gly Val Asn Leu Gly Leu Glu Ser Ser Leu Thr Leu Arg Arg Leu Leu
355 360 365

Val Trp Thr Tyr Asp Pro Lys Ile Arg Leu Lys Thr Leu Ala Ala Leu
370 375 380

Val Asp His Cys Gln Gly Arg Lys Gly Gly Glu Leu Ala Ser Ala Val
385 390 395 400

His Ala Tyr Thr Lys Thr Gly Asp Pro Tyr Met Arg Ser Leu Val Gln
405 410 415

His Ile Leu Ser Leu Val Ser His Pro Val Leu Ser Phe Leu Tyr Arg
420 425 430

Trp Ile Tyr Asp Gly Glu Leu Glu Asp Thr Tyr His Glu Phe Phe Val
435 440 445

Ala Ser Asp Pro Thr Val Lys Thr Asp Arg Leu Trp His Asp Lys Tyr
450 455 460

Thr Leu Arg Lys Ser Met Ile Pro Ser Phe Met Thr Met Asp Gln Ser
465 470 475 480

Arg Lys Val Leu Leu Ile Gly Lys Ser Ile Asn Phe Leu His Gln Val
485 490 495

Cys His Asp Gln Thr Pro Thr Thr Lys Met Ile Ala Val Thr Lys Ser
500 505 510

Ala Glu Ser Pro Gln Asp Ala Ala Asp Leu Phe Thr Asp Leu Glu Asn
515 520 525

Ala Phe Gln Gly Lys Ile Asp Ala Ala Tyr Phe Glu Thr Ser Lys Tyr
530 535 540

Leu Leu Asp Val Leu Asn Lys Lys Tyr Ser Leu Leu Asp His Met Gln
545 550 555 560

Ala Met Arg Arg Tyr Leu Leu Leu Gly Gln Gly Asp Phe Ile Arg His
565 570 575

Leu Met Asp Leu Leu Lys Pro Glu Leu Val Arg Pro Ala Thr Thr Leu
580 585 590

Tyr Gln His Asn Leu Thr Gly Ile Leu Glu Thr Ala Val Arg Ala Thr
595 600 605

Asn Ala Gln Phe Asp Ser Pro Glu Ile Leu Arg Arg Leu Asp Val Arg
610 615 620

Leu Leu Glu Val Ser Pro Gly Asp Thr Gly Trp Asp Val Phe Ser Leu
625 630 635 640

Asp Tyr His Val Asp Gly Pro Ile Ala Thr Val Phe Thr Arg Glu Cys
645 650 655

Met Ser His Tyr Leu Arg Val Phe Asn Phe Leu Trp Arg Ala Lys Arg
660 665 670

Met Glu Tyr Ile Leu Thr Asp Ile Arg Lys Gly His Met Cys Asn Ala

675 680 685

Lys Leu Leu Arg Asn Met Pro Glu Phe Ser Gly Val Leu His Gln Cys
690 695 700

His Ile Leu Ala Ser Glu Met Val His Phe Ile His Gln Met Gln Tyr
705 710 715 720

Tyr Ile Thr Phe Glu Val Leu Glu Cys Ser Trp Asp Glu Leu Trp Asn
725 730 735

Lys Val Gln Gln Ala Gln Asp Leu Asp His Ile Ile Ala Ala His Glu
740 745 750

Val Phe Leu Asp Thr Ile Ile Ser Arg Cys Leu Leu Asp Ser Asp Ser
755 760 765

Arg Ala Leu Leu Asn Gln Leu Arg Ala Val Phe Asp Gln Ile Ile Glu
770 775 780

Leu Gln Asn Ala Gln Asp Ala Ile Tyr Arg Ala Ala Leu Glu Glu Leu
785 790 795 800

Gln Arg Arg Leu Gln Phe Glu Glu Lys Lys Lys Gln Arg Glu Ile Glu
805 810 815

Gly Gln Trp Gly Val Thr Ala Ala Glu Glu Glu Glu Glu Asn Lys Arg
820 825 830

Ile Gly Glu Phe Lys Glu Ser Ile Pro Lys Met Cys Ser Gln Leu Arg
835 840 845

Ile Leu Thr His Phe Tyr Gln Gly Ile Val Gln Gln Phe Leu Val Leu
850 855 860

Leu Thr Thr Ser Ser Asp Glu Ser Leu Arg Phe Leu Ser Phe Arg Leu
865 870 875 880

<210> 37
<211> 534
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 110

<400> 37

Met Glu Lys Ser Leu Ala Asp Gln Ile Ser Asp Ile Ala Ile Lys Pro
1 5 10 15

Val Asn Lys Asp Phe Asp Ile Glu Asp Glu Glu Asn Ala Ser Leu Phe
20 25 30

Gln His Asn Glu Lys Asn Gly Glu Ser Asp Leu Ser Asp Tyr Gly Asn
35 40 45

Ser Asn Thr Glu Glu Thr Lys Lys Ala His Tyr Leu Glu Val Glu Lys
50 55 60

Ser Lys Leu Arg Ala Glu Lys Gly Leu Glu Leu Asn Asp Pro Lys Tyr
65 70 75 80

Thr Gly Val Lys Gly Ser Arg Gln Ala Leu Tyr Glu Glu Val Ser Glu
85 90 95

Asn Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Glu
100 105 110

Asp Ala Leu Ser Phe Arg Thr Asp Ser Glu Asp Glu Glu Val Glu Ile
115 120 125

Asp Glu Glu Glu Ser Asp Ala Asp Gly Gly Glu Thr Glu Glu Ala Gln
130 135 140

Gln Lys Arg His Ala Leu Ser Lys Leu Ile Gln Gln Glu Thr Lys Gln
145 150 155 160

Ala Ile Asn Lys Leu Ser Gln Ser Val Gln Arg Asp Ala Ser Lys Gly
 165 170 175

Tyr Ser Ile Leu Gln Gln Thr Lys Leu Phe Asp Asn Ile Ile Asp Leu
 180 185 190

Arg Ile Lys Leu Gln Lys Ala Val Ile Ala Ala Asn Lys Leu Pro Leu
 195 200 205

Thr Thr Glu Ser Trp Glu Glu Ala Lys Met Asp Asp Ser Glu Glu Thr
 210 215 220

Lys Arg Leu Leu Lys Glu Asn Glu Lys Leu Phe Asn Asn Leu Phe Asn
225 230 235 240

Arg Leu Ile Asn Phe Arg Ile Lys Phe Gln Leu Gly Asp His Ile Thr
 245 250 255

Gln Asn Glu Glu Val Ala Lys His Lys Leu Ser Lys Lys Arg Ser Leu
 260 265 270

Lys Glu Leu Tyr Gln Glu Thr Asn Ser Leu Asp Ser Glu Leu Lys Glu
 275 280 285

Tyr Arg Thr Ala Val Leu Asn Lys Trp Ser Thr Lys Val Ser Ser Ala
 290 295 300

Ser Gly Asn Ala Ala Leu Ser Ser Asn Lys Phe Lys Ala Ile Asn Leu
305 310 315 320

Pro Ala Asp Val Gln Val Glu Asn Gln Leu Ser Asp Met Ser Arg Leu
 325 330 335

Met Lys Arg Thr Lys Leu Asn Arg Arg Asn Ile Thr Pro Leu Tyr Phe

340 345 350

Gln Lys Asp Cys Ala Asn Gly Arg Leu Pro Glu Leu Ile Ser Pro Val
355 360 365

Val Lys Asp Ser Val Asp Asp Asn Glu Asn Ser Asp Asp Gly Leu Asp
370 375 380

Ile Pro Lys Asn Tyr Asp Pro Arg Arg Lys Asp Asn Asn Ala Ile Asp
385 390 395 400

Ile Thr Glu Asn Pro Tyr Val Phe Asp Asp Glu Asp Phe Tyr Arg Val
405 410 415

Leu Asn Asp Leu Ile Asp Lys Lys Ile Ser Asn Ala His Asn Ser
420 425 430

Glu Ser Ala Ala Ile Thr Ile Thr Ser Thr Asn Ala Arg Ser Asn Asn
435 440 445

Lys Leu Lys Lys Asn Ile Asp Thr Lys Ala Ser Lys Gly Arg Lys Leu
450 455 460

Asn Tyr Ser Val Gln Asp Pro Ile Ala Asn Tyr Glu Ala Pro Ile Thr
465 470 475 480

Ser Gly Tyr Lys Trp Ser Asp Asp Gln Ile Asp Glu Phe Phe Ala Gly
485 490 495

Leu Leu Gly Gln Arg Val Asn Phe Asn Glu Asn Glu Asp Glu Glu Gln
500 505 510

His Ala Arg Ile Glu Asn Asp Glu Glu Leu Glu Ala Val Lys Asn Asp
515 520 525

Asp Ile Gln Ile Phe Gly
530

<210> 38

<211> 480

<212> PRT

<213> *Candida albicans*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 111

<400> 38

Met Ser Phe Phe Gly Leu His Phe Gln Leu Asn Ser Leu Thr Leu Asn
 1 5 10 15

Ile Ser Asn Met Ala Lys Lys Ser Leu Ser Glu Gln Ile Ser Ser Leu
 20 25 30

Tyr Thr Pro Lys Thr Asp Tyr Asp Ile Glu Asp His Asp Leu Asp Val
 35 40 45

Ser Lys Asp Asn Gly Ile Phe Gln His His Asp Gly Gly Ser Glu Asn
 50 55 60

Glu Ser Glu Asp Glu Asp Thr Gly Leu Arg Asn Glu His Tyr Val Glu
 65 70 75 80

Ser Ser Lys Ser Lys Leu Arg Gln Gln Asn Glu Gly Val Asn Leu Gly
 85 90 95

Glu Lys Tyr Val Gly Asn Val Thr Ser Arg Ser Lys Leu Tyr Asp Asp
 100 105 110

Glu Asp Asp Lys Gln Pro Thr Glu Ala Ser Ser Gly Glu Glu Leu Asp
 115 120 125

Ala Glu Ser Ala Glu Glu Glu Asp Glu Glu Ser Glu Asp Val Ala
 130 135 140

Asp Asp Asp Glu Asp Asp Gln Glu Ser Asp Arg Ser Ser Ser Ser Asp

145 150 155 160
 Ala Glu Asn Asp Glu Asp Glu Asn Ile Ser His Lys Arg Glu Leu Leu
 165 170 175
 Lys Gln Leu Met Ser Lys Glu Arg Ser His Ile Val Asn Arg Leu Ser
 180 185 190
 Gln Ser Ala Thr Asn Asp Ala Leu Lys Gly Tyr Ser Ile Gln Gln Gln
 195 200 205
 Asn Lys Thr Phe Glu Lys Ile Ile Asp Val Arg Leu Lys Phe Gln Lys
 210 215 220
 Ser Val Thr Ser Ser Asn Met Leu Pro Ile Asn Thr Ser Thr Tyr Ser
 225 230 235 240
 Glu Thr Lys Ser Glu Asp Ser Asp Glu Leu Val Thr Lys Ala Lys Lys
 245 250 255
 Gln Leu Tyr Ser Leu Leu Asp His Leu Phe Thr Leu Arg Asn Glu Leu
 260 265 270
 Asp Glu Ser Thr Ser Val Lys Thr Pro Lys Lys Arg Ser Phe Ala Lys
 275 280 285
 Tyr Ser Glu Val Thr Ser Ala Ala Asp Ala Gln Leu Asn Ser Arg Arg
 290 295 300
 Asn Gln Ile Leu Thr Lys Trp Ser Ala Lys Val Ala Asn Ser Ser Gly
 305 310 315 320
 Arg Asn Ala Met Asn Ala Asn Lys Phe Lys Thr Ile Asn Gln Ser Phe
 325 330 335
 Glu Gln Gln Val Asn Asn Asn Leu Ser Asp Met Asp Arg Leu Ile Lys
 340 345 350

Arg Thr Lys Leu Asn Arg Arg Asn Val Thr Pro Ile Gly Tyr Thr Thr
 355 360 365

Lys Glu Glu Asp Asp His Glu Asn Gly Asn Lys Asn Lys Ser Ile Asp
 370 375 380

Glu Asp Asp Asp Asp Ile Pro Glu Asp Thr Ser Val Arg Lys Lys Thr
 385 390 395 400

Gln Gly Leu Glu Asn Asp Tyr Ile Phe Asp Asp Glu Asp Phe Tyr Arg
 405 410 415

Val Leu Leu Asn Asp Leu Val Asp Lys Lys Val Gln Thr Ser Asp Pro
 420 425 430

Thr Ser Gly Ile Thr Ile Ser Leu Arg Ala Ala Gln Lys Ser Asn Lys
 435 440 445

Leu Lys Asn Asn Val Asp Thr Lys Ala Ser Lys Gly Arg Lys Leu Arg
 450 455 460

Tyr His Val Gln Glu Pro Ile Ala Asn Phe Glu Thr Ser Arg Gly Ser
 465 470 475 480

<210> 39

<211> 558

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: NM_000055

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 112

<400> 39

Met Gly Arg Pro Leu Ala Leu Gln Leu Glu Gln Leu Leu Asn Pro Arg
 1 5 10 15

Pro Ser Glu Ala Asp Pro Glu Ala Asp Pro Glu Glu Ala Thr Ala Ala
 20 25 30

Arg Val Ile Asp Arg Phe Asp Glu Gly Glu Asp Gly Glu Gly Asp Phe
 35 40 45

Leu Val Val Gly Ser Ile Arg Lys Leu Ala Ser Ala Ser Leu Leu Asp
 50 55 60

Thr Asp Lys Arg Tyr Cys Gly Lys Thr Thr Ser Arg Lys Ala Trp Asn
 65 70 75 80

Glu Asp His Trp Glu Gln Thr Leu Pro Gly Ser Ser Asp Glu Glu Ile
 85 90 95

Ser Asp Glu Glu Gly Ser Gly Asp Glu Asp Ser Glu Gly Leu Gly Leu
 100 105 110

Glu Glu Tyr Asp Glu Asp Asp Leu Gly Ala Ala Glu Glu Gln Glu Cys
 115 120 125

Gly Asp His Arg Glu Ser Lys Lys Thr Arg Ser His Ser Ala Lys Thr
 130 135 140

Pro Gly Phe Ser Val Gln Ser Ile Ser Asp Phe Glu Lys Phe Thr Lys
 145 150 155 160

Gly Met Asp Asp Leu Gly Ser Ser Glu Glu Glu Asp Glu Glu Ser
 165 170 175

Gly Met Glu Glu Gly Asp Asp Ala Glu Asp Ser Gln Gly Glu Ser Glu
 180 185 190

Glu Asp Arg Ala Gly Asp Arg Asn Ser Glu Asp Asp Gly Val Val Met

195 200 205

Thr Phe Ser Ser Val Lys Val Ser Glu Glu Val Glu Lys Gly Arg Ala
210 215 220

Val Lys Asn Gln Ile Ala Leu Trp Asp Gln Leu Leu Glu Gly Arg Ile
225 230 235 240

Lys Leu Gln Lys Ala Leu Leu Thr Thr Asn Gln Leu Pro Gln Pro Asp
245 250 255

Val Phe Pro Val Phe Lys Asp Lys Gly Gly Pro Glu Phe Ala Ser Ala
260 265 270

Leu Lys Asn Ser His Lys Ala Leu Lys Ala Leu Leu Arg Ser Leu Val
275 280 285

Gly Leu Gln Glu Glu Leu Leu Phe Gln Tyr Pro Asp Thr Arg Tyr Val
290 295 300

Val Asp Gly Thr Lys Pro Asn Ala Gly Ser Glu Glu Ile Ser Ser Glu
305 310 315 320

Asp Asp Glu Leu Val Glu Glu Lys Lys Gln Gln Arg Arg Arg Val Pro
325 330 335

Ala Lys Arg Lys Leu Glu Met Glu Asp Tyr Pro Ser Phe Met Ala Lys
340 345 350

Ala Leu Pro Thr Leu Gln Ser Thr Gly Thr Thr Leu Gln Lys Trp His
355 360 365

Asp Lys Thr Lys Leu Ala Ser Gly Lys Leu Gly Lys Gly Phe Gly Ala
370 375 380

Phe Glu Arg Ser Ile Leu Thr Gln Ile Asp His Ile Leu Met Cys Lys
385 390 395 400

Glu Arg Leu Leu Arg Arg Thr Gln Thr Lys Arg Ser Val Tyr Arg Val
 405 410 415

Leu Gly Lys Pro Glu Pro Ala Ala Gln Pro Val Pro Glu Ser Leu Pro
 420 425 430

Gly Glu Pro Glu Ile Leu Pro Gln Ala Pro Ala Asn Ala His Leu Lys
 435 440 445

Asp Leu Asp Glu Glu Ile Phe Asp Asp Asp Asp Phe Tyr His Gln Leu
 450 455 460

Leu Arg Glu Leu Ile Glu Arg Lys Thr Ser Ser Leu Asp Pro Asn Asp
 465 470 475 480

Gln Val Ala His Gly Lys Ala Val Ala Cys Asn Pro Glu Val Thr Glu
 485 490 495

Ala Lys Ser Thr Lys Lys Val Asp Arg Lys Ala Ser Lys Gly Arg Lys
 500 505 510

Leu Arg Phe His Val Leu Ser Lys Leu Leu Ser Phe Met Ala Pro Ile
 515 520 525

Asp His Thr Thr Met Asn Asp Asp Ala Arg Thr Glu Leu Tyr Arg Ser
 530 535 540

Leu Phe Gly Gln Leu His Pro Pro Asp Glu Gly His Gly Asp
 545 550 555

<210> 40

<211> 300

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 113

<400> 40

Met Ala Thr Leu His Phe Val Pro Gln His Glu Glu Glu Gln Val Tyr
1 5 10 15

Ser Ile Ser Gly Lys Ala Leu Lys Leu Thr Thr Ser Asp Asp Ile Lys
20 25 30

Pro Tyr Leu Glu Glu Leu Ala Ala Leu Lys Thr Cys Thr Lys Leu Asp
35 40 45

Leu Ser Gly Asn Thr Ile Gly Thr Glu Ala Ser Glu Ala Leu Ala Lys
50 55 60

Cys Ile Ala Glu Asn Thr Gln Val Arg Glu Ser Leu Val Glu Val Asn
65 70 75 80

Phe Ala Asp Leu Tyr Thr Ser Arg Leu Val Asp Glu Val Val Asp Ser
85 90 95

Leu Lys Phe Leu Leu Pro Val Leu Leu Lys Cys Pro His Leu Glu Ile
100 105 110

Val Asn Leu Ser Asp Asn Ala Phe Gly Leu Arg Thr Ile Glu Leu Leu
115 120 125

Glu Asp Tyr Ile Ala His Ala Val Asn Ile Lys His Leu Ile Leu Ser
130 135 140

Asn Asn Gly Met Gly Pro Phe Ala Gly Glu Arg Ile Gly Lys Ala Leu
145 150 155 160

Phe His Leu Ala Gln Asn Lys Lys Ala Ala Ser Lys Pro Phe Leu Glu
165 170 175

Thr Phe Ile Cys Asn Thr Phe Thr Lys His Ala Ser Leu Ile Leu Ala
180 185 190

Lys Ala Leu Pro Thr Trp Lys Asp Ser Leu Phe Glu Leu Asn Leu Asn
 195 200 205

Asp Cys Leu Leu Lys Thr Ala Gly Ser Asp Glu Val Phe Lys Val Phe
 210 215 220

Thr Glu Val Lys Phe Pro Asn Leu His Val Leu Lys Phe Glu Tyr Asn
 225 230 235 240

Glu Met Ala Gln Glu Thr Ile Glu Val Ser Phe Leu Pro Ala Met Glu
 245 250 255

Lys Gly Asn Leu Pro Glu Leu Glu Lys Leu Glu Ile Asn Gly Asn Arg
 260 265 270

Leu Asp Glu Asp Ser Asp Ala Leu Asp Leu Leu Gln Ser Lys Phe Asp
 275 280 285

Asp Leu Glu Val Asp Asp Phe Glu Glu Val Asp Ser
 290 295 300

<210> 41

<211> 415

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 114

<400> 41

Met Ala Ser Val Glu Val Glu Leu Gly Val Thr Pro Glu Thr Thr Tyr
 1 5 10 15

Ser Ile Ser Gly Lys Gln Leu Lys Phe Asp Ser Glu Ser Asp Ile Ala
 20 25 30

Pro Tyr Ile Lys Glu Leu Thr Glu Lys Glu Asn Val Lys Lys Val Asp
35 40 45

Phe Ser Gly Asn Thr Ile Gly Ile Glu Ala Ser Lys Ala Leu Ser Glu
50 55 60

Ala Leu Leu Lys His Lys Asp Thr Ile Val Glu Ile Asn Phe Ser Asp
65 70 75 80

Leu Tyr Thr Gly Arg Leu Asn Thr Glu Ile Pro Gln Ser Leu Glu Tyr
85 90 95

Leu Leu Pro Ala Leu Ser Lys Leu Pro Asn Leu Lys Leu Ile Asn Leu
100 105 110

Ser Asp Asn Ala Phe Gly Leu Gln Thr Ile Asp Pro Ile Glu Ala Tyr
115 120 125

Leu Ala Lys Ala Val Ser Ile Glu His Leu Ile Leu Ser Asn Asn Gly
130 135 140

Met Gly Pro Phe Ala Gly Ser Arg Ile Gly Gly Ser Leu Phe Lys Leu
145 150 155 160

Ala Lys Ala Lys Lys Ala Glu Gly Lys Glu Ser Leu Lys Thr Phe Ile
165 170 175

Cys Gly Arg Asn Arg Leu Glu Asn Gly Ser Val Asn Tyr Leu Ser Val
180 185 190

Gly Leu Arg Asn His Lys Asp Leu Glu Val Val Arg Leu Tyr Gln Asn
195 200 205

Gly Ile Arg Pro Ala Gly Ile Ser Lys Leu Val Glu Gln Gly Leu Ser
210 215 220

Asn Asn Lys Lys Leu Lys Val Leu Asp Leu Gln Asp Asn Thr Ile Thr

225 230 235 240
 Thr Arg Gly Ala Ile His Ile Ala Glu Ser Leu Ser Asn Trp Pro Leu
 245 250 255
 Leu Val Glu Leu Asn Leu Asn Asp Ser Leu Leu Lys Asn Lys Gly Ser
 260 265 270
 Leu Lys Leu Val Glu Ala Phe His Ala Gly Asp Glu Lys Pro Gln Leu
 275 280 285
 Ile Thr Leu Lys Leu Gln Tyr Asn Glu Leu Glu Thr Asp Ser Leu Arg
 290 295 300
 Val Leu Ala Asp Ala Ile Ala Ser Lys Leu Pro Gln Leu Lys Phe Leu
 305 310 315 320
 Glu Leu Asn Gly Asn Arg Phe Glu Glu Asp Ser Glu His Ile Asp Lys
 325 330 335
 Ile Asn Gly Ile Phe Glu Glu Arg Gly Tyr Gly Glu Ile Asp Glu Leu
 340 345 350
 Asp Glu Leu Glu Glu Leu Asp Ser Glu Glu Glu Glu Asp Asp Glu Asp
 355 360 365
 Asp Glu Gly Glu Asp Asp Thr Leu Glu Glu Asp Leu Asp Leu Thr Gln
 370 375 380
 Leu Glu Glu Glu Leu Ala Gly Val Ser Leu Glu Asp Lys Asp Gly Asn
 385 390 395 400
 Val Asp Glu Ile Ala Glu Glu Leu Ser Lys Thr His Ile Lys Glx
 405 410 415

<210> 42

<211> 587

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: CAA57714

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 115

<400> 42

Met Ala Ser Glu Asp Ile Ala Lys Leu Ala Glu Thr Leu Ala Lys Thr
1 5 10 15

Gln Val Ala Gly Gly Gln Leu Ser Phe Lys Gly Lys Ser Leu Lys Leu
20 25 30

Asn Thr Ala Glu Asp Ala Lys Asp Val Ile Lys Glu Ile Glu Asp Phe
35 40 45

Asp Ser Leu Glu Ala Leu Arg Leu Glu Gly Asn Thr Val Gly Val Glu
50 55 60

Ala Ala Arg Val Ile Ala Lys Ala Leu Glu Lys Lys Ser Glu Leu Lys
65 70 75 80

Arg Cys His Trp Ser Asp Met Phe Thr Gly Arg Leu Arg Thr Glu Ile
85 90 95

Pro Pro Ala Leu Ile Ser Leu Gly Glu Gly Leu Ile Thr Ala Gly Ala
100 105 110

Gln Leu Val Glu Leu Asp Leu Ser Asp Asn Ala Phe Gly Pro Asp Gly
115 120 125

Val Gln Gly Phe Glu Ala Leu Leu Lys Ser Ser Ala Cys Phe Thr Leu
130 135 140

Gln Glu Leu Lys Leu Asn Asn Cys Gly Met Gly Ile Gly Gly Gly Lys
145 150 155 160

Ile Leu Ala Ala Ala Leu Thr Glu Cys His Arg Lys Ser Ser Ala Gln
 165 170 175

Gly Lys Pro Leu Ala Leu Lys Val Phe Val Ala Gly Arg Asn Arg Leu
 180 185 190

Glu Asn Asp Gly Ala Thr Ala Leu Ala Glu Ala Phe Arg Val Ile Gly
 195 200 205

Thr Leu Glu Glu Val His Met Pro Gln Asn Gly Ile Asn His Pro Gly
 210 215 220

Ile Thr Ala Leu Ala Gln Ala Phe Ala Val Asn Pro Leu Leu Arg Val
225 230 235 240

Ile Asn Leu Asn Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met
 245 250 255

Ala Glu Thr Leu Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly
 260 265 270

Asp Cys Leu Val Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile
 275 280 285

Arg Gly Gly Leu Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu
 290 295 300

Ile Lys Arg Asp Ala Ala Leu Ala Val Ala Glu Ala Met Ala Asp Lys
305 310 315 320

Ala Glu Leu Glu Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu
 325 330 335

Gly Cys Glu Gln Leu Gln Glu Val Leu Glu Gly Phe Asn Met Ala Lys
340 345 350

Val Leu Ala Ser Leu Ser Asp Asp Glu Asp Glu Glu Glu Glu Glu
355 360 365

Gly Glu Glu Glu Glu Glu Glu Ala Glu Glu Glu Glu Glu Asp Glu
370 375 380

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Pro Gln Gln
385 390 395 400

Arg Gly Gln Gly Glu Lys Ser Ala Thr Pro Ser Arg Lys Ile Leu Asp
405 410 415

Pro Asn Thr Gly Glu Pro Ala Pro Val Leu Ser Ser Pro Pro Pro Ala
420 425 430

Asp Val Ser Thr Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu Arg
435 440 445

Leu Gly Pro Lys Ser Ser Val Leu Ile Ala Gln Gln Thr Asp Thr Ser
450 455 460

Asp Pro Glu Lys Val Val Ser Ala Phe Leu Lys Val Ser Ser Val Phe
465 470 475 480

Lys Asp Glu Ala Thr Val Arg Met Ala Val Gln Asp Ala Val Asp Ala
485 490 495

Leu Met Gln Lys Ala Phe Asn Ser Ser Ser Phe Asn Ser Asn Thr Phe
500 505 510

Leu Thr Arg Leu Leu Val His Met Gly Leu Leu Lys Ser Glu Asp Lys
515 520 525

Val Lys Ala Ile Ala Asn Leu Tyr Gly Pro Leu Met Ala Leu Asn His

530 535 540

Met Val Gln Gln Asp Tyr Phe Pro Lys Ala Leu Ala Pro Leu Leu Leu
545 550 555 560

Ala Phe Val Thr Lys Pro Asn Ser Ala Leu Glu Ser Cys Ser Phe Ala
565 570 575

Arg His Ser Leu Leu Gln Thr Leu Tyr Lys Val
580 585

<210> 43
<211> 381
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 116

<400> 43

Met Ser Ser Gln Ala Phe Thr Ser Val His Pro Asn Ala Ala Thr Ser
1 5 10 15

Asp Val Asn Val Thr Ile Asp Thr Phe Val Ala Lys Leu Lys Arg Arg
20 25 30

Gln Val Gln Gly Ser Tyr Ala Ile Ala Leu Glu Thr Leu Gln Leu Leu
35 40 45

Met Arg Phe Ile Ser Ala Ala Arg Trp Asn His Val Asn Asp Leu Ile
50 55 60

Glu Gln Ile Arg Asp Leu Gly Asn Ser Leu Glu Lys Ala His Pro Thr
65 70 75 80

Ala Phe Ser Cys Gly Asn Val Ile Arg Arg Ile Leu Ala Val Leu Arg
85 90 95

Asp Glu Val Glu Glu Asp Thr Met Ser Thr Thr Val Thr Ser Thr Ser
100 105 110

Val Ala Glu Pro Leu Ile Ser Ser Met Phe Asn Leu Leu Gln Lys Pro
115 120 125

Glu Gln Pro His Gln Asn Arg Lys Asn Ser Ser Gly Ser Ser Ser Met
130 135 140

Lys Thr Lys Thr Asp Tyr Arg Gln Val Ala Ile Gln Gly Ile Lys Asp
145 150 155 160

Leu Ile Asp Glu Ile Lys Asn Ile Asp Glu Gly Ile Gln Gln Ile Ala
165 170 175

Ile Asp Leu Ile His Asp His Glu Ile Leu Leu Thr Pro Thr Pro Asp
180 185 190

Ser Lys Thr Val Leu Lys Phe Leu Ile Thr Ala Arg Glu Arg Ser Asn
195 200 205

Arg Thr Phe Thr Val Leu Val Thr Glu Gly Phe Pro Asn Asn Thr Lys
210 215 220

Asn Ala His Glu Phe Ala Lys Lys Leu Ala Gln His Asn Ile Glu Thr
225 230 235 240

Leu Val Val Pro Asp Ser Ala Val Phe Ala Leu Met Ser Arg Val Gly
245 250 255

Lys Val Ile Ile Gly Thr Lys Ala Val Phe Val Asn Gly Gly Thr Ile
260 265 270

Ser Ser Asn Ser Gly Val Ser Ser Val Cys Glu Cys Ala Arg Glu Phe
275 280 285

Arg Thr Pro Val Phe Ala Val Ala Gly Leu Tyr Lys Leu Ser Pro Leu
290 295 300

Tyr Pro Phe Asp Val Glu Lys Phe Val Glu Phe Gly Gly Ser Gln Arg
305 310 315 320

Ile Leu Pro Arg Met Asp Pro Arg Lys Arg Leu Asp Thr Val Asn Gln
325 330 335

Ile Thr Asp Tyr Val Pro Pro Glu Asn Ile Asp Ile Tyr Ile Thr Asn
340 345 350

Val Gly Gly Phe Asn Pro Ser Phe Ile Tyr Arg Ile Ala Trp Asp Asn
355 360 365

Tyr Lys Gln Ile Asp Val His Leu Asp Lys Asn Lys Ala
370 375 380

<210> 44

<211> 365

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 117

<400> 44

Met Ser Lys Leu Leu Thr Pro Glu Ile Leu Ala Leu Ile Asp Pro Val
1 5 10 15

Val Ser Ser Leu Lys Arg His Gln Leu Val Asp Asp Lys Glu Ile Ala
20 25 30

Leu Thr Ile Ala Gln Leu Leu Met Lys Val Ile Ser Ala Ala Arg Trp
35 40 45

Ser Asn Thr Tyr Asp Leu Ile Glu Leu Ile Arg Gln Val Gly Val Ile

50 55 60

Phe Thr Glu Ala Tyr Pro Arg Lys Val Ile Pro Gly Asn Ile Val Arg
65 70 75 80

Arg Val Leu Ala Leu Ile Arg Asp Glu Thr Glu Thr Glu Thr
85 90 95

Glu Thr Glu Gln Thr Asp Asn Ile Pro Met Met Ser Ser Met Phe Ser
100 105 110

Leu Leu Ala Thr His Asn Lys Asn Glu Thr Ile Lys Glu Gln Thr Gln
115 120 125

Leu Gln Leu Lys Lys Gln Thr Ser Asp Met Arg Ala Ile Ile Ile Gln
130 135 140

Gly Ile Arg Asp Leu Val Asp Glu Ile Ser Asn Val Asn Asp Gly Ile
145 150 155 160

Glu Thr Met Ala Val Asp Leu Ile His Asp Asp Glu Ile Leu Leu Thr
165 170 175

Pro Thr Pro Asn Ser Glu Thr Val Gln His Phe Leu Ile Lys Ala Arg
180 185 190

Leu Lys Arg Lys Phe Thr Val Val Val Thr Glu Asn Tyr Pro Asn Asp
195 200 205

Ile Lys Ala Ala His Lys Phe Val Lys Thr Leu Ala Glu His Asn Ile
210 215 220

Glu Thr Ile Leu Ile Pro Asp Thr Thr Ile Tyr Ala Val Met Ser Arg
225 230 235 240

Val Gly Lys Val Ile Ile Gly Thr Asn Ala Val Phe Ala Asn Gly Gly
245 250 255

Cys Leu Ser Asn Ser Gly Val Ala Asn Val Val Glu Cys Ala Lys Glu
 260 265 270

His Arg Thr Pro Val Phe Ala Val Ala Gly Leu Phe Lys Leu Ser Pro
 275 280 285

Leu Tyr Pro Phe Thr Arg Asn Asp Leu Ile Glu Val Gly Asn Ser Gly
 290 295 300

Lys Val Leu Asn Tyr Asp Asp Phe Glu Leu Val Gln Asn Val Asp Val
 305 310 315 320

Val Thr Asn Pro Leu Glu Asp Tyr Ile Pro Pro Gln His Ile Asp Ile
 325 330 335

Phe Met Thr Asn Ile Gly Gly Phe Ser Pro Ser Phe Ile Tyr Arg Ile
 340 345 350

Val Leu Asp Asn Tyr Lys Ala Glu Asp Asn Lys Leu Glu
 355 360 365

<210> 45

<211> 349

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: AAC42002

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 118

<400> 45

Met Pro Gly Ser Ala Ala Lys Gly Ser Glu Leu Ser Glu Arg Ile Glu
 1 5 10 15

Ser Phe Val Glu Thr Leu Lys Arg Gly Gly Gly Pro Arg Ser Ser Glu
 20 25 30

Glu Met Ala Arg Glu Thr Leu Gly Leu Leu Arg Gln Ile Ile Thr Asp
 35 40 45

His Arg Trp Ser Asn Ala Gly Glu Leu Met Glu Leu Ile Arg Arg Glu
 50 55 60

Gly Arg Arg Met Thr Ala Ala Gln Pro Ser Glu Thr Thr Val Gly Asn
 65 70 75 80

Met Val Arg Arg Val Leu Lys Ile Ile Arg Glu Glu Tyr Gly Arg Leu
 85 90 95

His Gly Arg Ser Asp Glu Asp Gln Gln Glu Ser Leu His Lys Leu Leu
 100 105 110

Thr Ser Gly Gly Leu Asn Glu Asp Phe Ser Phe His Tyr Ala Gln Leu
 115 120 125

Gln Ser Asn Ile Ile Glu Ala Ile Asn Glu Leu Leu Val Glu Leu Glu
 130 135 140

Gly Thr Met Glu Asn Ile Ala Ala Gln Ala Leu Glu His Ile His Ser
 145 150 155 160

Asn Glu Val Ile Met Thr Ile Gly Phe Ser Arg Thr Val Glu Ala Phe
 165 170 175

Leu Lys Glu Ala Ala Arg Lys Arg Lys Phe His Val Ile Val Ala Glu
 180 185 190

Cys Ala Pro Phe Cys Gln Gly His Glu Met Ala Val Asn Leu Ser Lys
 195 200 205

Ala Gly Ile Glu Thr Thr Val Met Thr Ala Ala Ile Phe Ala Val Met

210 215 220

Ser Arg Val Asn Lys Val Ile Ile Gly Thr Lys Thr Ile Leu Ala Asn
225 230 235 240

Gly Ala Leu Arg Ala Val Thr Gly Thr His Thr Leu Ala Leu Ala Ala
 245 250 255

Lys His His Ser Thr Pro Leu Ile Val Cys Ala Pro Met Phe Lys Leu
 260 265 270

Ser Pro Gln Phe Pro Asn Glu Glu Asp Ser Phe His Lys Phe Val Ala
 275 280 285

Pro Glu Glu Val Leu Pro Phe Thr Glu Gly Asp Ile Leu Glu Lys Val
 290 295 300

Ser Val His Cys Pro Val Phe Asp Tyr Val Pro Pro Glu Leu Ile Thr
305 310 315 320

Leu Phe Ile Ser Asn Ile Gly Gly Asn Ala Pro Ser Tyr Ile Tyr Arg
 325 330 335

Leu Met Ser Glu Leu Tyr His Pro Asp Asp His Val Leu
 340 345

<210> 46

<211> 246

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 119

<400> 46

Met Ser Arg Leu Glu Ile Tyr Ser Pro Glu Gly Leu Arg Leu Asp Gly
1 5 10 15

Arg Arg Trp Asn Glu Leu Arg Arg Phe Glu Ser Ser Ile Asn Thr His
20 25 30

Pro His Ala Ala Asp Gly Ser Ser Tyr Met Glu Gln Gly Asn Asn Lys
35 40 45

Ile Ile Thr Leu Val Lys Gly Pro Lys Glu Pro Arg Leu Lys Ser Gln
50 55 60

Met Asp Thr Ser Lys Ala Leu Leu Asn Val Ser Val Asn Ile Thr Lys
65 70 75 80

Phe Ser Lys Phe Glu Arg Ser Lys Ser Ser His Lys Asn Glu Arg Arg
85 90 95

Val Leu Glu Ile Gln Thr Ser Leu Val Arg Met Phe Glu Lys Asn Val
100 105 110

Met Leu Asn Ile Tyr Pro Arg Thr Val Ile Asp Ile Glu Ile His Val
115 120 125

Leu Glu Gln Asp Gly Gly Ile Met Gly Ser Leu Ile Asn Gly Ile Thr
130 135 140

Leu Ala Leu Ile Asp Ala Gly Ile Ser Met Phe Asp Tyr Ile Ser Gly
145 150 155 160

Ile Ser Val Gly Leu Tyr Asp Thr Thr Pro Leu Leu Asp Thr Asn Ser
165 170 175

Leu Glu Glu Asn Ala Met Ser Thr Val Thr Leu Gly Val Val Gly Lys
180 185 190

Ser Glu Lys Leu Ser Leu Leu Leu Val Glu Asp Lys Ile Pro Leu Asp
195 200 205

Arg Leu Glu Asn Val Leu Ala Ile Gly Ile Ala Gly Ala His Arg Val
 210 215 220

Arg Asp Leu Met Asp Glu Glu Leu Arg Lys His Ala Gln Lys Arg Val
 225 230 235 240

Ser Asn Ala Ser Ala Arg
 245

<210> 47

<211> 180

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 120

<400> 47

Met Glu Leu Tyr Ser Pro Glu Gly Leu Arg Ile Asp Gly Arg Arg Trp
 1 5 10 15

Asn Glu Leu Arg Arg Phe Glu Cys Arg Ile Asn Thr His Pro Asn Ser
 20 25 30

Ser Asp Gly Ser Ser Tyr Val Glu Gln Gly Asn Thr Lys Val Met Cys
 35 40 45

Thr Val Gln Gly Pro Ile Glu Pro Ala Leu Arg Ser Gln Gln His Ser
 50 55 60

Glu Arg Ala Asn Ile Glu Val Asn Leu Asn Ile Ala Ser Phe Ser Thr
 65 70 75 80

Phe Glu Arg Lys Lys Arg Ser Arg Asn Glu Arg Arg Leu Val Glu Leu
 85 90 95

Lys Thr Thr Leu Glu Lys Thr Phe Glu Glu Ser Val Met Ile Asn Leu

100 105 110

Tyr Pro Arg Thr Asn Ile Val Ile Asn Val Gln Val Leu Cys Gln Asp
115 120 125

Gly Gly Met Leu Ala Ala Val Ile Asn Ser Ile Thr Leu Ala Leu Ile
130 135 140

Asp Ala Gly Ile Ser Met Tyr Asp Tyr Val Ser Gly Val Ser Cys Gly
145 150 155 160

Leu Tyr Asp Gln Thr Pro Leu Leu Asp Val Asn Asn Leu Glu Glu His
165 170 175

Asp Met Ser Cys
180

<210> 48

<211> 245

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: BAA91279

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 121

<400> 48

Met Ala Gly Leu Glu Leu Leu Ser Asp Gln Gly Tyr Arg Val Asp Gly
1 5 10 15

Arg Arg Ala Gly Glu Leu Arg Lys Ile Gln Ala Arg Met Gly Val Phe
20 25 30

Ala Gln Ala Asp Gly Ser Ala Tyr Ile Glu Gln Gly Asn Thr Lys Ala

35 40 45

Leu Ala Val Val Tyr Gly Pro His Glu Ile Arg Ser Arg Ala Arg Ala
50 55 60

Leu Pro Asp Arg Ala Leu Val Asn Cys Gln Tyr Ser Ser Ala Thr Phe
65 70 75 80

Ser Thr Gly Glu Arg Lys Arg Arg Pro His Gly Asp Arg Lys Ser Cys
85 90 95

Glu Met Gly Leu Gln Leu Arg Gln Thr Phe Glu Ala Ala Ile Leu Thr
100 105 110

Gln Leu His Pro Arg Ser Gln Ile Asp Ile Tyr Val Gln Val Leu Gln
115 120 125

Ala Asp Gly Gly Thr Tyr Ala Ala Cys Val Asn Ala Ala Thr Leu Ala
130 135 140

Val Leu Asp Ala Gly Ile Pro Met Arg Asp Phe Val Cys Ala Cys Ser
145 150 155 160

Ala Gly Phe Val Asp Gly Thr Ala Leu Ala Asp Leu Ser His Val Glu
165 170 175

Glu Ala Ala Gly Gly Pro Gln Leu Ala Leu Ala Leu Leu Pro Ala Ser
180 185 190

Gly Gln Ile Ala Leu Leu Glu Met Asp Ala Arg Leu His Glu Asp His
195 200 205

Leu Glu Arg Val Leu Glu Ala Ala Ala Gln Ala Ala Arg Asp Val His
210 215 220

Thr Leu Leu Asp Arg Val Val Arg Gln His Val Arg Glu Ala Ser Ile
225 230 235 240

Leu Leu Gly Asp Gly
245

<210> 49

<211> 720

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 122

<400> 49

Met Ser Arg Phe Phe Ser Ser Asn Tyr Glu Tyr Asp Val Ala Ser Ser
1 5 10 15

Ser Ser Glu Glu Asp Leu Leu Ser Ser Ser Glu Glu Asp Leu Leu Ser
20 25 30

Ser Ser Ser Ser Glu Ser Glu Leu Asp Gln Glu Ser Asp Asp Ser Phe
35 40 45

Phe Asn Glu Ser Glu Ser Glu Ser Glu Ala Asp Val Asp Ser Asp Asp
50 55 60

Ser Asp Ala Lys Pro Tyr Gly Pro Asp Trp Phe Lys Lys Ser Glu Phe
65 70 75 80

Arg Lys Gln Gly Gly Gly Ser Asn Lys Phe Leu Lys Ser Ser Asn Tyr
85 90 95

Asp Ser Ser Asp Glu Glu Ser Asp Glu Glu Asp Gly Lys Lys Val Val
100 105 110

Lys Ser Ala Lys Glu Lys Leu Leu Asp Glu Met Gln Asp Val Tyr Asn
115 120 125

Lys Ile Ser Gln Ala Glu Asn Ser Asp Asp Trp Leu Thr Ile Ser Asn
130 135 140

Glu Phe Asp Leu Ile Ser Arg Leu Leu Val Arg Ala Gln Gln Gln Asn
145 150 155 160

Trp Gly Thr Pro Asn Ile Phe Ile Lys Val Val Ala Gln Val Glu Asp
165 170 175

Ala Val Asn Asn Thr Gln Gln Ala Asp Leu Lys Asn Lys Ala Val Ala
180 185 190

Arg Ala Tyr Asn Thr Thr Lys Gln Arg Val Lys Lys Val Ser Arg Glu
195 200 205

Asn Glu Asp Ser Met Ala Lys Phe Arg Asn Asp Pro Glu Ser Phe Asp
210 215 220

Lys Glu Pro Thr Ala Asp Leu Asp Ile Ser Ala Asn Gly Phe Thr Ile
225 230 235 240

Ser Ser Ser Gln Gly Asn Asp Gln Ala Val Gln Glu Asp Phe Phe Thr
245 250 255

Arg Leu Gln Thr Ile Ile Asp Ser Arg Gly Lys Lys Thr Val Asn Gln
260 265 270

Gln Ser Leu Ile Ser Thr Leu Glu Glu Leu Leu Thr Val Ala Glu Lys
275 280 285

Pro Tyr Glu Phe Ile Met Ala Tyr Leu Thr Leu Ile Pro Ser Arg Phe
290 295 300

Asp Ala Ser Ala Asn Leu Ser Tyr Gln Pro Ile Asp Gln Trp Lys Ser
305 310 315 320

Ser Phe Asn Asp Ile Ser Lys Leu Leu Ser Ile Leu Asp Gln Thr Ile

325 330 335

Asp Thr Tyr Gln Val Asn Glu Phe Ala Asp Pro Ile Asp Phe Ile Glu
340 345 350

Asp Glu Pro Lys Glu Asp Ser Asp Gly Val Lys Arg Ile Leu Gly Ser
355 360 365

Ile Phe Ser Phe Val Glu Arg Leu Asp Asp Glu Phe Met Lys Ser Leu
370 375 380

Leu Asn Ile Asp Pro His Ser Ser Asp Tyr Leu Ile Arg Leu Arg Asp
385 390 395 400

Glu Gln Ser Ile Tyr Asn Leu Ile Leu Arg Thr Gln Leu Tyr Phe Glu
405 410 415

Ala Thr Leu Lys Asp Glu His Asp Leu Glu Arg Ala Leu Thr Arg Pro
420 425 430

Phe Val Lys Arg Leu Asp His Ile Tyr Tyr Lys Ser Glu Asn Leu Ile
435 440 445

Lys Ile Met Glu Thr Ala Ala Trp Asn Ile Ile Pro Ala Gln Phe Lys
450 455 460

Ser Lys Phe Thr Ser Lys Asp Gln Leu Asp Ser Ala Asp Tyr Val Asp
465 470 475 480

Asn Leu Ile Asp Gly Leu Ser Thr Ile Leu Ser Lys Gln Asn Asn Ile
485 490 495

Ala Val Gln Lys Arg Ala Ile Leu Tyr Asn Ile Tyr Tyr Thr Ala Leu
500 505 510

Asn Lys Asp Phe Gln Thr Ala Lys Asp Met Leu Leu Thr Ser Gln Val
515 520 525

Gln Thr Asn Ile Asn Gln Phe Asp Ser Ser Leu Gln Ile Leu Phe Asn
530 535 540

Arg Val Val Val Gln Leu Gly Leu Ser Ala Phe Lys Leu Cys Leu Ile
545 550 555 560

Glu Glu Cys His Gln Ile Leu Asn Asp Leu Leu Ser Ser Ser His Leu
565 570 575

Arg Glu Ile Leu Gly Gln Gln Ser Leu His Arg Ile Ser Leu Asn Ser
580 585 590

Ser Asn Asn Ala Ser Ala Asp Glu Arg Ala Arg Gln Cys Leu Pro Tyr
595 600 605

His Gln His Ile Asn Leu Asp Leu Ile Asp Val Val Phe Leu Thr Cys
610 615 620

Ser Leu Leu Ile Glu Ile Pro Arg Met Thr Ala Phe Tyr Ser Gly Ile
625 630 635 640

Lys Val Lys Arg Ile Pro Tyr Ser Pro Lys Ser Ile Arg Arg Ser Leu
645 650 655

Glu His Tyr Asp Ser Leu Lys Thr Tyr Phe Phe Ser Phe Lys Arg Phe
660 665 670

Tyr Ser Ser Phe Ser Val Ala Lys Leu Ala Glu Leu Phe Asp Leu Pro
675 680 685

Glu Asn Lys Val Val Glu Val Leu Gln Ser Val Ile Ala Glu Leu Glu
690 695 700

Ile Pro Ala Lys Leu Asn Asp Glu Lys Thr Ile Phe Val Val Glu Lys
705 710 715 720

<210> 50
 <211> 874
 <212> PRT
 <213> Candida albicans

 <220>
 <221> misc_feature
 <223> Corresponds to SEQ ID NO: 123

<400> 50

Met Ser Arg Phe Phe Val Ser Gly Tyr Thr Ser Asp Ser Ser Ser Glu
 1 5 10 15

Glu Glu Asp Leu Leu Ser Thr Ser Glu Glu Glu Leu Leu Ser Ser Ser
 20 25 30

Asp Glu Gly Glu Asp Asn Glu Ser Asp Ser Ser Phe Phe Gly Glu Asp
 35 40 45

Asp Asp Glu Ser Glu Glu Ser Ser Ser Asp Asp Glu Asp Gly Arg Pro
 50 55 60

Ser Gly Pro Ala Tyr Phe Leu Lys Lys Ser Phe Leu Lys Gly Ala Gly
 65 70 75 80

Gly Asp Asp Ser Asp Ser Asp Ser Asp Asp Glu Gly Arg Lys Val Val
 85 90 95

Lys Ser Ala Lys Asp Lys Leu Leu Asp Asp Met Lys Ser Ser Ile Glu
 100 105 110

Ile Ile Asn Ser Asn Lys Tyr Asn Asn Asn Trp Ser Ile Val Leu Gly
 115 120 125

Glu Phe Asp Lys Phe Gly Arg Phe Leu Ile Arg Cys Asn Gln Thr Asn
 130 135 140

Leu Gly Thr Pro Lys Phe Tyr Ile Lys Leu Leu Thr Ser Leu Asp Asn
 145 150 155 160

Ser Ile Thr Glu Thr Ser Asn Asn Glu Arg Asp Asp Lys Thr Leu Lys
165 170 175

Ala Asp Glu Ala Arg Ala Phe Asn Thr Leu Arg Gln Arg Ile Lys Lys
180 185 190

Gln Ile Arg Glu Phe Gln Val Tyr Tyr Asp Leu Tyr Lys Glu Asn Pro
195 200 205

Glu Glu Phe Asp Glu Asn Glu Asp Glu Pro Leu Glu Ser Val Gln Ala
210 215 220

Gly Leu Asn Asp Asn Val Lys Asn Glu Ala Asp Asn Ser Asn Val Gly
225 230 235 240

Ala Leu Ala Ser Asn Arg Val Leu Ser Pro Ile Phe His Thr Leu Lys
245 250 255

Thr Ile Ser Glu Ser Arg Gly Lys Lys Asn Ile Asp Lys Leu Glu Gln
260 265 270

Ile Ala Thr Leu Glu Lys Leu Leu Glu Ala Asn Val Ser Lys Ser Ser
275 280 285

Pro Phe Glu Leu Ile Ser Ile Tyr Gln Met Leu Leu Ser Val Arg Phe
290 295 300

Asp Ala Ser Ser Asn Gln Ala Phe Met Pro Leu Glu Gln Trp Gln Lys
305 310 315 320

Asn Glu His Asp Leu Gly Lys Leu Leu Asp Leu Leu Glu Ala Asn Val
325 330 335

Asp Thr Tyr Gln Val Ser Glu Leu Gly Ser Thr Thr Asp Asp Ile Asp
340 345 350

Ile Glu Pro Val Ala Asn Ala Gln Gly Val Lys Val Ile Phe Gly Ser
355 360 365

Ile Thr Ser Ser Ile Asp Arg Leu Asp Asp Glu Leu Thr Lys Ser Leu
370 375 380

Gln His Thr Asp Pro His Ser Ile Glu Tyr Val Glu Arg Leu Lys Asp
385 390 395 400

Glu Ser Thr Ile Tyr Asn Leu Ile Val Arg Gly Gln Ala Tyr Val Glu
405 410 415

Ser Ile Thr Pro Glu Asp Val Lys Tyr Asn Ser Glu Gln Leu Ala Arg
420 425 430

Ile Val Leu Arg Arg Leu Glu His Ile Tyr Tyr Lys Pro Lys Gln Leu
435 440 445

Ile Lys Ala Asn Glu Glu Glu Ala Trp Arg Asn Ile Glu Tyr Asn Ser
450 455 460

Ser Ile Val Ser Lys Gly Ser Ser Val Asp Glu Val Ile Asp Gln Leu
465 470 475 480

Thr Glu Phe Leu Gln Lys Gln Gln Lys Asn Lys Thr Tyr Gly Lys His
485 490 495

Ala Ile Leu Phe Ser Ile Tyr Tyr Tyr Ala Val Asn Ser Gln Tyr Glu
500 505 510

Lys Ala Lys Glu Leu Phe Leu Arg Ser Gln Phe Tyr Ser Asn Ile Asn
515 520 525

Ser Ala Glu Ser Ser Leu Gln Val Gln Tyr Asn Arg Ala Leu Val Gln
530 535 540

Leu Gly Leu Ser Ala Phe Arg Ala Gly Ser Ile Glu Glu Ser His Lys

545 550 555 560

Ile Leu Asn Glu Ile Val Asn Ser Gln Arg Ser Lys Glu Leu Leu Gly
 565 570 575

Gln Gly Phe Asn Ser Lys Phe Pro Asn Gln Ala Thr Val Leu Glu Arg
 580 585 590

Gln Lys Leu Leu Pro Phe His Gln His Ile Asn Leu Glu Leu Leu Glu
 595 600 605

Cys Val Phe Met Thr Cys Ser Leu Leu Ile Glu Ile Pro Thr Leu Ala
 610 615 620

Ala Ile Ala Asn Asn His Lys Asp Ser Lys Arg Lys Asn Ala Ser Leu
625 630 635 640

Lys Ser Phe Lys Ser Lys Leu Asp Phe His Asp Arg Gln Phe Phe Thr
 645 650 655

Gly Pro Pro Glu Ser Ile Lys Asp His Ile Val His Ala Ser Ile Ala
 660 665 670

Leu Gln Lys Gly Asp Trp Leu Lys Ser Tyr Asn Leu Leu Ser Ser Ile
 675 680 685

Lys Ile Trp Lys Leu Phe Pro Asp Asn Asp Lys Leu Leu Ala Met Met
 690 695 700

Lys Asn Gln Leu Gln Ile Glu Gly Leu Arg Thr Tyr Ile Phe Thr Tyr
705 710 715 720

Lys Ser Val Phe Lys Lys Leu Ser Ile Glu Lys Leu Gln Gln Ile Phe
 725 730 735

Gln Leu Ser Lys Asp Glu Val Val Ser Ile Leu Glu Lys Met Ile Thr
 740 745 750

Thr Gly Asn Val Ser Gly Gly Glu Ile Ile Asp Asn Lys Phe Ile Ser
755 760 765

Phe Thr Ser Thr Thr Glu Pro Gln Arg Ser Lys Leu Gln Glu Leu Ala
770 775 780

Ile Val Leu Asn Glu Lys Ile Gln Leu Leu Thr Glu Lys Asn Glu Lys
785 790 795 800

Thr Gln Ser Asn Gly Tyr Gly Lys Lys Gln Gln Asn Lys Asp Gln Gln
805 810 815

Asn Gln Gln Gln Gln Asn Gln Asn Gln Asn Gln Gln Gln Gln Asn
820 825 830

Gln Gln Gln Gln Gln Gln Gln Gln Ser Ser Gln Gln Gln Ser Asn Asn
835 840 845

Ile Leu Ser Glu Glu Ser Ala Asn Lys Phe Arg Tyr Ala Asn Val Asn
850 855 860

Ser Asn Asn Asp Glu Phe Gln Ala Thr Ala
865 870

<210> 51

<211> 853

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: AAD03462

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 124

<400> 51

Met Ser Arg Phe Phe Thr Thr Gly Ser Asp Ser Glu Ser Glu Ser Ser
 1 5 10 15

Leu Ser Gly Glu Glu Leu Val Thr Lys Pro Val Gly Gly Asn Tyr Gly
 20 25 30

Lys Gln Pro Leu Leu Leu Ser Glu Asp Glu Glu Asp Thr Lys Arg Val
 35 40 45

Val Arg Ser Ala Lys Asp Lys Arg Phe Glu Glu Leu Thr Asn Leu Ile
 50 55 60

Arg Thr Ile Arg Asn Ala Met Lys Ile Arg Asp Val Thr Lys Cys Leu
 65 70 75 80

Glu Glu Phe Glu Leu Leu Gly Lys Ala Tyr Gly Lys Ala Lys Ser Ile
 85 90 95

Val Asp Lys Glu Gly Val Pro Arg Phe Tyr Ile Arg Ile Leu Ala Asp
 100 105 110

Leu Glu Asp Tyr Leu Asn Glu Leu Trp Glu Asp Lys Glu Gly Lys Lys
 115 120 125

Lys Met Asn Lys Asn Asn Ala Lys Ala Leu Ser Thr Leu Arg Gln Lys
 130 135 140

Ile Arg Lys Tyr Asn Arg Asp Phe Glu Ser His Ile Thr Ser Tyr Lys
 145 150 155 160

Gln Asn Pro Glu Gln Ser Ala Asp Glu Asp Ala Glu Lys Asn Glu Glu
 165 170 175

Asp Ser Glu Gly Ser Ser Asp Glu Asp Glu Asp Glu Asp Gly Val Ser
 180 185 190

Ala Ala Thr Phe Leu Lys Lys Lys Ser Glu Ala Pro Ser Gly Glu Ser

195 200 205

Arg Lys Phe Leu Lys Lys Met Asp Asp Glu Asp Glu Asp Ser Glu Asp
210 215 220

Ser Glu Asp Asp Glu Asp Trp Asp Thr Gly Ser Thr Ser Ser Asp Ser
225 230 235 240

Asp Ser Glu Glu Glu Glu Gly Lys Gln Thr Ala Leu Ala Ser Arg Phe
245 250 255

Leu Lys Lys Ala Pro Thr Thr Asp Glu Asp Lys Lys Ala Ala Glu Lys
260 265 270

Lys Arg Glu Asp Lys Ala Lys Lys Lys His Asp Arg Lys Ser Lys Arg
275 280 285

Leu Asp Glu Glu Glu Glu Asp Asn Glu Gly Gly Glu Ala Ala Glu Asn
290 295 300

Asn Leu Gly Glu Gly Val Ile Val Lys Ile Lys Phe Asn Ile Ile Ala
305 310 315 320

Ser Leu Tyr Asp Tyr Asn Pro Asn Leu Ala Thr Tyr Met Lys Pro Glu
325 330 335

Met Trp Gly Lys Cys Leu Asp Cys Ile Asn Glu Leu Met Asp Ile Leu
340 345 350

Phe Ala Asn Pro Asn Ile Phe Val Gly Glu Asn Ile Leu Glu Glu Ser
355 360 365

Glu Asn Leu His Asn Ala Asp Gln Pro Leu Arg Val Arg Gly Cys Ile
370 375 380

Leu Thr Leu Val Glu Arg Met Asp Glu Glu Phe Thr Lys Ile Met Gln
385 390 395 400

Asn Thr Asp Pro His Ser Gln Glu Tyr Val Glu His Leu Lys Asp Glu
405 410 415 :

Ala Gln Val Cys Ala Ile Ile Glu Arg Val Gln Arg Tyr Leu Glu Glu
420 425 430

Lys Gly Thr Thr Glu Glu Val Cys Arg Ile Tyr Leu Leu Arg Ile Leu
435 440 445

His Thr Tyr Tyr Lys Phe Asp Tyr Lys Ala His Gln Arg Gln Leu Thr
450 455 460

Pro Pro Glu Gly Ser Ser Lys Ser Glu Gln Asp Gln Ala Glu Asn Glu
465 470 475 480

Gly Glu Asp Ser Ala Val Leu Met Glu Arg Leu Cys Lys Tyr Ile Tyr
485 490 495

Ala Lys Asp Arg Thr Asp Arg Ile Arg Thr Cys Ala Ile Leu Cys His
500 505 510

Ile Tyr His His Ala Leu His Ser Arg Trp Tyr Gln Ala Arg Asp Leu
515 520 525

Met Leu Met Ser His Leu Gln Asp Asn Ile Gln His Ala Asp Pro Pro
530 535 540

Val Gln Ile Leu Tyr Asn Arg Thr Met Val Gln Leu Gly Ile Cys Ala
545 550 555 560

Phe Arg Gln Gly Leu Thr Lys Asp Ala His Asn Ala Leu Leu Asp Ile
565 570 575

Gln Ser Ser Gly Arg Ala Lys Glu Leu Leu Gly Gln Gly Leu Leu Leu
580 585 590

Arg Ser Leu Gln Glu Arg Asn Gln Glu Gln Glu Lys Val Glu Arg Arg
595 600 605

Arg Gln Val Pro Phe His Leu His Ile Asn Leu Glu Leu Leu Glu Cys
610 615 620

Val Tyr Leu Val Ser Ala Met Leu Leu Glu Ile Pro Tyr Met Ala Ala
625 630 635 640

His Glu Ser Asp Ala Arg Arg Arg Met Ile Ser Lys Gln Phe His His
645 650 655

Gln Leu Arg Val Gly Glu Arg Gln Pro Leu Leu Gly Pro Pro Glu Ser
660 665 670

Met Arg Glu His Val Val Ala Ala Ser Lys Ala Met Lys Met Gly Asp
675 680 685

Trp Lys Thr Cys His Ser Phe Ile Ile Asn Glu Lys Met Asn Gly Lys
690 695 700

Val Trp Asp Leu Phe Pro Glu Ala Asp Lys Val Arg Thr Met Leu Val
705 710 715 720

Arg Lys Ile Gln Glu Glu Ser Leu Arg Thr Tyr Leu Phe Thr Tyr Ser
725 730 735

Ser Val Tyr Asp Ser Ile Ser Met Glu Thr Leu Ser Asp Met Phe Glu
740 745 750

Leu Asp Leu Pro Thr Val His Ser Ile Ile Ser Lys Met Ile Ile Asn
755 760 765

Glu Glu Leu Met Ala Ser Leu Asp Gln Pro Thr Gln Thr Val Val Met
770 775 780

His Arg Thr Glu Pro Thr Ala Gln Gln Asn Leu Ala Leu Gln Leu Ala

785 790 795 800

Glu Lys Leu Gly Ser Leu Val Glu Asn Asn Glu Arg Val Phe Asp His
 805 810 815

Lys Gln Gly Thr Tyr Gly Gly Tyr Phe Arg Asp Gln Lys Asp Gly Tyr
 820 825 830

Arg Lys Asn Glu Gly Tyr Met Arg Arg Gly Gly Tyr Arg Gln Gln Gln
 835 840 845

Ser Gln Thr Ala Tyr
 850

<210> 52

<211> 297

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 125

<400> 52

Met Ser Glu Leu Asn Ala Leu Leu Lys Asp Ile Asn Gly Ser Leu Thr
1 5 10 15

Ala Thr Ser Glu Ser Leu Glu Arg Leu Ser Gly Ile Tyr Ser Asn Ser
 20 25 30

Ala Thr Asp Glu Ile Pro Glu Ser Asn Gln Leu His Glu His Leu Phe
 35 40 45

Tyr Asp Ala Lys Lys Pro Ala Glu Lys Val Ser Leu Leu Ser Leu Lys
 50 55 60

Asn Gly Ser Met Leu Gly Tyr Ile Asn Ser Leu Leu Met Leu Ile Gly
65 70 75 80

Asn Arg Leu Asp Asp Glu Cys Lys Asp Pro Ser Ala Met Asp Ala Arg
85 90 95

Glu Arg Ser Ile Gln His Arg Val Val Leu Glu Arg Gly Val Lys Pro
100 105 110

Leu Glu Lys Lys Leu Ala Tyr Gln Leu Asp Lys Leu Thr Arg Ala Tyr
115 120 125

Val Lys Met Glu Lys Glu Tyr Lys Asp Ala Glu Lys Arg Ala Leu Glu
130 135 140

Lys Ser Thr Leu Val Asn His Ser Gly Asn Asp Asp Ser Glu Asp Asp
145 150 155 160

Glu Ser Ser Glu Asp Glu Ile Ala Tyr Arg Pro Asn Thr Ser Gly Ile
165 170 175

Ile Asn Thr Asn Lys Lys Ser Ser Ala Tyr Arg Val Glu Glu Thr Ala
180 185 190

Lys Gln Glu Asn Gly Glu Glu Asn Asp Asp Asn Glu Thr Gly Val Tyr
195 200 205

Lys Pro Pro Lys Ile Thr Ala Val Leu Pro Pro Gln Gln Thr His Phe
210 215 220

Glu Asp Arg Phe Asp Ala Arg Glu His Lys Asp Arg Ser Asn Lys Ser
225 230 235 240

Asn Lys Ala Glu Lys Arg Lys Gln Lys Gln Arg Glu Arg Asn Ala Arg
245 250 255

Met Asn Val Ile Gly Gly Glu Asp Phe Gly Ile Phe Ser Ser Lys Arg
260 265 270

Lys Leu Glu Asp Ser Thr Ser Arg Arg Gly Ala Lys Lys Thr Arg Ser
 275 280 285

Ala Trp Asp Arg Ala Gln Arg Arg Leu
 290 295

<210> 53

<211> 300

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 126

<400> 53

Met Ser Lys Val Asp Thr Val Leu Lys Glu Ile Ile Ser Ser Thr Lys
 1 5 10 15

Ser Thr Glu Ala Ser Val Lys Glu Leu Ile Ala Phe Val Lys Asp Ser
 20 25 30

Ser Ser Gln His Pro Glu Leu Val Arg Asn Leu Leu Ala Lys Ser Asn
 35 40 45

Ser Ser Leu Glu Gly Val Ser Leu Leu Gly Leu Lys Asn Glu Ser Leu
 50 55 60

Val Ser Tyr Ile Asn Asn Ile Val Leu Val Val Leu Ser His Leu Glu
 65 70 75 80

Arg Leu Glu Ser Asp Ser Glu Thr Gly Ser Ser Ala Val Glu Arg Ser
 85 90 95

Ile Ile Gln Arg Val Thr Leu Glu Lys Gly Val Lys Pro Leu Glu Lys
 100 105 110

Lys Leu Ser Tyr Gln Leu Asp Lys Met Ile Arg Ala Tyr Gly Arg Met

115 120 125

Glu Gln Asp Glu Ile Lys Ala Glu Gln Lys Leu Asn Asp Arg Gly Ser
130 135 140

Gly Glu Asn Asp Glu Asn Asp Glu Asn Asp Ser Glu Glu Asp Ser Glu
145 150 155 160

Glu Asp Ser Glu Asp Asp Ser Glu Asp Asp Glu Leu Ala Tyr Arg Pro
165 170 175

Asp Ala Ser Ser Phe Ala Lys Leu Thr Ser Ala Lys Thr Lys Ser Lys
180 185 190

Pro Thr Ser Ser Ala Val Ser Thr Ser Asn Glu Lys Tyr Arg Pro Pro
195 200 205

Lys Ile Ser Ala Met Ala Pro Pro Thr Ala Val Lys Ser His Asp Leu
210 215 220

Asp Ala Asn Thr Thr Ser Ser Lys Asn Arg Lys Leu Gln Ser Met Glu
225 230 235 240

Glu Tyr Leu Gln Glu Gln Ser Asp Met Pro Met Val Glu Ala Ser Val
245 250 255

Gly Ser Thr Ile Val Glu His Gly Arg Gly Gly Val Lys Thr Gln His
260 265 270

Asp Arg Lys Lys Glu Arg Glu Ile Gln Thr Tyr Glu Glu Asp Asn Phe
275 280 285

Val Arg Leu Pro Thr Ser Gln Thr Lys Lys Ser Phe
290 295 300

<210> 54
<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: AL050003

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 127

<400> 54

Met Ala Ala Leu Gly Val Leu Glu Ser Asp Leu Pro Ser Ala Val Thr
 1 5 10 15

Leu Leu Lys Asn Leu Gln Glu Gln Val Met Ala Val Thr Ala Gln Val
 20 25 30

Lys Ser Leu Thr Gln Lys Val Gln Ala Gly Ala Tyr Pro Thr Glu Lys
 35 40 45

Gly Leu Ser Phe Leu Glu Val Lys Asp Gln Leu Leu Leu Met Tyr Leu
 50 55 60

Met Asp Leu Thr His Leu Ile Leu Asp Lys Ala Ser Gly Gly Ser Leu
 65 70 75 80

Gln Gly His Asp Ala Val Leu Arg Leu Val Glu Ile Arg Thr Val Leu
 85 90 95

Glu Lys Leu Arg Pro Leu Asp Gln Lys Leu Lys Tyr Gln Ile Asp Lys
 100 105 110

Leu Ile Lys Thr Ala Val Thr Gly Ser Leu Ser Glu Asn Asp Pro Leu
 115 120 125

Arg Phe Lys Pro His Pro Ser Asn Met Met Ser Lys Leu Ser Ser Glu
 130 135 140

Asp Glu Glu Glu Asp Glu Ala Glu Asp Asp Gln Ser Glu Ala Ser Gly
 145 150 155 160

Lys Lys Ser Val Lys Gly Val Ser Lys Lys Tyr Val Pro Pro Arg Leu
 165 170 175

Val Pro Val His Tyr Asp Glu Thr Glu Ala Glu Arg Glu Lys Lys Arg
 180 185 190

Leu Glu Arg Ala Lys Arg Arg Ala Leu Ser Ser Ser Val Ile Arg Glu
 195 200 205

Leu Lys Glu Gln Tyr Ser Asp Ala Pro Glu Glu Ile Arg Asp Ala Arg
 210 215 220

His Pro His Val Thr Arg Gln Ser Gln Glu Asp Gln His Arg Ile Asn
 225 230 235 240

Tyr Glu Glu Ser Met Met Val Arg Leu Ser Val Ser Lys Arg Glu Lys
 245 250 255

Gly Arg Arg Lys Arg Ala Asn Val Met Ser Ser Gln Leu His Ser Leu
 260 265 270

Thr His Phe Ser Asp Ile Ser Ala Leu Thr Gly Gly Thr Val His Leu
 275 280 285

Asp Glu Asp Gln Asn Pro Ile Lys Lys Arg Lys Lys Ile Pro Gln Lys
 290 295 300

Gly Arg Lys Lys Lys Gly Gln
 305 310

<210> 55
 <211> 221
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 128

<400> 55

Met Ser Ala Thr Glu Ser Ser Ser Ile Phe Thr Leu Ser His Asn Ser
1 5 10 15

Asn Leu Gln Asp Ile Leu Ala Ala Asn Ala Lys Trp Ala Ser Gln Met
20 25 30

Asn Asn Ile Gln Pro Thr Leu Phe Pro Asp His Asn Ala Lys Gly Gln
35 40 45

Ser Pro His Thr Leu Phe Ile Gly Cys Ser Asp Ser Arg Tyr Asn Glu
50 55 60

Asn Cys Leu Gly Val Leu Pro Gly Glu Val Phe Thr Trp Lys Asn Val
65 70 75 80

Ala Asn Ile Cys His Ser Glu Asp Leu Thr Leu Lys Ala Thr Leu Glu
85 90 95

Phe Ala Ile Ile Cys Leu Lys Val Asn Lys Val Ile Ile Cys Gly His
100 105 110

Thr Asp Cys Gly Gly Ile Lys Thr Cys Leu Thr Asn Gln Arg Glu Ala
115 120 125

Leu Pro Lys Val Asn Cys Ser His Leu Tyr Lys Tyr Leu Asp Asp Ile
130 135 140

Asp Thr Met Tyr His Glu Glu Ser Gln Asn Leu Ile His Leu Lys Thr
145 150 155 160

Gln Arg Glu Lys Ser His Tyr Leu Ser His Cys Asn Val Lys Arg Gln
165 170 175

Phe Asn Arg Ile Ile Glu Asn Pro Thr Val Gln Thr Ala Val Gln Asn
 180 185 190

Gly Glu Leu Gln Val Tyr Gly Leu Leu Tyr Asn Val Glu Asp Gly Leu
 195 200 205

Leu Gln Thr Val Ser Thr Tyr Thr Lys Val Thr Pro Lys
 210 215 220

<210> 56

<211> 281

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 129

<400> 56

Met Gly Arg Glu Asn Ile Leu Lys Tyr Gln Leu Glu His Asp His Glu
 1 5 10 15

Ser Asp Leu Val Thr Glu Lys Asp Gln Ser Leu Leu Leu Asp Asn Asn
 20 25 30

Asn Asn Leu Asn Gly Met Asn Asn Thr Ile Lys Thr His Pro Val Arg
 35 40 45

Val Ser Ser Gly Asn His Asn Asn Phe Pro Phe Thr Leu Ser Ser Glu
 50 55 60

Ser Thr Leu Gln Asp Phe Leu Asn Asn Asn Lys Phe Phe Val Asp Ser
 65 70 75 80

Ile Lys His Asn His Gly Asn Gln Ile Phe Asp Leu Asn Gly Gln Gly
 85 90 95

Gln Ser Pro His Thr Leu Trp Ile Gly Cys Ser Asp Ser Arg Ala Gly
100 105 110

Asp Gln Cys Leu Ala Thr Leu Pro Gly Glu Ile Phe Val His Arg Asn
115 120 125

Ile Ala Asn Ile Val Asn Ala Asn Asp Ile Ser Ser Gln Gly Val Ile
130 135 140

Gln Phe Ala Ile Asp Val Leu Lys Val Lys Lys Ile Ile Val Cys Gly
145 150 155 160

His Thr Asp Cys Gly Gly Ile Trp Ala Ser Leu Ser Lys Lys Lys Ile
165 170 175

Gly Gly Val Leu Asp Leu Trp Leu Asn Pro Val Arg His Ile Arg Ala
180 185 190

Ala Asn Leu Lys Leu Leu Glu Glu Tyr Asn Gln Asp Pro Lys Leu Lys
195 200 205

Ala Lys Lys Leu Ala Glu Leu Asn Val Ile Ser Ser Val Thr Ala Leu
210 215 220

Lys Arg His Pro Ser Ala Ser Val Ala Leu Lys Lys Asn Glu Ile Glu
225 230 235 240

Val Trp Gly Met Leu Tyr Asp Val Ala Thr Gly Tyr Leu Ser Gln Val
245 250 255

Glu Ile Pro Gln Asp Glu Phe Glu Asp Leu Phe His Val His Asp Glu
260 265 270

His Asp Glu Glu Glu Tyr Asn Pro His
275 280

<210> 57

<211> 281

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 130

<400> 57

Met Lys Ala Arg Lys Ser Gln Arg Lys Ala Gly Ser Lys Pro Asn Leu
1 5 10 15

Ile Gln Ser Lys Leu Gln Val Asn Asn Gly Ser Lys Ser Asn Lys Ile
20 25 30

Val Lys Cys Asp Lys Cys Glu Met Ser Tyr Ser Ser Thr Ser Ile Glu
35 40 45

Asp Arg Ala Ile His Glu Lys Tyr His Thr Leu Gln Leu His Gly Arg
50 55 60

Lys Trp Ser Pro Asn Trp Gly Ser Ile Val Tyr Thr Glu Arg Asn His
65 70 75 80

Ser Arg Thr Val His Leu Ser Arg Ser Thr Gly Thr Ile Thr Pro Leu
85 90 95

Asn Ser Ser Pro Leu Lys Lys Ser Ser Pro Ser Ile Thr His Gln Glu
100 105 110

Glu Lys Ile Val Tyr Val Arg Pro Asp Lys Ser Asn Gly Glu Val Arg
115 120 125

Ala Met Thr Glu Ile Met Thr Leu Val Asn Asn Glu Leu Asn Ala Pro
130 135 140

His Asp Glu Asn Val Ile Trp Asn Ser Thr Thr Glu Glu Lys Gly Lys
145 150 155 160

Ala Phe Val Tyr Ile Arg Asn Asp Arg Ala Val Gly Ile Ile Ile Ile
165 170 175

Glu Asn Leu Tyr Gly Gly Asn Gly Lys Thr Ser Ser Arg Gly Arg Trp
180 185 190

Met Val Tyr Asp Ser Arg Arg Leu Val Gln Asn Val Tyr Pro Asp Phe
195 200 205

Lys Ile Gly Ile Ser Arg Ile Trp Val Cys Arg Thr Ala Arg Lys Leu
210 215 220

Gly Ile Ala Thr Lys Leu Ile Asp Val Ala Arg Glu Asn Ile Val Tyr
225 230 235 240

Gly Glu Val Ile Pro Arg Tyr Gln Val Ala Trp Ser Gln Pro Thr Asp
245 250 255

Ser Gly Gly Lys Leu Ala Ser Lys Tyr Asn Gly Ile Met His Lys Ser
260 265 270

Gly Lys Leu Leu Leu Pro Val Tyr Ile
275 280

<210> 58

<211> 260

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 131

<400> 58

Met Gly Ser Ile Asn Ser Gln Lys Ala Gln Lys Ile Gln Ser Ile Leu
1 5 10 15

Ala Leu Pro Ser Asn Phe Lys Lys Ile Thr Cys Ser Thr Cys Asp Met
20 25 30

Thr Tyr Asn Pro His Ile Ser Gln Asp Lys Leu Leu His Asn Lys Tyr
35 40 45

His Thr Asn Phe Ile Asn Gly Ile Pro Trp Asn Tyr Lys Thr Asp Asn
50 55 60

Asp Val Leu Ile Ile Glu Asn Phe Thr Leu Val Glu Thr Pro Lys Leu
65 70 75 80

Asn Ser Thr Gly Lys Ser Leu Lys Leu Thr Lys Thr Arg Gln Thr Phe
85 90 95

Lys Gly Ser Ile Ile Cys Ile Asn Lys Ser Asn Lys Arg His Ile Gln
100 105 110

Lys Val Glu Leu Leu Leu Asn Met Val Asn Gln Glu Leu Asn Ala Ser
115 120 125

Gln Asp Ser Gly Gln Trp Lys Lys Pro Glu Phe Asp Arg Ser Lys Ala
130 135 140

Phe Val Ile Ile Ile Asp Ser Lys Ala Ile Gly Leu Cys Thr Thr Asp
145 150 155 160

Thr Ile Gln Pro Asp Gln Gly Arg Trp Met Ile His Lys Thr Gln Ser
165 170 175

Ile Val Pro Asn Gln Ile Asn Lys Asn Val Val Ile Gly Ile Ser Arg
180 185 190

Ile Trp Ile Ser Arg Lys Trp Arg Gln Tyr Gly Leu Gly Lys Lys Leu
195 200 205

Leu Asn Val Val Leu Lys Asn Ser Ile Tyr Ser Val Gln Leu Leu Lys

210 215 220

Asn Gln Val Ala Phe Ser Gln Pro Ser Phe Ser Gly Gly Met Leu Ala
225 230 235 240

Lys Ser Phe Asn Gly Val Lys His Lys Ser Gly Glu Met Leu Leu Pro
 245 250 255

Val Tyr Ile Glu
 260

<210> 59
<211> 620
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 132

<400> 59

Met Leu Asn Gly Glu Asp Phe Val Glu His Asn Asp Ile Leu Ser Ser
1 5 10 15

Pro Ala Lys Ser Arg Asn Val Thr Pro Lys Arg Val Asp Pro His Gly
 20 25 30

Glu Arg Gln Leu Arg Arg Ile His Ser Ser Lys Lys Asn Leu Leu Glu
 35 40 45

Arg Ile Ser Leu Val Gly Asn Glu Arg Lys Asn Thr Ser Pro Asp Pro
 50 55 60

Ala Leu Lys Pro Lys Thr Pro Ser Lys Ala Pro Arg Lys Arg Gly Arg
65 70 75 80

Pro Arg Lys Ile Gln Glu Glu Leu Thr Asp Arg Ile Lys Lys Asp Glu
 85 90 95

Lys Asp Thr Ile Ser Ser Lys Lys Lys Arg Lys Leu Asp Lys Asp Thr
100 105 110

Ser Gly Asn Val Asn Glu Glu Ser Lys Thr Ser Asn Asn Lys Gln Val
115 120 125

Met Glu Lys Thr Gly Ile Lys Glu Lys Arg Glu Arg Glu Lys Ile Gln
130 135 140

Val Ala Thr Thr Thr Tyr Glu Asp Asn Val Thr Pro Gln Thr Asp Asp
145 150 155 160

Asn Phe Val Ser Asn Ser Pro Glu Pro Pro Glu Pro Ala Thr Pro Ser
165 170 175

Lys Lys Ser Leu Thr Thr Asn His Asp Phe Thr Ser Pro Leu Lys Gln
180 185 190

Ile Ile Met Asn Asn Leu Lys Glu Tyr Lys Asp Ser Thr Ser Pro Gly
195 200 205

Lys Leu Thr Leu Ser Arg Asn Phe Thr Pro Thr Pro Val Pro Lys Asn
210 215 220

Lys Lys Leu Tyr Gln Thr Ser Glu Thr Lys Ser Ala Ser Ser Phe Leu
225 230 235 240

Asp Thr Phe Glu Gly Tyr Phe Asp Gln Arg Lys Ile Val Arg Thr Asn
245 250 255

Ala Lys Ser Arg His Thr Met Ser Met Ala Pro Asp Val Thr Arg Glu
260 265 270

Glu Phe Ser Leu Val Ser Asn Phe Phe Asn Glu Asn Phe Gln Lys Arg
275 280 285

Pro Arg Gln Lys Leu Phe Glu Ile Gln Lys Lys Met Phe Pro Gln Tyr
290 295 300

Trp Phe Glu Leu Thr Gln Gly Phe Ser Leu Leu Phe Tyr Gly Val Gly
305 310 315 320

Ser Lys Arg Asn Phe Leu Glu Glu Phe Ala Ile Asp Tyr Leu Ser Pro
325 330 335

Lys Ile Ala Tyr Ser Gln Leu Ala Tyr Glu Asn Glu Leu Gln Gln Asn
340 345 350

Lys Pro Val Asn Ser Ile Pro Cys Leu Ile Leu Asn Gly Tyr Asn Pro
355 360 365

Ser Cys Asn Tyr Arg Asp Val Phe Lys Glu Ile Thr Asp Leu Leu Val
370 375 380

Pro Ala Glu Leu Thr Arg Ser Glu Thr Lys Tyr Trp Gly Asn His Val
385 390 395 400

Ile Leu Gln Ile Gln Lys Met Ile Asp Phe Tyr Lys Asn Gln Pro Leu
405 410 415

Asp Ile Lys Leu Ile Leu Val Val His Asn Leu Asp Gly Pro Ser Ile
420 425 430

Arg Lys Asn Thr Phe Gln Thr Met Leu Ser Phe Leu Ser Val Ile Arg
435 440 445

Gln Ile Ala Ile Val Ala Ser Thr Asp His Ile Tyr Ala Pro Leu Leu
450 455 460

Trp Asp Asn Met Lys Ala Gln Asn Tyr Asn Phe Val Phe His Asp Ile
465 470 475 480

Ser Asn Phe Glu Pro Ser Thr Val Glu Ser Thr Phe Gln Asp Val Met

485 490 495

Lys Met Gly Lys Ser Asp Thr Ser Ser Gly Ala Glu Gly Ala Lys Tyr
500 505 510

Val Leu Gln Ser Leu Thr Val Asn Ser Lys Lys Met Tyr Lys Leu Leu
515 520 525

Ile Glu Thr Gln Met Gln Asn Met Gly Asn Leu Ser Ala Asn Thr Gly
530 535 540

Pro Lys Arg Gly Thr Gln Arg Thr Gly Val Glu Leu Lys Leu Phe Asn
545 550 555 560

His Leu Cys Ala Ala Asp Phe Ile Ala Ser Asn Glu Ile Ala Leu Arg
565 570 575

Ser Met Leu Arg Glu Phe Ile Glu His Lys Met Ala Asn Ile Thr Lys
580 585 590

Asn Asn Ser Gly Met Glu Ile Ile Trp Val Pro Tyr Thr Tyr Ala Glu
595 600 605

Leu Glu Lys Leu Leu Lys Thr Val Leu Asn Thr Leu
610 615 620

<210> 60

<211> 600

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 133

<400> 60

Met Ser His Ser Asn Ala Leu Pro Asn Ser Pro Phe Arg Ser Pro Lys
1 5 10 15

Lys Gln Arg Met Glu Val Ile Gly Pro Leu Asn Ala Ser Arg Phe Ser
20 25 30

Phe Ser Pro Val Lys Thr Pro Pro His Gly Arg Ala Gly Leu Ser Ser
35 40 45

Pro Glu Lys Arg Leu Val Lys Asp Leu Asp Lys Ala Arg Lys Arg Ala
50 55 60

Asn Asn Ser Leu Tyr Asn Arg Leu Met Asp Glu Tyr Leu Asp Thr Asp
65 70 75 80

Asp Tyr Leu Asp Glu Gln Asp Arg Ile Leu Ala Asp Arg Ile Ile Lys
85 90 95

Gln Ser Arg Gly Glu Pro Asp Glu Val Asn Tyr Gly Ser Asp Val Glu
100 105 110

Leu Glu Ile Asp Leu Thr Gln Gln Arg Arg Thr Arg Arg Arg Glu Lys
115 120 125

Lys Val Val Tyr Ser Ser Asp Ser Ser Asn Glu Tyr Glu Asp Thr Gly
130 135 140

Met Pro Glu Glu Ser Ser Ser Glu Glu Glu Glu Ala Asp Asp Asp Asp
145 150 155 160

Gly Asn Val Glu Phe Val Tyr Gly Pro Pro Lys Glu Arg Lys Thr Ser
165 170 175

Leu Ser Ser Ser Pro Pro Thr Val Lys Pro Thr Val Arg Arg Thr Lys
180 185 190

Arg Gly Arg Pro Ser Lys Ser Glu Leu Val Leu Gly Gln Ile Lys Ser
195 200 205

Ile Phe His Gln Asp Asp Val Leu Phe Ser Thr Asp Arg Lys Thr Phe
210 215 220

Thr Pro Thr Lys Pro Thr Ala Ala Lys Lys Pro Val Ser Asn Tyr Leu
225 230 235 240

Thr Ser Ile Phe Asp Gln Asn Phe Asp Arg Ser Lys Val Pro Ser Leu
245 250 255

Ser Gly Ile Pro Lys Ser Thr Asn Thr His Glu Glu Lys Lys Thr Phe
260 265 270

Val Pro Leu Pro Ile Pro Thr Leu Asp Ala Asp Gly Asn Ile Thr Asp
275 280 285

Lys Glu Tyr Ile Ser Lys Tyr Phe Asp Gly Val Asp Pro Ala Lys Phe
290 295 300

Lys Glu Gly Arg Phe Val Asp Glu Lys Val Phe Tyr Leu Glu Gly Pro
305 310 315 320

Glu Gly Tyr Phe Glu Gln Gln Thr Thr Arg Val Lys Gln Ser Gly Asn
325 330 335

Ser Leu Thr Ala Leu Ala Pro Gln Ile Glu Tyr Lys Asp Phe Ala Arg
340 345 350

Leu Val Lys Leu Gly Asp Asn Leu Ser Phe Gln Arg Lys Arg His Leu
355 360 365

Phe Glu Leu His Lys Tyr Ile Tyr His Gln Trp Cys Phe Glu Met Ser
370 375 380

Gln Gly Phe Asn Leu Asn Phe Tyr Gly Val Gly Ser Lys Ile Asp Leu
385 390 395 400

Leu Arg Asp Phe Ala Thr Asn Tyr Phe Gly Ile Trp Trp Glu Asn Val

405 410 415

Val His Ala Asp Leu Pro Lys Val Leu Val Val Asn Gly Phe Asn Pro
420 425 430

Ser Ile Asn Ile Lys Lys Leu Ile Leu Glu Ile Ala Ser Ile Leu Leu
435 440 445

Pro Asn Glu Leu Tyr Pro Lys His Ile Ala Gly Thr Val Pro Phe Val
450 455 460

Val Asp Tyr Leu Asn Asn His Arg Leu Pro Cys Gly Ser Ile Gly Phe
465 470 475 480

His Lys Pro Lys Ile Leu Leu Ile Ile His Asn Leu Asp Gly Glu Val
485 490 495

Phe Arg Val Asp Lys Thr Gln Thr Leu Leu Ser Gln Leu Met Thr Leu
500 505 510

Pro Glu Val Trp Ala Met Ser Ser Thr Asp His Ile Asn Ala Ser Leu
515 520 525

Leu Trp Asp Leu Ser Lys Val Lys Asn Leu Asn Phe Ile Trp His Asn
530 535 540

Leu Thr Thr Tyr Ala Thr Tyr Gln Arg Glu Thr Ser Phe Arg Asp Val
545 550 555 560

Ile Ser Leu Gly Lys Ser Lys Lys Phe Val Gly Gly Leu Gly Ala Lys
565 570 575

Tyr Val Leu Arg Ser Leu Thr Asp Asn His Arg Asn Leu Tyr Arg Glu
580 585 590

Leu Leu Ile Ala Gln Leu Asp Lys
595 600

<210> 61

<211> 577

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: Q13416

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 134

<400> 61

Met Ser Lys Pro Glu Leu Lys Glu Asp Lys Met Leu Glu Val His Phe
1 5 10 15

Val Gly Asp Asp Asp Val Leu Asn His Ile Leu Asp Arg Glu Gly Gly
20 25 30

Ala Lys Leu Lys Lys Glu Arg Ala Gln Leu Leu Val Asn Pro Lys Lys
35 40 45

Ile Ile Lys Lys Pro Glu Tyr Asp Leu Glu Glu Asp Asp Gln Glu Val
50 55 60

Leu Lys Asp Gln Asn Tyr Val Glu Ile Met Gly Arg Asp Val Gln Glu
65 70 75 80

Ser Leu Lys Asn Gly Ser Ala Thr Gly Gly Gly Asn Lys Val Tyr Ser
85 90 95

Phe Gln Asn Arg Lys His Ser Glu Lys Met Ala Lys Leu Ala Ser Glu
100 105 110

Leu Ala Lys Thr Pro Gln Lys Ser Val Ser Phe Ser Leu Lys Asn Asp
115 120 125

Pro Glu Ile Thr Ile Asn Val Pro Gln Ser Ser Lys Gly His Ser Ala
130 135 140

Ser Asp Lys Val Gln Pro Lys Asn Asn Asp Lys Ser Glu Phe Leu Ser
145 150 155 160

Thr Ala Pro Arg Ser Leu Arg Lys Arg Leu Ile Val Pro Arg Ser His
165 170 175

Ser Asp Ser Glu Ser Glu Tyr Ser Ala Ser Asn Ser Glu Asp Asp Glu
180 185 190

Gly Val Ala Gln Glu His Glu Glu Asp Thr Asn Ala Val Ile Phe Ser
195 200 205

Gln Lys Ile Gln Ala Gln Asn Arg Val Val Ser Ala Pro Val Gly Lys
210 215 220

Glu Thr Pro Ser Lys Arg Met Lys Arg Asp Lys Thr Ser Asp Leu Val
225 230 235 240

Glu Glu Tyr Phe Glu Ala His Ser Ser Ser Lys Val Leu Thr Ser Asp
245 250 255

Arg Thr Leu Gln Lys Leu Lys Arg Ala Lys Leu Asp Gln Gln Thr Leu
260 265 270

Arg Asn Leu Leu Ser Lys Val Ser Pro Ser Phe Ser Ala Glu Leu Lys
275 280 285

Gln Leu Asn Gln Gln Tyr Glu Lys Leu Phe His Lys Trp Met Leu Gln
290 295 300

Leu His Leu Gly Phe Asn Ile Val Leu Tyr Gly Leu Gly Ser Lys Arg
305 310 315 320

Asp Leu Leu Glu Arg Phe Arg Thr Thr Met Leu Gln Asp Ser Ile His

325 330 335

Val Val Ile Asn Gly Phe Phe Pro Gly Ile Ser Val Lys Ser Val Leu
340 345 350Asn Ser Ile Thr Glu Glu Val Leu Asp His Met Gly Thr Phe Arg Ser
355 360 365Ile Leu Asp Gln Leu Asp Trp Ile Val Asn Lys Phe Lys Glu Asp Ser
370 375 380Ser Leu Glu Leu Phe Leu Leu Ile His Asn Leu Asp Ser Gln Met Leu
385 390 395 400Arg Gly Glu Lys Ser Gln Gln Ile Ile Gly Gln Leu Ser Ser Leu His
405 410 415Asn Ile Tyr Leu Ile Ala Ser Ile Asp His Leu Asn Ala Pro Leu Met
420 425 430Trp Asp His Ala Lys Gln Ser Leu Phe Asn Trp Leu Trp Tyr Glu Thr
435 440 445Thr Thr Tyr Ser Pro Tyr Thr Glu Glu Thr Ser Tyr Glu Asn Ser Leu
450 455 460Leu Val Lys Gln Ser Gly Ser Leu Pro Leu Ser Ser Leu Thr His Val
465 470 475 480Leu Arg Ser Leu Thr Pro Asn Ala Arg Gly Ile Phe Arg Leu Leu Ile
485 490 495Lys Tyr Gln Leu Asp Asn Gln Asp Asn Pro Ser Tyr Ile Gly Leu Ser
500 505 510Phe Gln Asp Phe Tyr Gln Gln Cys Arg Glu Ala Phe Leu Val Asn Ser
515 520 525

Asp Leu Thr Leu Arg Ala Gln Leu Thr Glu Phe Arg Asp His Lys Leu
530 535 540

Ile Arg Thr Lys Lys Gly Thr Asp Gly Val Glu Tyr Leu Leu Ile Pro
545 550 555 560

Val Asp Asn Gly Thr Leu Thr Asp Phe Leu Glu Lys Glu Glu Glu
565 570 575

Ala

<210> 62

<211> 385

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 135

<400> 62

Met Ser Ser Val Asn Ala Asn Gly Gly Tyr Thr Lys Pro Gln Lys Tyr
1 5 10 15

Val Pro Gly Pro Gly Asp Pro Glu Leu Pro Pro Gln Leu Ser Glu Phe
20 25 30

Lys Asp Lys Thr Ser Asp Glu Ile Leu Lys Glu Met Asn Arg Met Pro
35 40 45

Phe Phe Met Thr Lys Leu Asp Glu Thr Asp Gly Ala Gly Gly Glu Asn
50 55 60

Val Glu Leu Glu Ala Leu Lys Ala Leu Ala Tyr Glu Gly Glu Pro His
65 70 75 80

Glu Ile Ala Glu Asn Phe Lys Lys Gln Gly Asn Glu Leu Tyr Lys Ala
85 90 95

Lys Arg Phe Lys Asp Ala Arg Glu Leu Tyr Ser Lys Gly Leu Ala Val
100 105 110

Glu Cys Glu Asp Lys Ser Ile Asn Glu Ser Leu Tyr Ala Asn Arg Ala
115 120 125

Ala Cys Glu Leu Glu Leu Lys Asn Tyr Arg Arg Cys Ile Glu Asp Cys
130 135 140

Ser Lys Ala Leu Thr Ile Asn Pro Lys Asn Val Lys Cys Tyr Tyr Arg
145 150 155 160

Thr Ser Lys Ala Phe Phe Gln Leu Asn Lys Leu Glu Glu Ala Lys Ser
165 170 175

Ala Ala Thr Phe Ala Asn Gln Arg Ile Asp Pro Glu Asn Lys Ser Ile
180 185 190

Leu Asn Met Leu Ser Val Ile Asp Arg Lys Glu Gln Glu Leu Lys Ala
195 200 205

Lys Glu Glu Lys Gln Gln Arg Glu Ala Gln Glu Arg Glu Asn Lys Lys
210 215 220

Ile Met Leu Glu Ser Ala Met Thr Leu Arg Asn Ile Thr Asn Ile Lys
225 230 235 240

Thr His Ser Pro Val Glu Leu Leu Asn Glu Gly Lys Ile Arg Leu Glu
245 250 255

Asp Pro Met Asp Phe Glu Ser Gln Leu Ile Tyr Pro Ala Leu Ile Met
260 265 270

Tyr Pro Thr Gln Asp Glu Phe Asp Phe Val Gly Glu Val Ser Glu Leu

275 280 285

Thr Thr Val Gln Glu Leu Val Asp Leu Val Leu Glu Gly Pro Gln Glu
290 295 300

Arg Phe Lys Lys Glu Gly Lys Glu Asn Phe Thr Pro Lys Lys Val Leu
305 310 315 320

Val Phe Met Glu Thr Lys Ala Gly Gly Leu Ile Lys Ala Gly Lys Lys
325 330 335

Leu Thr Phe His Asp Ile Leu Lys Lys Glu Ser Pro Asp Val Pro Leu
340 345 350

Phe Asp Asn Ala Leu Lys Ile Tyr Ile Val Pro Lys Val Glu Ser Glu
355 360 365

Gly Trp Ile Ser Lys Trp Asp Lys Gln Lys Ala Leu Glu Arg Arg Ser
370 375 380

Val
385

<210> 63
<211> 300
<212> PRT
<213> Candida albicans

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 136

<400> 63

Met Ser Lys Ile Glu Pro Val Thr Glu Lys Glu Glu Glu Tyr Val Ser
1 5 10 15

Glu Trp Asp Arg Arg Arg Tyr Val Pro Lys Ala Gly Glu Pro Glu Leu
20 25 30

Pro Pro Gln Leu Ser Glu Phe Ser Asn Lys Thr Thr Asp Glu Val Ile
35 40 45

Glu Glu Leu Asn Arg Leu Pro Phe Phe Met Thr Leu Asp Glu Thr Asp
50 55 60

Gly Asp Gly Gly Glu Asn Val Asn Leu Glu Ala Leu Lys Ser Leu Ala
65 70 75 80

Tyr Glu Gly Asp Pro Asp Glu Ile Ala Ser Asn Phe Lys Asn Gln Gly
85 90 95

Asn Asn Cys Tyr Lys Phe Lys Lys Tyr Lys Asp Ala Ile Ile Phe Tyr
100 105 110

Thr Lys Gly Leu Glu Val Asn Cys Asp Val Asp Ala Ile Asn Ser Ala
115 120 125

Leu Tyr Leu Asn Arg Ala Ala Cys Asn Leu Glu Leu Lys Asn Tyr Arg
130 135 140

Arg Cys Ile Glu Asp Cys Lys Lys Val Leu Met Leu Asp Glu Lys Asn
145 150 155 160

Ile Lys Ala Cys Phe Arg Ser Gly Lys Ala Phe Phe Ala Ile Glu Lys
165 170 175

Tyr Asp Glu Ala Ile Lys Val Leu Glu Tyr Gly Leu Asn Ile Glu Pro
180 185 190

Glu Asn Lys Asp Leu Gln Lys Leu Leu Gln Gln Val Gln Lys Arg Gln
195 200 205

Glu Thr Leu Ala Gln Ile Lys Ala Lys Lys Ala Gln Glu Glu Glu Gln
210 215 220

Glu Arg Leu Lys Asn Ile Val Leu Glu Asn Ser Ile Lys Leu Arg His
225 230 235 240

Ile Glu Ile Val Lys Ser Ser Ser Pro Pro Glu Val Leu Lys Thr Ala
 245 250 255

Lys Ile Arg Leu Glu Asp Pro Lys Asp Tyr Gln Ser Gln Leu Ile Phe
 260 265 270

Pro Ala Met Ile Leu Tyr Pro Thr Thr Asp Glu Phe Asp Phe Ile Ala
 275 280 285

Glu Ile Ser Glu Leu Thr Thr Pro Leu Glu Leu Leu
 290 295 300

<210> 64

<211> 356

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: NP_004614

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 137

<400> 64

Met Glu Gln Pro Gly Gln Asp Pro Thr Ser Asp Asp Val Met Asp Ser
1 5 10 15

Phe Leu Glu Lys Phe Gln Ser Gln Pro Tyr Arg Gly Gly Phe His Glu
 20 25 30

Asp Gln Trp Glu Lys Glu Phe Glu Lys Val Pro Leu Phe Met Ser Arg
 35 40 45

Ala Pro Ser Glu Ile Asp Pro Arg Glu Asn Pro Asp Leu Ala Cys Leu
50 55 60

Gln Ser Ile Ile Phe Asp Glu Glu Arg Ser Pro Glu Glu Gln Ala Lys
65 70 75 80

Thr Tyr Lys Asp Glu Gly Asn Asp Tyr Phe Lys Glu Lys Asp Tyr Lys
85 90 95

Lys Ala Val Ile Ser Tyr Thr Glu Gly Leu Lys Lys Lys Cys Ala Asp
100 105 110

Pro Asp Leu Asn Ala Val Leu Tyr Thr Asn Arg Ala Ala Ala Gln Tyr
115 120 125

Tyr Leu Gly Asn Phe Arg Ser Ala Leu Asn Asp Val Thr Ala Ala Arg
130 135 140

Lys Leu Lys Pro Cys His Leu Lys Ala Ile Ile Arg Gly Ala Leu Cys
145 150 155 160

His Leu Glu Leu Ile His Phe Ala Glu Ala Val Asn Trp Cys Asp Glu
165 170 175

Gly Leu Gln Ile Asp Ala Lys Glu Lys Lys Leu Leu Glu Met Arg Ala
180 185 190

Lys Ala Asp Lys Leu Lys Arg Ile Glu Gln Arg Asp Val Arg Lys Ala
195 200 205

Asn Leu Lys Glu Lys Lys Glu Arg Asn Gln Asn Glu Ala Leu Leu Gln
210 215 220

Ala Ile Lys Ala Arg Asn Ile Arg Leu Ser Glu Ala Ala Cys Glu Asp
225 230 235 240

Glu Asp Ser Ala Ser Glu Gly Leu Gly Glu Leu Phe Leu Asp Gly Leu

245 250 255

Ser Thr Glu Asn Pro His Gly Ala Arg Leu Ser Leu Asp Gly Gln Gly
260 265 270

Arg Leu Ser Trp Pro Val Leu Phe Leu Tyr Pro Glu Tyr Ala Gln Ser
275 280 285

Asp Phe Ile Ser Ala Phe His Glu Asp Ser Arg Phe Ile Asp His Leu
290 295 300

Met Val Met Phe Gly Glu Thr Pro Ser Trp Asp Leu Glu Gln Lys Tyr
305 310 315 320

Cys Leu Ile Ile Trp Arg Ser Thr Leu Arg Met Arg Thr Gly Gln Asn
325 330 335

Tyr Thr Gly Cys Leu Pro Arg Ala Pro Cys Tyr Arg Phe Tyr Ser Thr
340 345 350

Arg Gly Thr Leu
355

<210> 65
<211> 167
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> Corresponds to SEQ ID NO: 138

<400> 65

Met Ser Thr Ile Pro Ser Glu Ile Ile Asn Trp Thr Ile Leu Asn Glu
1 5 10 15

Ile Ile Ser Met Asp Asp Asp Asp Ser Asp Phe Ser Lys Gly Leu Ile
20 25 30

Ile Gln Phe Ile Asp Gln Ala Gln Thr Thr Phe Ala Gln Met Gln Arg
35 40 45

Gln Leu Asp Gly Glu Lys Asn Leu Thr Glu Leu Asp Asn Leu Gly His
50 55 60

Phe Leu Lys Gly Ser Ser Ala Ala Leu Gly Leu Gln Arg Ile Ala Trp
65 70 75 80

Val Cys Glu Arg Ile Gln Asn Leu Gly Arg Lys Met Glu His Phe Phe
85 90 95

Pro Asn Lys Thr Glu Leu Val Asn Thr Leu Ser Asp Lys Ser Ile Ile
100 105 110

Asn Gly Ile Asn Ile Asp Glu Asp Asp Glu Glu Ile Lys Ile Gln Val
115 120 125

Asp Asp Lys Asp Glu Asn Ser Ile Tyr Leu Ile Leu Ile Ala Lys Ala
130 135 140

Leu Asn Gln Ser Arg Leu Glu Phe Lys Leu Ala Arg Ile Glu Leu Ser
145 150 155 160

Lys Tyr Tyr Asn Thr Asn Leu
165

<210> 66

<211> 184

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 139

<400> 66

Met Ser Glu Asp Lys Leu Gln Lys Leu Gln Asp Ser Gly Leu Val Asp
 1 5 10 15

Trp Ala Val Phe Ser Glu Ile Val Thr Met Asp Glu Asp Glu Glu Gly
 20 25 30

Phe Ser Lys Ser Leu Val Glu Val Phe Val Ser Gln Val Glu Glu Thr
 35 40 45

Phe Glu Glu Ile Asp Lys Tyr Leu Lys Glu Lys Asn Leu Glu Lys Leu
 50 55 60

Ser Ser Ser Gly His Phe Leu Lys Gly Ser Ala Ala Ala Leu Gly Leu
 65 70 75 80

Thr Lys Ile Ser Asn Gln Cys Glu Arg Ile Gln Asn Tyr Gly His Lys
 85 90 95

Ile Asn Phe Asp Asn Phe Gln Leu Glu Asp Ile Lys Thr Lys Gly Asp
 100 105 110

Ser Ala Val Ser Ala Glu Asn Val Ala Val Asn Asp Gly Glu Thr Asn
 115 120 125

Pro Glu Asn Gly Ser Asn Gly Asn Glu Thr Ser Asn Asn Lys Thr Asn
 130 135 140

Thr Ser Asn Ile Pro Asp Glu Ser Ser Asp Asp Phe Trp Ile Ala Leu
 145 150 155 160

Ile Glu Asp Ala Leu Ala Lys Ala Arg Asp Gly Phe Asp Gln Ser Arg
 165 170 175

Arg Ala Leu Asp Glu Tyr Tyr Glu
 180

<210> 67

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: CAA78727

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 140

<400> 67

Thr Asp Lys Leu Ser Asn Met Gln Lys Asp Leu Glu Asn Ser Asn Ala
1 5 10 15

Lys Leu Gln Glu Lys Ile Gln Glu Leu Lys Ala Asn Glu His Gln Leu
20 25 30

Ile Thr Leu Lys Lys Asp Val Asn Glu Thr Gln Lys Lys Val Ser Glu
35 40 45

Met Glu Gln Leu Lys Lys Gln Ile Lys Asp Gln Ser Leu Thr Leu Ser
50 55 60

Lys Leu Glu Ile Glu Asn Leu Asn Leu Ala Gln Glu Leu His Glu Asn
65 70 75 80

Leu Glu Glu Met Lys Ser Val Met Lys Glu Arg Asp Asn Leu Arg Arg
85 90 95

Val Glu Glu Thr Leu Lys Leu Glu Arg Asp Gln Leu Lys Glu Ser Leu
100 105 110

Gln Glu Thr Lys Ala Arg Asp Leu Glu Ile Gln Gln Glu Leu Lys Thr
115 120 125

Ala Arg Met Leu Ser Lys Glu His Lys Glu Thr Val Asp Lys Leu Arg

130 135 140

Glu Lys Ile Ser Glu Lys Thr Ile Gln Ile Ser Asp Ile Gln Lys Asp
145 150 155 160

Leu Asp Lys Ser Lys Asp Glu Leu Gln Lys Lys Ile Gln Glu Leu Gln
 165 170 175

Lys Lys Glu Leu Gln Leu Leu Arg Val Lys Glu Asp Val Asn Met Ser
 180 185 190

His Lys Lys Ile Asn Glu Met Glu Gln Leu Lys Lys Gln Phe Glu Pro
 195 200 205

Asn Tyr Leu Cys Lys Cys Glu Met Asp Asn Phe Gln Leu Thr Lys Lys
 210 215 220

Leu His Glu Ser Leu Glu Glu Ile Arg Ile Val Ala Lys Glu Arg Asp
225 230 235 240

<210> 68

<211> 93

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 141

<400> 68

Met Ser Phe Leu Gly Phe Gly Gly Gly Gln Pro Gln Leu Ser Ser Gln
1 5 10 15

Gln Lys Ile Gln Ala Ala Glu Ala Glu Leu Asp Leu Val Thr Asp Met
 20 25 30

Phe Asn Lys Leu Val Asn Asn Cys Tyr Lys Lys Cys Ile Asn Thr Ser
 35 40 45

Tyr Ser Glu Gly Glu Leu Asn Lys Asn Glu Ser Ser Cys Leu Asp Arg
 50 55 60

Cys Val Ala Lys Tyr Phe Glu Thr Asn Val Gln Val Gly Glu Asn Met
 65 70 75 80

Gln Lys Met Gly Gln Ser Phe Asn Ala Ala Gly Lys Phe
 85 90

<210> 69

<211> 91

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 142

<400> 69

Met Phe Gly Leu Gly Gly Thr Thr Pro Gln Ile Ser Ser Gln Gln Lys
 1 5 10 15

Leu Gln Ala Ala Glu Ala Glu Leu Asp Met Val Thr Gly Met Phe Asn
 20 25 30

Ala Leu Val Ser Gln Cys His Thr Lys Cys Ile Asn Lys Ser Tyr Asn
 35 40 45

Glu Ala Asp Ile Ser Lys Gln Glu Ser Leu Cys Leu Asp Arg Cys Val
 50 55 60

Ala Lys Tyr Phe Glu Thr Asn Val Gln Val Gly Glu Asn Met Gln Lys
 65 70 75 80

Leu Gly Gln Ser Gly Gln Phe Met Gly Arg Arg
 85 90

<210> 70

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> human genbank accession #: NP_036588

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 143

<400> 70

Met Asp Pro Leu Arg Ala Gln Gln Leu Ala Ala Glu Leu Glu Val Glu
1 5 10 15

Met Met Ala Asp Met Tyr Asn Arg Met Thr Ser Ala Cys His Arg Lys
 20 25 30

Cys Val Pro Pro His Tyr Lys Glu Ala Glu Leu Ser Lys Gly Glu Ser
 35 40 45

Val Cys Leu Asp Arg Cys Val Ser Lys Tyr Leu Asp Ile His Glu Arg
 50 55 60

Met Gly Lys Lys Leu Thr Glu Leu Ser Met Gln Asp Glu Glu Leu Met
65 70 75 80

Lys Arg Val Gln Gln Ser Ser Gly Pro Ala
 85 90

<210> 71

<211> 600

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 144

<400> 71

Met Thr Thr Glu Asp Pro Asp Ser Asn His Leu Ser Ser Glu Thr Gly
1 5 10 15

Ile Lys Leu Ala Leu Asp Pro Asn Leu Ile Thr Leu Ala Leu Ser Ser
20 25 30

Asn Pro Asn Ser Ser Leu His Ser Pro Thr Ser Asp Glu Pro Val Pro
35 40 45

Glu Ser Ala Gly Lys Ala Asp Thr Ser Ile Arg Leu Glu Gly Asp Glu
50 55 60

Leu Glu Asn Lys Thr Lys Lys Asp Asn Asp Lys Asn Leu Lys Phe Leu
65 70 75 80

Lys Asn Lys Asp Ser Leu Val Ser Asn Pro His Glu Ile Tyr Gly Ser
85 90 95

Met Pro Leu Glu Gln Leu Ile Pro Ile Ile Leu Arg Gln Arg Gly Pro
100 105 110

Gly Phe Lys Phe Val Asp Leu Asn Glu Lys Glu Leu Gln Asn Glu Ile
115 120 125

Lys Gln Leu Gly Ser Asp Ser Ser Asp Gly His Asn Ser Glu Lys Lys
130 135 140

Asp Thr Asp Gly Ala Asp Glu Asn Val Gln Ile Gly Glu Asp Phe Met
145 150 155 160

Glu Val Asp Tyr Glu Asp Lys Asp Asn Pro Val Asp Ser Arg Asn Glu
165 170 175

Thr Asp His Lys Thr Asn Glu Asn Gly Glu Thr Asp Asp Asn Ile Glu
180 185 190

Thr Val Met Thr Gln Glu Gln Phe Val Lys Arg Arg Arg Asp Met Leu
195 200 205

Glu His Ile Asn Leu Ala Met Asn Glu Ser Ser Leu Ala Leu Glu Phe
210 215 220

Val Ser Leu Leu Leu Ser Ser Val Lys Glu Ser Thr Gly Met Ser Ser
225 230 235 240

Met Ser Pro Phe Leu Arg Lys Val Val Lys Pro Ser Ser Leu Asn Ser
245 250 255

Asp Lys Ile Pro Tyr Val Ala Pro Thr Lys Lys Glu Tyr Ile Glu Leu
260 265 270

Asp Ile Leu Asn Lys Gly Trp Lys Leu Gln Ser Leu Asn Glu Ser Lys
275 280 285

Asp Leu Leu Arg Ala Ser Phe Asn Lys Leu Ser Ser Ile Leu Gln Asn
290 295 300

Glu His Asp Tyr Trp Asn Lys Ile Met Gln Ser Ile Ser Asn Lys Asp
305 310 315 320

Val Ile Phe Lys Ile Arg Asp Arg Thr Ser Gly Gln Lys Leu Leu Ala
325 330 335

Ile Lys Tyr Gly Tyr Glu Asp Ser Gly Ser Thr Tyr Lys His Asp Arg
340 345 350

Gly Ile Ala Asn Ile Arg Asn Asn Ile Glu Ser Gln Asn Leu Asp Leu
355 360 365

Ile Pro His Ser Ser Ser Val Phe Lys Gly Thr Asp Phe Val His Ser
370 375 380

Val Lys Lys Phe Leu Arg Val Arg Ile Phe Thr Lys Ile Glu Ser Glu
385 390 395 400

Asp Asp Tyr Ile Leu Ser Gly Glu Ser Val Met Asp Arg Asp Ser Glu
405 410 415

Ser Glu Glu Ala Glu Thr Lys Asp Ile Arg Lys Gln Ile Gln Leu Leu
420 425 430

Lys Lys Ile Ile Phe Glu Lys Glu Leu Met Tyr Gln Ile Lys Lys Glu
435 440 445

Cys Ala Leu Leu Ile Ser Tyr Gly Val Ser Ile Glu Asn Glu Asn Lys
450 455 460

Val Ile Ile Glu Leu Pro Asn Glu Lys Phe Glu Ile Glu Leu Leu Ser
465 470 475 480

Leu Asp Asp Asp Ser Ile Val Asn His Glu Gln Asp Leu Pro Lys Ile
485 490 495

Asn Asp Lys Arg Ala Asn Leu Met Leu Val Met Leu Arg Leu Leu Leu
500 505 510

Val Val Ile Phe Lys Lys Thr Leu Arg Ser Arg Ile Ser Ser Pro His
515 520 525

Gly Leu Ile Asn Leu Asn Val Asp Asp Asp Ile Leu Ile Ile Arg Pro
530 535 540

Ile Leu Gly Lys Val Arg Phe Ala Asn Tyr Lys Leu Leu Leu Lys Lys
545 550 555 560

Ile Ile Lys Asp Tyr Val Leu Asp Ile Val Pro Gly Ser Ser Ile Thr
565 570 575

Glu Thr Glu Val Glu Arg Glu Gln Pro Gln Glu Asn Lys Asn Ile Asp

580 585 590

Asp Glu Asn Ile Thr Lys Leu Asn
595 600

<210> 72

<211> 587

<212> PRT

<213> Candida albicans

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 145

<400> 72

Met Val Glu Lys Gln Phe Asn Ile Asp Leu Glu Leu Asn Asp Thr Gly
1 5 10 15

His Ile Asp Pro Phe Leu Gln Asp Glu Tyr Val Cys Phe Leu Thr Leu
20 25 30

Leu Val Phe Leu Val Leu Phe Phe Ser Leu Leu Thr Leu Pro Arg Asp
35 40 45

Lys Leu Lys Leu Glu Glu Leu Ile Pro Arg Ile Phe Glu Arg Lys Ser
50 55 60

Phe Leu Asn Val Thr Glu Asp Ser Leu Arg Lys Glu Ile Asp Asn Ser
65 70 75 80

Leu Lys Ile Ser Glu Glu Asp Ala Leu Asp Thr Glu Glu Ser Arg Glu
85 90 95

Asp Thr Val Glu Ala Asp Gln Gln Glu Val Phe Asn Lys His Lys Phe
100 105 110

Glu Leu Ser Lys Asn Ile Asn Asn Ala Leu Asn Glu Thr Gln Leu Ser
115 120 125

Leu Asp Phe Val Ser Leu Leu Ile Ser Ser Val Lys Pro Ser Leu Ala
130 135 140

Lys Ser Thr Ile Ser Pro His Leu Ser Lys Phe Val Lys Pro Thr Ser
145 150 155 160

Leu Asn Ser Asp Arg Leu Gly Gln Asp Ser Asn Asp Asn Gln Glu Ser
165 170 175

Lys Ala Thr Asp Ser Phe Gly Gln Gly Trp Lys Leu Glu Ser Leu Gly
180 185 190

Lys Ile Thr Asp Leu Phe Arg Glu Ala Ser Thr Asn Leu Asn Asp Gln
195 200 205

Val Ile Lys Glu Arg Arg Tyr Trp Asn Met Ile Asn Leu Val Leu Ala
210 215 220

Asn Asp Glu Val Leu Phe Arg Met Arg Asp Pro Gln Asn Asn Ala Arg
225 230 235 240

Ala Ile Gly Val Lys Tyr Gly Tyr Gly Asp Ser Gly Ser Asn Phe His
245 250 255

Asp Gln Gly Leu Ala Leu Leu Arg Lys Asp Asn Gln Thr Gly Glu Ile
260 265 270

Ser Phe His Pro Ile Ser Ser Ile Asn Asn Ala Lys Ile Val Glu Lys
275 280 285

Val Ser Arg Phe Ile Arg Val Lys Ile Leu Ser Gln Ile Asp Gly Asp
290 295 300

Tyr Met Leu Thr Gly Gln Ser Ile Phe Asn Phe Asp Phe Glu Lys Ser
305 310 315 320

Lys Gln Ser Ile Ile Asn Asp Ile Glu Lys Ala Arg Phe Phe Leu Phe
325 330 335

Glu Glu Asp Leu Phe His Gln Leu Ile Arg Glu Ala Lys Leu Leu Val
340 345 350

Asn Tyr Asn Val Ser Ile Ile Ser Asn Lys Ile Ile Ile Glu Ile Asn
355 360 365

Asn Ile Ile Ile Glu Ile Glu Ser Ile Val Tyr Asp Glu Leu Asn Glu
370 375 380

Glu Glu Leu Glu Asn Tyr Tyr Gln Asn Val Asn Glu Tyr Ser Thr Leu
385 390 395 400

His Asn Lys Lys Cys Gln Leu Ile Leu Asn Tyr Leu Lys Leu Met Leu
405 410 415

Cys Cys Tyr Tyr Lys Tyr Asn Leu Lys Leu Lys Gln Lys Val Pro Thr
420 425 430

Ala Leu Thr Lys Trp Lys Gln Ser Asn Ser His Pro Leu Ile Leu Arg
435 440 445

Pro Leu Val Gly Asn Met Arg His Glu Leu Asn Leu Leu Asn Met Lys
450 455 460

Ser Val Leu Asp Arg Leu Met His Ala His Glu Ser Glu Leu Ser Tyr
465 470 475 480

Ser Lys Leu Asp Val Glu Lys Phe Ile Asn Leu Ala Thr Arg Ser Lys
485 490 495

Lys Gln Asn Pro Phe Gln Lys Ser Ile Glu Lys Pro Ile Ser Lys Phe
500 505 510

His Leu Val Leu Cys Asn Lys Thr Ser Asn Met Leu Asp Val Asn Ile

515 520 525

Gln Leu Asp Asn Tyr Glu Leu Phe Val Asn Leu Ile Ile Asn Met Thr
530 535 540

Ile Ile Arg Phe Glu Thr Glu His Asp Phe Lys Asn Asn Val Asn Gly
545 550 555 560

Ile Asn Val Leu Gln Leu Gly Phe Ser Asp Phe Asn Glu Ile Glu Glu
565 570 575

Cys Leu Asp Trp Ser Ile Gln Asn Phe Val Leu
580 585

<210> 73

<211> 888

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Corresponds to SEQ ID NO: 146

<400> 73

Met Tyr Gly Ser Ala Arg Ser Val Gly Lys Val Glu Pro Ser Ser Gln
1 5 10 15

Ser Pro Gly Arg Ser Pro Arg Leu Pro Arg Ser Pro Arg Leu Gly His
20 25 30

Arg Arg Thr Asn Ser Thr Gly Gly Ser Ser Gly Ser Ser Val Gly Gly
35 40 45

Gly Ser Gly Lys Thr Leu Ser Met Glu Asn Ile Gln Ser Leu Asn Ala
50 55 60

Ala Tyr Ala Thr Ser Gly Pro Met Tyr Leu Ser Asp His Glu Asn Val
65 70 75 80

Gly Ser Glu Thr Pro Lys Ser Thr Met Thr Leu Gly Arg Ser Gly Gly
 85 90 95

Arg Leu Pro Tyr Gly Val Arg Met Thr Ala Met Gly Ser Ser Pro Asn
 100 105 110

Ile Ala Ser Ser Gly Val Ala Ser Asp Thr Ile Ala Phe Gly Glu His
 115 120 125

His Leu Pro Pro Val Ser Met Ala Ser Thr Val Pro His Ser Leu Arg
 130 135 140

Gln Ala Arg Asp Asn Thr Ile Met Asp Leu Gln Thr Gln Leu Lys Glu
 145 150 155 160

Val Leu Arg Glu Asn Asp Leu Leu Arg Lys Asp Val Glu Val Lys Glu
 165 170 175

Ser Lys Leu Ser Ser Ser Met Asn Ser Ile Lys Thr Phe Trp Ser Pro
 180 185 190

Glu Leu Lys Lys Glu Arg Ala Leu Arg Lys Asp Glu Ala Ser Lys Ile
 195 200 205

Thr Ile Trp Lys Glu Gln Tyr Arg Val Val Gln Glu Glu Asn Gln His
 210 215 220

Met Gln Met Thr Ile Gln Ala Leu Gln Asp Glu Leu Arg Ile Gln Arg
 225 230 235 240

Asp Leu Asn Gln Leu Phe Gln Gln Asp Ser Ser Ser Arg Thr Gly Glu
 245 250 255

Pro Cys Val Ala Glu Leu Thr Glu Glu Asn Phe Gln Arg Leu His Ala
 260 265 270

Glu His Glu Arg Gln Ala Lys Glu Leu Phe Leu Leu Arg Lys Thr Leu
275 280 285

Glu Glu Met Glu Leu Arg Ile Glu Thr Gln Lys Gln Thr Leu Asn Ala
290 295 300

Arg Asp Glu Ser Ile Lys Lys Leu Leu Glu Met Leu Gln Ser Lys Gly
305 310 315 320

Leu Ser Ala Lys Ala Thr Glu Glu Asp His Glu Arg Thr Arg Arg Leu
325 330 335

Ala Glu Ala Glu Met His Val His His Leu Glu Ser Leu Leu Glu Gln
340 345 350

Lys Glu Lys Glu Asn Ser Met Leu Arg Glu Glu Met His Arg Arg Phe
355 360 365

Glu Asn Ala Pro Asp Ser Ala Lys Thr Lys Ala Leu Gln Thr Val Ile
370 375 380

Glu Met Lys Asp Ser Lys Ile Ser Ser Met Glu Arg Gly Leu Arg Asp
385 390 395 400

Leu Glu Glu Glu Ile Gln Met Leu Lys Ser Asn Gly Ala Leu Ser Thr
405 410 415

Glu Glu Arg Glu Glu Glu Met Lys Gln Met Glu Val Tyr Arg Ser His
420 425 430

Ser Lys Phe Met Lys Asn Lys Ile Gly Gln Val Lys Gln Glu Leu Ser
435 440 445

Arg Lys Asp Thr Glu Leu Leu Ala Leu Gln Thr Lys Leu Glu Thr Leu
450 455 460

Thr Asn Gln Phe Ser Asp Ser Lys Gln His Ile Glu Val Leu Lys Glu

465 470 475 480

Ser Leu Thr Ala Lys Glu Gln Arg Ala Ala Ile Leu Gln Thr Glu Val
 485 490 495

Asp Ala Leu Arg Leu Arg Leu Glu Glu Lys Glu Thr Met Leu Asn Lys
 500 505 510

Lys Thr Lys Gln Ile Gln Asp Met Ala Glu Glu Lys Gly Thr Gln Ala
 515 520 525

Gly Glu Ile His Asp Leu Lys Asp Met Leu Asp Val Lys Glu Arg Lys
 530 535 540

Val Asn Val Leu Gln Lys Lys Ile Glu Asn Leu Gln Glu Gln Leu Arg
545 550 555 560

Asp Lys Glu Lys Gln Met Ser Ser Leu Lys Glu Arg Val Lys Ser Leu
 565 570 575

Gln Ala Asp Thr Thr Asn Thr Asp Thr Ala Leu Thr Thr Leu Glu Glu
 580 585 590

Ala Leu Ala Glu Lys Glu Arg Thr Ile Glu Arg Leu Lys Glu Gln Arg
 595 600 605

Asp Arg Asp Glu Arg Glu Lys Gln Glu Glu Ile Asp Asn Tyr Lys Lys
 610 615 620

Asp Leu Lys Asp Leu Lys Glu Lys Val Ser Leu Leu Gln Gly Asp Leu
625 630 635 640

Ser Glu Lys Glu Ala Ser Leu Leu Asp Leu Lys Glu His Ala Ser Ser
 645 650 655

Leu Ala Ser Ser Asp Glu Ser Ser Lys Ala Gln Ala Glu Val Asp Arg
 660 665 670

Leu Leu Glu Ile Leu Lys Glu Val Glu Asn Glu Lys Asn Asp Lys Asp
675 680 685

Lys Lys Ile Ala Glu Leu Glu Ser Leu Thr Ser Arg Gln Val Lys Asp
690 695 700

Gln Asn Lys Lys Val Ala Asn Leu Lys His Lys Glu Gln Val Glu Lys
705 710 715 720

Lys Lys Ser Ala Gln Met Leu Glu Glu Ala Arg Arg Arg Glu Asp Asn
725 730 735

Leu Asn Asp Ser Ser Gln Gln Leu Gln Val Glu Glu Leu Leu Met Ala
740 745 750

Met Glu Lys Val Lys Gln Glu Leu Glu Ser Met Lys Ala Lys Leu Ser
755 760 765

Ser Thr Gln Gln Ser Leu Ala Glu Lys Glu Thr His Leu Thr Asn Leu
770 775 780

Arg Ala Glu Arg Arg Lys His Leu Glu Glu Val Leu Glu Met Lys Gln
785 790 795 800

Glu Ala Leu Leu Ala Ala Ile Ser Glu Lys Asp Ala Asn Ile Ala Leu
805 810 815

Leu Glu Leu Ser Ser Ser Lys Lys Lys Thr Gln Glu Glu Val Ala Ala
820 825 830

Leu Lys Arg Glu Lys Asp Arg Leu Val Gln Gln Leu Lys Gln Gln Thr
835 840 845

Gln Asn Arg Met Lys Leu Met Ala Asp Asn Tyr Glu Asp Asp His Phe
850 855 860

Lys Ser Ser His Ser Asn Gln Thr Asn His Lys Pro Ser Pro Asp Gln
 865 870 875 880

Asp Glu Glu Glu Gly Ile Trp Ala
 885

<210> 74

<211> 900

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number:CAA96279.1

<400> 74

atgagtggaa tgalagaaaa tgggttacag ctatcggaca atgctaaaac cttacatagc 60

cagatgatgt cgaaaggaat aggcgcatta ttacacagc aagaactcca aaaacaaatg 120

ggaatcgggt cgftaacaga ctfgatgtcc attgtacagg aattgctaga caagaacttg 180

atcaaattag taaaacaaaa cgacgaatta aaattcaag gtgtcttaga atctgaggcg 240

caaaagaaag ccaccatgtc ggctgaagag gcactggtat attcttatat cgaggctagc 300

ggtagagaag ggatatgttc caagactatc aaggcaagaa ccaatctcca tcagcatgta 360

gttcttaaat gcttgaagag tttagaatcc caagatacg tgaagagtgt taagagtgt 420

aagtttccca caaggaaaat ctacatgttg tacagcttac aacctctgt ggacatcaca 480

ggagggtccat gggtcacaga tggagagctg gatatagaat ttatcaatag tttattgact 540

attgtttgga gggtcatatc agagaacacc ttcctaatag gcttcaagaa ttcgaaaat 600

ggacccaaaa aaaacgtctt ttatgtcca aacgtaaaaa attactctac cacacaagaa 660

attttggaat ttattacagc ggcacaagtg gccaatgtcg agttaacccc ttcaaatatc 720

agatctttgt gtgaagtctt agtgtacgac gacaagctgg aaaaagtcac gcatgactgc 780

tatagagtga ccttagagag cattctacaa atgaaccaag gtgaggcgga gccggaggca 840

ggtaataagg ctttgaggga tgaagaagaa ttttccatct ttaactactt caagatgttt 900

<210> 75

<211> 993

<212> DNA

<213> *Candida albicans*

<400> 75

```

atgagtgaga tgttagtattc agataaagca cgtcatcttt atacaaagat gagggagtat   60
ccaacttcca aactttttga tcaagatgaa ttacaaacac tatttgatat taaaaaggga   120
tcagaattaa tggaatattt acaagaatta gtcaatggta aatatgttaa aattagtaaa   180
atgggagatc aattaaatt tcaaactgtt gctgaagaag aagccaaaa agtatcgtca   240
atgtctgatg atgaagcaat gatttattct tatattgaag cttcaggctg tgaagggatt   300
tggaactaaa ccattaaagc taaaactaat ttacatcaac atattgttca aaaatgttta   360
aaaaatttag aaaataatcg atacattaaa agtattaaat cagtgaacaa tccaacaaga   420
aaaatttata tgttgtataa ttacaacct agtattgatg ttactgggtg tccttggttt   480
actgattcag aattagatac tgaatttata gaaactttat tggaagtgtg ttggagattt   540
attgttgga aaacctatga tataaaggat gaagaagctg ataatagaata taaaatcca   600
cttcaacaa catatcacia tcatcatcca ggggtgaatt tggatcaact tgttgaattt   660
ataacaata gtaatatcac cagtgttgag ttgggtatta atgatattag atcattatgt   720
gatgtgctaa tctatgacga tagaatagaa gaagttgggt ggaatcaaga aaatagtggg   780
atttttaag ctacttggca aagtataata gataaaggta acactatttt gcaaaataat   840
tatcaggatt tgaaaaatgt tgttctgaa gattgtttta attattaca acaaaatcaa   900
tcagalilla gtgttttca atataaatct actattcaag atcttcaaga tgaatcggat   960
ctagtgtatt tagatagctg gataaatgaa taa                                     993

```

<210> 76

<211> 2203

<212> DNA

<213> *Homo sapiens*

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: U93869

<220>
 <221> misc_feature
 <222> (1657)..(1658)
 <223> n is unknown

<220>
 <221> misc_feature
 <222> (1661)..(1661)
 <223> n is unknown

<400> 76
 cgaccgggt tccgccgtt gctaccgggc tgctccgtgc atcttcccc ccaggcgta 60
 ggaactgcgc ctcatgggag aggtgaaggt gaaggtgcag ccgcctgacg ccgatccggt 120
 cgaaatagaa aacaggatta tagaattatg tcaccagttc cctcatggaa tcacagacca 180
 agtaattcag aatgaaatgc ctcaatatag aagcccagca gcgggcagta gcatcaatag 240
 gttgttgtct atgggtcagt tggatctctt aaggagcaat acgggccttt tatatagaat 300
 aaaggacict cagaatgctg gtaaaatgaa gggatccgat aaccaagaaa aactagtata 360
 tcaaatcata gaggatgcag gaaataaagg aatatggagc agagatatcc gctataaaag 420
 taatttgcca ttaacagaaa tcaacaaaat tctgaagaat ctggaaagta aaaagcttat 480
 caaagctgtt aagtctgtag cagcctcaaa aaagaagggt tatatgctct ataacctgca 540
 gccagaccgg tctgtgactg gtggagcctg gtacagtgc caggattttg aatctgaatt 600
 tgtagagggt citaaccaac agtgttttaa attcctacag tccaaggcag aaacagcacg 660
 agaaagcaaa cagaacccaa tgatacaaag aaatagtica ttgcctcat cacatgaagt 720
 gtggaaatat atctgcgaat tgggaatcag taaggtagag ttatccatgg aagacattga 780
 aaccatcctg aatacactca ttatgatgg aaaagtggag atgacgatta ttgcctgcaa 840
 aagaaggcac agttggcagt gtagatggac acatgaaact gtacagggca gtcaatccaa 900
 tcatccctcc cacaggtttg gtccgggcca ccctgtggac tctgccccgg ttttgatga 960
 ctgccacgaa ggtggtgaga ttccacalc taactgtatt tacatgacag agtggctcga 1020
 attttaatag agagctatga actttattga cattttgcaa atgaagttac ttagggagca 1080

gataatttaa ttcgatgg aacacgaaat ctccttgaaa gcaaacttca caataatgga 1140
 cgtagacttg ctgctatgaa aacataat tttatattat gaagactaaa ttatattgg 1200
 taaaatagcc agtagaatat gaaagaaata aggttagtag tgaaattcat tcttcaataa 1260
 ataaaacaat ttgaaactcc ggaggaccac atcttcaag acttctgatg ggcgaagccc 1320
 ccggcttcaa aacacgacaa ggaagtggc tattctgatg aatggacaat ttgaaaagat 1380
 gccaacatac ccgtatttac caagtactat gataatggct agagtataaa aatgttctt 1440
 ttaaagttat ttattaagtt cttcattgga cgctttttt tatactgtgt tcaactaccac 1500
 catttctgt tcttacttt ctcagtgggt tcattgaaaa gaaattagaa ggggttaaag 1560
 gcaggaatag caaagagtgc aaactgggg tatgactggg ggagagtga acatgcctt 1620
 tccgcacaat attaatcct tttgtatca gaaaggnct ntaggagtt atgctaccat 1680
 acttactica aacccaatga ctactgtcaa ggcatattt tcagtacata aatactatca 1740
 ttctattct aaagaatatt ttcactgttc cttctttct aaagtctat gtttactct 1800
 ttaactcaaa tgtattctt gtagaattt accctagatt cttatataat gtctgcagta 1860
 gactgaatgt ttgtgtgcc ccagaattct aatgtgaaa tctcattcc aatgtgatg 1920
 tattggagg tggggcttt ggtaagtgt aggtcaggag agtaacagcg ctcagatg 1980
 ggattagtgc cctatataa agagaccag agagctccat cacccttct gccatgtgaa 2040
 agggagaaga caaacatcca cgaaccagga agtgggicct caccagaaa caaatctgta 2100
 agcacctga tcttgactt ccagccctc agaattgtga gaaataaatt tctgtgtg 2160
 attttttt tttttttt tttttttt tttttttt ttt 2203

<210> 77

<211> 588

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc feature

<223> GENBANK Accession Number: CAA96194.1

<400> 77

atgtccgggt cgtaaatac tctagacaag aaaatagcta aaagaaggca ggtgtataag 60
 cccgtgctag acaatccgtt cacaacgaa gcacatatgt ggccgcgcgt gcatgatcag 120
 ccattgattt ggcagctgct gcaatcctct atcataaata agttgattca cattcaatcg 180
 aaggagaact acccttggga gctgtataca gatttcaatg aaattgtgca gtattgagc 240
 ggcgctcacg gaaacagcga ccagtatgt ctatttgtgt gcaataagga ccctgatgta 300
 ccgcttgctc tcttgacgca aatcccgcta ttatgctata tggcgcccat gacgggtaaa 360
 ctggtgcagt tgcccaagag tgccatggat accctcaagt cggtttctaa atatggaatg 420
 ctgctgctgc ggtgcgacga tagggtcgac aagaaattcg tatcgcatat ccagaagaac 480
 gttgatctgc ttacgtttcc ctggttaaat gctatcaagt atcgcccac atctgtcaag 540
 ctgttgaaaa ctacagtgcc aattgtctcg aagaagaggc aaaagtag 588

<210> 78

<211> 663

<212> DNA

<213> *Candida albicans*

<400> 78

atgaataaat caaataaagt caagaaacct tcggtggcca aagtctcaac taaagctgct 60
 tcatcatcac tcaagtctca ggaagcaaag agaaaacaag ttctccgtcc aattctgat 120
 aactcattta cacaatcaaa ccaatggcca ttatagaac caactattgc aaacgatatt 180
 gttgatctac tagaagtatt gctaaaaatg caagactcta cattlaaata ccgtgggttt 240
 aatccaactg tgctctgctt tgaaaaacaa gcagctgcta atcgtgggat acataaaaat 300
 gcttggttac aaataaagta tgtatttggt tgcaagtacg atatatccc agcaacgctc 360
 acaaatgtgt ttctacgtt gtgtttcacg gcgtcaaaaa gtgctgaaga tcgggttaag 420
 ctaatccagt taccaagagg aagtctagaa cggttatcga aagcacttgg ggtagataga 480
 gtiggtatat ttggtctaac taaagatact gaaggggcac aaccgttatt tgatctata 540
 aatgaaaaatg tcaagatat tgaagctcct tggctagact gtattttccg tgaggagatg 600
 gtatttaac aacctaacac aaagcatgtg gcaagtactg taggtagaaa gaaaaacaag 660

tag

663

<210> 79

<211> 960

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA82141.1

<400> 79

atgagtaaaa acagggaccc tctactggct aatttgaacg ctttcaaaag caaagtgaag 60
tctgccccgg tgatgcgacc cgctaaagt ggacagaaga agaccaatga cacagtgatt 120
actatagatg gaaacactag gaagaggacg gcctccgaac gtgcgcaaga aaacactttg 180
aactctgcga aaaatcctgt gttagtggat atcaagaaag aagctgggag caatagctct 240
aatgtatttt cattagatga cgacgatgac gacgaagatt ttggtagctc tctttcaaaa 300
aaagtaaggc ctggctctat tgtgcagcc gctttacaag caaatcaaac agatatltcc 360
aagagtcacg attcttcaaa gttgctttgg gcgactgaat acattcaaaa gaaaggtaag 420
cccgttttgg tgaatgagtt attggactac ttgtcaatga aaaaagatga caaggttatt 480
gagcttttaa aaaaattaga tagaatagag ttgacccca agaaggggac tttcaaatat 540
ctttccacct acgatgtcca ttcccttcg gaactgctga agttgttacg ttcacaagta 600
acattcaag gtatttcctg caaagacttg aaagacggtt ggccacaatg cgatgaaacg 660
attaaccaac tggaggaaga cagcaaaatt ttggtgttaa gaactaaaaa ggataaaact 720
ccaagatacg ttgtgtataa cagcgggtgg aacttgaat gtattgacga ggagtttgtt 780
aaaatgtggg aaaatgtgca attaccgcaa ttgcagaat tgccaagaaa gctgcaagat 840
ttaggtctaa agcctgctag tgtcgatcct gctactatca aaagacaaac aaagagagtt 900
gaagttaaaa agaagagaca aagaaagggt aagattacta acactcatat gaccggtatc 960

<210> 80

<211> 855

<212> DNA

<213> *Candida albicans*

<400> 80

```

atgtccgact tatcagctca actttcagct tttagaata agatcaaaag tggaccatcg   60
gtgattgttc ctgaaaggc aacttttact caatctccat catcaccatt atcatcatca  120
accacaacaa caacactgaa gaatgacgcc aatgtgaaga agagatcaac gacggattca  180
gtaacccgag tattgaagaa acaaaaggca aatatgggag aatgacggg atcacattta  240
tcgacacaat tacaccttgc tgttgaatat atcaaggaa atgaccaacc aatatcgggtg  300
gagaagtgtc agaattattt atcatttgat atatcacata ctttattgcc attattgaat  360
gaaattgac gagtgaaata cgacgaatct aagggtacat tggaatatgt ttcattgcat  420
aatattcgta gtagtgatga tttattggaa ttttgagac gtcaaaccac attcaagggc  480
acttccgtaa aagaattaaa agatggttgg gctggttgtg ttgccgctat agacgaatta  540
gaatcacaag gcaaaatttt ggtgttgcgt aacaagaagg aaaatgctcc aagattagta  600
tgggctaata atggttgtga gttgggttat attgacacag aattcaagga tatgtgggat  660
caagtgaat tgccggaacc agatgtattg taccagaaat tattggatca aggattgaaa  720
cctacgggag ctgacctaata ttgatcaaa aagcaaccac acaaaaagga aaagaacaa  780
aagaaagcaa gaagaggaaa gattacaaat acacatatga aaggtatttt gaaggattat  840
tctcaattag ttga                                     855

```

<210> 81

<211> 1500

<212> DNA

<213> *Homo sapiens*

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: NM_002095.1

<400> 81

```

cttaaatc cactacgtt gtccagtcgc cgctcagct accgccgtg ccgccgcgc   60
cgccgccacc gccagtgtg agaccccgac ctggcgggtc agcgtgggc gtgcgtgcgg  120

```

gcaggcgggg gcgctgacga gaagcaggaa gagggcgag tgcggcggtg ggcggccggc 180
cgaggcggag gcgcaggaag ggggcggcga gtcgtgcgag gctgcccttc tcactcagca 240
ttatggatcc aagcctgttg agagaaagg agctgttcaa aaaacgagct cttctactc 300
ctgtagtaga aaaacgttca gcatctctg agtcacatc atcatctca aagaagaaga 360
aaacaaaggt agaacatgga ggaicgtcag gctctaaaca aaattctgat catagcaatg 420
gatcatttaa ctgaaagct ttgtcaggaa gcctcggata taagtttggg gttcttgcta 480
agattgtgaa ttacatgaag acacggcatc agcgaggaga tacgcacct ctaaccttag 540
atgaaatttt ggatgaaaca caacatttag atattggact caagcagaaa caatggctaa 600
tgactgaggc tttagtcaac aatcccaaaa ttgaagtaat agatgggaag tatgctttca 660
agcccaagta caacgtgaga gataagaagg ccctacttag gctcttagat cagcatgacc 720
agcgaggatt aggaggaatt ctttagaag acatagaaga agcactgccc aattccaga 780
aagctgtcaa ggctttgggg gaccagatac tattgtaaa tcgtcccgat aagaagaaaa 840
tactttctt caatgataag agcgtcagt ttctgtgga tgaagaatt cagaaactgt 900
ggaggagtgt cactgtagat tccatggacg aggagaaaat tgaagaatat ctgaagcgac 960
agggtatttc ttcatgcag gaatctggac caaagaaagt ggccctatt cagagaagga 1020
aaaagcctgc ttcacagaaa aagcgacgt ttaagactca taacgaacac ttggctggag 1080
tgctgaagga ttactctgac attactcca gcaaataggg aacagtttg ccctggaaca 1140
gagttacaga tacacaatca agagtgtct tgctgatgct cggggtctga agactgtctt 1200
cctatctgct tcttcggct gaggagagga gcagtcagt ttacaaaaca agtcaaatt 1260
accaaactca aagcttatt gagtagaat ggctcatggg caatgtgatg ttccctgta 1320
acctctgtt actccctggg agaaaggcg tgagcgtggc atgcaggtgt cttgtctgtg 1380
ttttctcca ctctaaatg gttctggtt ctttctcc tcgttgta ctttagagca 1440
agttgccca tagtctgaa tgcaatatt gttattcca aaagaacata ttataataa 1500

<210> 82

<211> 1560

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA96830.1

<400> 82

atgtctcaag aacagtacac agaaaacttg aaggttatcg ttgccgaaaa actggctggt 60
 ataccaaact ttaacgaaga tatcaagtat gttgcggagt atattgtctt attgatcggt 120
 aacggtggtta ctgttgaatc tgtcgtagac gagctggcta gtttgttga tagtgtttcg 180
 agagatacgc ttgcaaatgt tgtcaaaca gcctttttcg cattagaagc tctgcaacag 240
 ggagaaagtg ctgaaaatat tgtttccaaa attagaatga tgaatgcgca aagcttgggg 300
 caatcggata tcgcacaaca gcaacaacag caacaacaac aacagcaacc agacatcgcg 360
 caacgcaac ctcaacagca acctcaacag caacctcaac agcaacctca acagcaacct 420
 caacgcaac ctcaacagca acctcaacag caacctcaac agcaacctca acttcaacca 480
 cttcagccac aactagggac ccagaatgca atgcagacag atgctcctgc aactccatcc 540
 cccatatcag cctttccgg cgttgttaac gctgcagctc cccctcagtt tgcgcctgta 600
 gataacagcc aaaggttcac tcaacgtggc ggaggcgccg ttggaaagaa tcgtagaggt 660
 ggtcgcggtg ggaaccgtgg aggacgcaac aataattcca cacgttttaa tccgtagca 720
 aaagcacttg gaatggcggg tgagagtaat atgaactca ctccaacaa gaaagagggg 780
 cgttcagat tgtttcctca ctgtcctctt ggtagatcat gccacatgc acaccaact 840
 aaggtatgta atgaatatcc aaattgtcca aagcctcccg gaacttgtga gttttacat 900
 ccaaatgaag atgaagagtt gatgaaggaa atggaaagaa ctctgtgaaga atttcaaaaa 960
 agaaaagctg atttattggc ggcaaaaagg aaaccggtac aaactggtat cgttctgtgt 1020
 aaatttgggg ctctgtgttc caatccatca tgcccatgtg gtcacccaac accagcaaat 1080
 gaagatgcga aagtcattga tctaatgtgg tgtgacaaga atttgacatg tgataalcct 1140
 gagtgtagaa aggcccactc ttcatgtcg aagatcaagg aagtaaaacc aataagccag 1200

aagaaagcag ctccacctcc ggtgaaaag tccttagaac aatgtaagtt cggtagcac 1260
 tgcaccaata aacgttgcaa atatagacat gctcgtctc atattatgtg ccgtgaagga 1320
 gcaaactgta ctagaattga ttgtttattt ggccatccaa ttaatgaaga tttagatt 1380
 ggtgtcaatt gtaagaatat ttactgtcta ttacagacatc ctccaggcag agtacttccg 1440
 gaaaagaaag gcgctgcacc caaltcaaac gticctacca atgaaaggcc atttgattg 1500
 ccagaaaacg caataattga aaatgctcct ccgcaaacca gtlttacgca ccaagaacaa 1560

<210> 83
 <211> 1296
 <212> DNA
 <213> Candida albicans

<400> 83
 atgcaattg ctccagataa ccaaataggc aaagagttac agcaaaactt gattcaagaa 60
 atacaaaggc gttcaataa accggctgat gatgccgtag atattgtga ctatatcatc 120
 tacttgattg tggcaaaaa gagcgaacaa gaaatagtcg cagaagtcaa agatattgct 180
 gacatatcta ttgatgttg gtttattggg gatgtttatc tggaaatcag aaagttggaa 240
 gtaaaatata atcaacctcc tgctgcagtg gaggaagctt ctcaacctca acaagaacag 300
 caacagcaat ctcaagcttc ttagtggct ccacaaatc ctattggctc taagaacaa 360
 ttaactgagg aagagaagat tgcccttga agtcaaagat ttggaactac tactagattg 420
 agtgggcgag gtggacgtgg tggataact aaaactagaa ccgatttcag aaatgggcac 480
 aataataaga acttcctaga ccctaaaaaa ttagacaaa taatttctgg tgccaataat 540
 ggggtatta agttgtacc actcccacca aaaggtagat gtccagattt cccatattgt 600
 aagaatcaga attgtgaaaa agctcalcca acaaaaaact gtticaacta cccgattgc 660
 cctaaccac cggaacatg taatttttg catccggatc aagaccaaga gttgattgct 720
 aaattagaaa catctaaaaa agaattgaa gaaaagaaa agaactcaat tatggtcaaa 780
 caaggctcat gtaaatatgg ttgaaatgt gctaaagaaa attgtccatt tgctaccca 840
 acaccagcta atcctgaatc tggtaagatt gaaacttgg aatggtgtcc acaaggaag 900

aattgtcaag atagaaattg tactaaatca catccacctc cacctacggc aaactcagaa 960
aaattattat cagctgctga ctggcattg gaacaatgta aatttggtc acaatgtact 1020
aatctcaaat gtccaagaag acatgcaact tcggctgtgc catgtcgtgc tgggtctgaa 1080
tgtagaagag tcgattgtac atttcccat ccattgaaag aacctgccc ttttgaaca 1140
aaatgtacaa ataaagtgtg tatgtacaa catcctgaag gaagaactat tgcctctcac 1200
acttgacca aggatggtag tggcaataat aacagtacct caaatcgatc atttctgtt 1260
tctgaagatc agattatgga acaagttgct caatag 1296

<210> 84

<211> 680

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: AF155107.1

<400> 84

acccacagca gttgcacttg ctgagcaggc agcttgagga cccaaatggt agcttttcta 60
acgctgagat gagtgaactg agtgtggcac agaaaccaga aaaacttttg gagcgctgca 120
agtactggcc tgcttgtaaa aatggggatg agtgtgccta ccatcacccc atctcacctt 180
gcaaaacctt cccaattgt aaatttgctg aaaaatgitt gttgttcac ccaaattgta 240
gatacggaaa tgaactgaaa tatgatgcaa agtgtactaa accagattgt cccctcactc 300
atgtgagtag aagaattcca gtactgtctc caaaaccagt tgcaccacca gcaccacctt 360
ccagtagtca gctctgccgt tacttcctg ctgtgaagaa gatggaatgt cccctctatc 420
atccaaaaca tttaggttt aacctcaat gtacaagacc ggactgcaca ttctaccatc 480
ccaccattaa tgtccacca cgacatgcct tgaatggat tcgacctcaa accagcgaat 540
agcaccagt cctgcctggc agaagatcat gcagtttga agtttcatg tctgatgaaa 600
gatctctaca gaacttgta aatctttgaa acttgaata tattgcttc alaatatgaa 660
ggtttattgg ctatctaaaa 680

<210> 85
<211> 1140
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> GENBANK Accession Number:CAA88520.1

<400> 85
atggcaaatt cgccgaaaa gccatctgat ggcactggag tatcagcgtc agacacgcct 60
aaatatcaac ataccgtccc agaaacgaaa ccagcattta attgtcacc aggtaaagct 120
agtgagctat cacatagcct tccgtgcct agccagataa aatcaaccgc acatgtatct 180
tcaactcaca atgatgcggc aggtaatacg gatgattctg ttcttcctaa aaatgtatca 240
cccacaacta atttgagagt tgaaagtaat ggagatacaa acaatatgtt ctctagccct 300
gctggactag ctctaccaa aaaggatgat aaaaaaaaa acaagggtac gagtaaagca 360
gattctaaag atggcaaagc atccaactcc tcaggacaga atgcacaaca acaatcagac 420
ccaaataaaa tgcaagatgt ccttttticc gcaggatcgc atgttaggga ggaggaggct 480
cttctaaatt catctattaa tgcccaaaa tccaagttc aaacaaataa cgtaagatc 540
cccaaccatt taccattcct tcacccggaa caagtttcca attatatgag gaaagtcgga 600
aaagagcaaa acttcaacct gacccctaca aagaatcctg aaattttgga catgatgtca 660
agtgccctgcg aaaactatat gagagatc ctaacaaatg ccattgtcat ctccgacat 720
agaagaaaag cagtcaagat aaattcggg agaagaagtg aagtttctgc ggccttaaga 780
gccattgcac taattcaaaa aaaagaagaa gaaaggcgtg tgaaaaaag aattgcgttg 840
ggactcgaga aggaagatta tgaaaataag attgattccg aagagacgtt acacagagca 900
tcgaacgtta cggctggcct tagagcaggt agtaaaaaac agtatggttg gctaacttca 960
tcagtaaata agccgacgtc ctggggagca aaatcttcag gcaaagtcgc ctccgacatc 1020
acggctagag gagaagtg gctaaagtt agagaagcta gagaggagcc tggtagta 1080
atgagggatt tactctttgc tctcgaaaat aggcgcaaca gcgttcagac tattatttca 1140

<210> 86

<211> 1119

<212> DNA

<213> Candida albicans

<400> 86

aatcaccgaa ttatatacaca taaatccatg acaagtacac ctcaagaatc ctctaattta 60

aagagacaat tagaaaacag tgaggactcc agctaccaa ataaggaatc taaaacagag 120

actaccacgg aaaaccagag ctcatgggag tctgacttta atagtttacc agtggaatta 180

ctacaaactg aaacaaatgg tacatcacca gcaccagcac cagcaacacc gatcgatacc 240

accaatgcat caagcacaaa ggaacgtgat caggatactt cttaattaaa tgacgcgatt 300

gctgctgcag gaggatgat tcaacaagaa gaagagatat tattacaaca acaattaat 360

agaaaatctg cagagggtat ggcaagcaat ctaaaaagtg tgatcaggtc cagcaaactg 420

cctccatttc tacacaatta ccatttagct gccittattg ataaagtggc taaacaaaat 480

ggaattcaac agaatttctt aatggatggt gagatgttgg aattaatttc agctgcttgt 540

gagacitggt taagtaatct agcaacaaaa acgataatct tgtcacgcca caggagaagg 600

ggaatacctg ttattaataa gaagtcagga agtagttcag ttccaagatc agaaatttca 660

aaagaattga gaagcttggc cttaaaacaa aaggaaatgg aagagaaacg agtgaataaa 720

agagtgatgt tgggggttga aaaaagcacc aaagacgcat ccaaaaatga cgaaaatggt 780

gaatcaaaag ctggtgctga agaaacatta catcgtgcag caaatgctac agctgcaatg 840

atgactatga atccccggag aaagaaatat agttggatga ctcaagtgc tacagcaggc 900

ggtgggtcag acitttgtaa atcaagtggg ggctcatcaa aggactcggg aaaacaccaa 960

agtcctatta tticagtacg tggatgataat ggccttaggt ttagagaaat aaggtcaggt 1020

aattccatta ttatgaaaga ttgttaggc gcaattgaag atgaaaaaat gggtacgaga 1080

aatgctgtaa taaaaggata tgcaaaattg aaagattaa 1119

<210> 87

<211> 2307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: Y11354.1

<400> 87

```

atggcggcgg gctcggatct gctggacgag gtcttctca acagcgaggt ggacgagaaa   60

gtggtgagcg acctggtggg ctgctggag tcgcagctgg cggccagcgc ggcccaccac   120

caccacctcg cgccgcgcac gcccgaggtg cgggcgcggg ccgccggcgc gtcgggaac   180

catgttgtga gcggcagccc ggccggagcc gcgggcgcag ggccggccgc cccgccgag   240

ggcgcgcccc gagcggcgcc ggagccgccc ccgcaggtg gagcgcggcc ggggggcggg   300

ggggcgagc gcccgggccc cccctaccg cgccgcccc ttgtcccgcc agggcccgcg   360

ccgccgccc cgaagctgag gccgccgccc gagggcagcg cgggggcctg cgccccggtg   420

ccgccgccc cgccgtcgc gcggggccc gagccgccc ccgccggccc cgccaagccc   480

gccggcccc cgcgctggc cgccgcgccc ggccccggcc ccggggcccg ccccgcccc   540

ggccccggcc ctggcaagcc cgccggcccc ggcgccgcgc aaactttgaa tgggagcgcc   600

gcgtgtga actgcacca cgccgccga cctgtgtca gcctgtgtaa caacgggccc   660

gccgcgtgc tgccgtgcc caagcccgc gccccggca ctgtatcca gacgcccc   720

ttcgtggcg cgccgcgccc cccgcgccc gccgcgccc cgccccgc cgccccgcg   780

ccgccgccc cgccgccgc cccgccccg ccacccccg cgccgccac cctggcccg   840

ccgccggcc acccgccgg accccgacc gccgcgccc cgtgcccgc ccccgccgc   900

aagggttatg ccaagatcag agattaagcc cagaacgggg gcagcgccgg ggagcccc   960

ggccccccc cggcgccgg ggccccgct ggggtcagcg gccagcccg gcccggcgc   1020

gcggctcgg cgccggcgcc ggggglcaag gccgagtcg ccaagagggt ggtgcaggcg   1080

gcgccccgg cggcgcagc cctggcgccc agcgcccg ccagcacggc ggccagcatg   1140

gtcatcgggc caactatga aggggcgtg ccagcccg ccgcccgc gccgcccgc   1200

ccggggacc ccaccgggt gcccaaagg gcggccggcg cagtgacca gagcctgtcc   1260

```

cggacgcca cggccaccac cagcgggatt cgggccaccc tgacgcccac cgtgctggcc 1320
 ccccgttgc cgcagccgcc tcagaacccg accaacaacc agaactcca gctgccccca 1380
 ggaatgggcc tcgtccgaag tgagaatggg cagtgttaa tgattcctca gcaggccttg 1440
 gcccagatgc aggcgcaggc ccatgccag cctcagacca ccatggcgcc tcgccctgcc 1500
 acccccacaa gtgcccctcc cgtccagatc tccaccgtac aggcacctgg aacacctatc 1560
 attgcacggc aggtgacccc aactaccata attaagcaag tgtctcaggc ccagacaacg 1620
 gtgcagccca gtgcaaccct gcagcgctcg cccggcgctc agcctcagct cgttctgggt 1680
 ggcgctgccc agacggcttc acttgggacg gcgacggctg ttcagacggg gactcctcag 1740
 cgcacggtag cagggggcgac caccacttcc tcagtgcca cggaaactat ggaaaacgtg 1800
 aagaaatgta aaaatttctt atctacgta ataaaactgg ctcatctgg caagcagtct 1860
 acagagacag cagctaattg gaaagagctc gtgcagaatt tactggatgg aaaaatagaa 1920
 gcagaagatt tcacaagcag gttataccga gaacttaatt ctccacctca accttacctt 1980
 gtgcctttcc tgaagaggag ctaccgcc ttgagacagc tgacccccga ctccgcggcc 2040
 ttcatccagc agagccagca gcagccgcca ccgccacct cgcaggccac cactgcgtc 2100
 acggccgtgg tgctgagtag ctccgtccag cgcacggccg ggaagacggc ggccaccgtg 2160
 accagtcccc tcagcccc tgtgtcagc ctacgcagc ccacgcaggt cggcgtcggc 2220
 aagcaggggc aaccacacc gctggtatc cagcagctc cgaagccagg agccctgatc 2280
 cggccccgc aggtgacgtt gacgcag 2307

<210> 88

<211> 555

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA82029.1

<400> 88

atgaacacca atagtaatac tatggtaatg aatgacgcaa atcaagcaca aataacggcc 60

acatttacga agaagatatt agcgcatgtg gatgatccgg actccaacaa attggcccaa 120
 ttcgtacagc tttttaatcc aaacaactgc agaataatat ttaatgctac ccccttcgcg 180
 caagcaacag ttttctgca aatgtggcaa aaccaggctg tacaacaca acatgcccta 240
 acaggagtag actatcacgc tattccggga tccggcacgt tgatagcaa cgtaattgc 300
 aaagtcagat tcgacgaaag cggcagagac aagatggggc aagacgcgac tgttccatt 360
 caaccaaata acactgggaa cagaaatcga cccaacgata tgaacaagcc aagacctcta 420
 tgggggccat attttggcat ttccctgcag ctgatcatcg acgaccgcat atttagaat 480
 gattttaatg gtgtaatatc ggggtttaac tataacatgg ttacaacc cgaggattct 540
 ctgctaaaaa ttag 555

<210> 89
 <211> 540
 <212> DNA
 <213> *Candida albicans*

<400> 89
 catcctatag cacaacaact agagccggtt ctcaaagat ttcttgcac gttagattta 60
 ctgtacacac agccaacatc acaaccattc cccaacgttg aatcgtatgc cactcagtta 120
 ggatcaaact taaagcggtc aagtgcatt atagtgaacg gccagcctat tataccgagc 180
 ccacaagaag actgtaaatt acaattccaa aagaatggt tacaactcc gttatcgta 240
 caccaatga caagttacga tgggcattta attcaggca cggggacctt tgcgttcat 300
 ttttcagcaa aagtaagatt tgatcaaagt ggaaggaacc ggtaggtga atctgccgac 360
 ttgtttcagg aaaataatc aatgtttcc aaaaccaatc aaagacctat ttggggttcg 420
 tggtttgag tcgacgtcaa ttgggttgt gacgaaaacg ttatgcaaga tggagagatt 480
 ataaatagta tggattatag atttacctat gtacctaacg atagcattat aaaagtataa 540

<210> 90
 <211> 720
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA97636.1

<400> 90

atgaacgctc ttacaacca tgctgtgaag caaaaaaatc aactacaaca agagttggcc 60

aggtttgaag agaattctgt gaccgccctt attctttac aagggtccat ctctgcaact 120

ctggtctcac tggagaaaac agttaagcaa tatgcagaac atttaacag atataaagaa 180

gatactaatg cagaggaaat tgatcctaag ttcgctaac gactagcaac ttaacacag 240

gatctgcacg actttactgc caagttaag galftaaac aatcctacaa cgaaaalaat 300

tccagaactc agttgtttgg ctgaggagca tcgcatgta tggactccga taacccttt 360

agtacatcag agaccatcat gaataaaagg aacgttggtg gtgcgagtgc aaatggtaaa 420

gagggcicta gcaacggtgg gggactaccg ttgtaccaag ggctacaaaa ggaacagtct 480

gttttcgaag ggggtaacgc tcaattagat tacattctag aaatgggcca acaatcattc 540

gaaaatatag tgaacaaaa caaaattta tccaaggtaac aagatagaat gtcaaatggc 600

ctaagaacat tgggtgtttc ggaacaaact atcacctcta tcaataaacg ggtgttcaaa 660

gataaactag tcttttgat cgcgttaatt ctctgatca taggtattta ttatgtgtg 720

<210> 91

<211> 483

<212> DNA

<213> Candida albicans

<400> 91

atgaattcaa tatataatca tggtttaaaa caaacccaaa ctataactaa agatttaact 60

caattcgaga aaaacttaic cacatcacca ttatcattac aagtgcatac acaacatcat 120

taactgcatt caggaaaact atcgaagaat atgatgattt attggaagta aatgtctatg 180

atacatctga taccatagat gagggtagat tagatatatt caatccagat ttaaatgaat 240

acactctgaa atatgatact ttaaataagc tacgtgagtt tcttctccat caagctaata 300

aacaagaatt attaggagaa ggacacttat caccaacagc aacagcagca ttggatcgac 360

atcatcagat aatccgtatg aatctagctc aaatccatct caacaacaac aacagcaatt 420

acaagatgaa caaaacacca tgtcttatag agaaggatta tatcatgaaa agaattctct 480

aga 483

<210> 92

<211> 1560

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: NM_003569.1

<400> 92

gaggagccg tggaggcca ggtgactgct tagaaaactg cacagcatct gatgaaatta 60

gcgaataaga acatcaacca tgtcttacac tccaggagtt ggtggtgacc ccaccagtt 120

ggcccagagg atctcttcta acatccagaa gatcacacag tgttctgtgg aaatacaaag 180

aactctgaat caacttgga caccicaaga ttcacctgaa ttgaggcaac agttgcaaca 240

gaagcagcag tatactaacc agcttgccaa agaacagat aagtaatta aagagtttgg 300

atctctgccc accaccccca gtgaacagcg tcaaaggaaa atacagaagg atcgcttagt 360

ggcagagttc acaacatcac tgacaaactt ccagaaggtc cagaggcagg ctgctgagcg 420

agagaaagag ttgtgtgctc gagtaagagc cagttccaga gtgtctggca gtttctga 480

ggacagctca aaagaaagga atctgtatc ctgggaaagc caaactcaac ctcaagtga 540

ggtgcaggat gaagaaatta cagaggatga cctccgtctt atcatgaga gagaatcttc 600

tatcaggcaa ctgaagctg atattatga tatfaatgaa atatttaaag atttggaat 660

gatgattcat gaacaaggag atgtaataga tagcatagaa gccaatgtgg aaaatgcaga 720

ggtgcacgtt cagcaagcaa atcagcagct gtcaagggca gcagattatc agcgcaaatc 780

cagaaaaacc ctgtgcatca tcattcttat cctgtcalt ggagttgcga ttatcagtct 840

catcatatgg ggattgaacc actgaagtta taaaggagca cactgtcgca ctacattgtc 900

taaattatgt aggaagattc ctgtaatcat gtttttttaa ttattatttt aaagctattg 960

tataaaggat ggttcccata ctttgttatt ttattgggg gggtgggcg ggttccttg 1020
 gattaaatct gatatctct aatactgaaa galtttctaa atgtcacatg tgacataact 1080
 cccttggtct tcaatttaat agttgttaag ttgtgggcca cattgcatat gccttcatt 1140
 tataatttat ttaccctgct tgacitagti tggggaattc ggaaatttaa ggtgtgtgta 1200
 ttctgtggg atctccctgc cacgtgaaca caccaagatg tgtgttactt caagttaaaa 1260
 ctcccaaaaa tttaattttt gatttgcttc caccagggga aaatattctc caataatgta 1320
 aaataattaa ggiccaatac atgggttgta ttctctggt tcacaacagc acaaagtgc 1380
 ttcatTTTT ttgtggatt tccttaaga tctttttac cctgaagtcg gtgaacactt 1440
 ttctagttaa ttgatactc ttctgtgta tataataagc ttgtctgta gattgcctag 1500
 taaaattact aaggataggt tgtttttaca tatgtctat ttaagtctga tgtttacggg 1560

<210> 93

<211> 720

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA85038.1

<400> 93

atgttagaag caaaattga agaagcatcc ctttcaaga gaataattga tggltcaaa 60
 gattgtgtcc agttgtcaa ttccaatgt aaagaagatg gtatcattgc acaagctgc 120
 gatgactcaa gagtctatt ggtctccttg gaaatagggtg tcgaagcctt ccaagaatat 180
 agatgtgacc atcctgttac gttaggtatg gatctaacct cactaagtaa aatcctacgt 240
 tgtggttaaca acaccgatac attaacacta attgctgaca acacaccgga ttcatcatc 300
 ttattatttg aggataccaa gaaagaccgt atagccgaat actctctgaa attgatggat 360
 atcgatgctg atttcttaaa gattgaagaa ttacagtacg actccaccct gtcattgcc 420
 tctccgaat tctctaaaat tgtcgtgac ttgtccaat tgagtgttc tattaatata 480
 atgatcacca aagaacaat aaagtttga gctgacggtg atacggatc aggttcagtc 540

ataataaac cattcgtgga tatggaacat cctgaaacaa gcatcaaact tgaaatggat 600
caacctgtcg acttgacgtt cggagctaaa tatttattgg acatcattaa gggctcctcc 660
ctttctgata gagggtgat caggctctcc agcgaagctc ctgctttatt ccaattgat 720

<210> 94
<211> 780
<212> DNA
<213> Candida albicans

<400> 94
atgttagaag gtaaaattga agaagctgct ttattaaaaa aagttgtga agccattaaa 60
gattgtgta aaaaatgtaa ctcaattgt tcagagcatg ggattactgt acaagcagtg 120
gatgattctc gtgtattatt agtttcatta ttaattggtc aaactcttt cagtgaatat 180
agatgtgaca gagacgttac attaggtatt gacttggaag gtttcagtaa gattatcaaa 240
tctgctaaca algaagattt ctgaccctt ttagctgaag attcaccaga tcaaataatg 300
gctattcttg aagaaaaaca aaaagagaaa atcagtgaat attctttaa attaatggat 360
attgattctg aattttaca aattgatgat atggaatacg atgctgttg gaatatgcca 420
agtagtgatt ttgctaaact tgtgagggat ttgaaaaatt taagtgaatc ttacgtgtt 480
gttgttacta aagattccgt caagtttaca tctgaagggtg attctgggtc cggaagtgtt 540
atcttgaaac ctacaccaa ctgaaaaat gaaagagaaa gtgtcactat tagtttagat 600
gaccagtg attgacttt tggttgaaa tacttgaatg atatttgaa ggcagctaca 660
ttatccgatg tcaccacat caaattggcc gataaaactc ctgcattgtt tgaatttaa 720
atgcaatctg gaggttattt gagattctac ttggcaccaa aattcgatga tgatgagtag 780

<210> 95
<211> 1200
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: GI:181271

<400> 95

aggtctcagc cggctgctgc gacgttcgcc cgctcgctct gaggctcctg aagccgaanc 60

tagctagact ttcttccttc ccgctgcct gtagcggcgt tgttgccact ccgccaccat 120

gttcgaggcg cgcctggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180

cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240

ctcgtccac gtctctttg tgcagctcac cctgcggctt gagggttcg acacctaccg 300

ctgcgaccgc aacctggcca tgggcgtgaa cctcaccagt atgtccaaa tactaaaatg 360

cgccggcaat gaagatatca ttactaag gccgaagat aacgcggata cttggcgct 420

agtattgaa gcaccaaacc aggagaaagt ttgagactat gaaatgaagt tgatggatti 480

agatgtgaa caacttgaa ttccagaaca ggagtacagc tgtglagtaa agatgccitc 540

tggatgattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600

ctgtgcaaaa gacggagtga aattttctgc aagtggagaa ctggaaatg gaaacattaa 660

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720

accagticaa ctaacttttg cactgaggta cctgaacttc ttacaaaag ccactccact 780

ctctcaacg gtgacctca gtatgctgc agatgtacc cttgttag agtataaaat 840

tgcggatatg ggacacttaa aatactactt ggctcccaag atcaggatg aagaaggatc 900

ttaggcattc ttaaaattca agaaaataa actaagctct ttgagaactg cttctaagat 960

gccagcatat actgaagtct ttctgtcac caaatttga cctctaagta catatgtaga 1020

tattgtttc tgtaaataac ctatTTTT tctctattct ctccaattg tttaaagaat 1080

aaagtccaaa gtctgatctg gtctagtaa cctagaagta ttttgtctc ttagaaatac 1140

ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtgtttt 1200

<210> 96

<211> 1500

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA88556.1

<400> 96

```

atgtcgaaaa ggtctatcga ggtcaacgag gaacaagata gagggtctc tgctaaaaca   60
gaatctcact ctgttcctgc tattcccgcc tctgaagagc aagatgctcc caagaatgac   120
ctagaagaac aattgagtga tgaattgat agtgatggtg aaattattga aattgatggc   180
gatgatgaga ttaatgacga agatgacctt aggaaaaagc aagaagaagc tgaaacttta   240
gtacaaaagg accaatccga aggcaacaaa gaaaagatcc aggagcttta ctaccccat   300
atgtctctgc cattagggcc agatgaagtc ctgaggctg atccactgt ttatgaaatg   360
ctacataatg tcaatatgcc atggccatgc ttgacattag atgtattcc agatacacta   420
ggttctgaac gtagaaacta tccacagtct attttgtga ccacggctac tcaatcttcc   480
aggaaaaagg agaatgaact aatggttcta gcactttcta atttagcgaa aacacttttg   540
aaagacgata atgaaggatg agatgatgaa gaggatgatg aagatgatgt ggatccagtc   600
attgagaatg aaaatatacc attgagagat acaaccaata gattaaaggt ttctcctt   660
gccatttcta atcaaggagt gtaaccgct acaatgagcg aaaatggtga tgtttatata   720
tacaatctag ctccacaaag caaagctttt tccacaccag gttatcagat tccgaagtct   780
gctaagcgtc ctattcacac tgtaaaaaat catgggaatg ttgaaggcta cgggttggtat   840
tggtcaccat tgatcaagac tgggtcggtt ctatcagggtg attgctcagg acaaatatat   900
tttaccctaa ggcacacatc gagatgggtg actgataaac aaccatttac tgtttcaaac   960
aataaatcca tagaagatat ccagtgggtc cgcactgaat ccaccgtttt tgcaaccgca  1020
ggatgtgatg gatataaag gatttgggac acaagatcaa aaaaacataa acctgctatc  1080
tctgttaaag ctctaatatc tgacgtaat gtcataagtt ggagtataa aattggttac  1140
ttgctagcaa gcggtgacga taacggtaca tggggagtat gggatttaag acagtttacg  1200
ccaagtaatg ctgacgccgt ccaaccggtt gctcaatatg acttcataa gggagccatt  1260
acttcattg cattcaacc attagatgag tctatcgttg cggtaggctc agaagataa  1320
actgtgactt tgtgggattt gctctagaa gctgacgatg aggaaataa acaacaggcc  1380

```

gccgaacaa aagagctaca agaaattcca ccacaattat tgtttgtca ctggcaaaag 1440

gaagttaag atgtcaaatg gcataagcaa atcccagggt gtttagtaag taccgggtact 1500

<210> 97

<211> 1554

<212> DNA

<213> Candida albicans

<400> 97

atgtcaaaaa gatcagctga agatgattta agtggcaata gatccaccag tcatactgcc 60

attanaacta ataaagattc tttccaact actacaaatg gaaaggaaga agaaccagac 120

aatatggata ttggggaatt tgaagatcca tacggtgatg aattgaaag tgatgaagaa 180

attatagaat tagacgataa caatgatgaa gaagatgatg aatgattga tgaaaattca 240

acacaagcca aaattgaaga attagaagcc aaagaacaag aacaagaaca acaatcatca 300

atataattac tcataaatc aaaaccatta ggaccagatg aagtcttaga agccgatcca 360

acagtctatg aaatgttgca taatatcaat ttacatggc catgttgac tgttgatatt 420

ttaccagatt ctttaggtaa tgaaagaaga tcatatccag caacagtta ttagctact 480

gcgactcaag ctgctaaagc caagataat gaattgttag ctatgaaagc atcttcattg 540

gccaaaacat tagttaaga tgaaaatgaa gaagatgagg aagatgaaga cgatgacgat 600

gatgttgata gtgatccaat attagattca gaatctattc cattaagaca tactacaaat 660

agaataagag taagtcctca tgctcaacaa actggggaat acttaactgc ticaatgtca 720

gaaaatgggtg aagtttatat atttgattta ctggcacaat ataaggcaat tgacacacca 780

ggttatatga ttccataatc atcgaaaaga ccaattcata ctattcgtgc ccatgggaat 840

gttgaagggt atggattaga ttggtctcca ttagtaaata caggggcttt attatctgga 900

gatatgicag ggagaattta tttaactaat agaacgacat caagttggac cactgataaa 960

actccatttt ttgcatcaca atcttcaatt gaagatattc aatggtaac tggtgaaact 1020

acagtgtttg ccacgggtgg atgtgatgga tatatttgta ttgggatac aagatcgaaa 1080

aaacataaac ctgcattatc agtaattgct tctaaatctg atgttaatgt gatattctgg 1140

agttctaaaa tcaatcattt attggcatca ggacatgacg atggtagttg ggggtgatgg 1200
 gatttaagaa atttcacaaa caataccacc agtaatcctt cacctgtggc taattatgat 1260
 ttccataaat cgccaatcac atcaattca ttcaatccat tagatgaatc aatcattgct 1320
 gtticatcag aagataatac tgttacatla tgggatcttg ctgttgaagc tgatgatgaa 1380
 gaaatttctc aacaaagaaa agaagctcaa gaattacatg atattccacc acaattatta 1440
 ttgtccatt ggcaaagaga tgttaaagat gttagatggc atccacaaat tcttggttgt 1500
 ttggtatcta ctggtggtga tggattaaac atttgaaaa ctatatctgt gtaa 1554

<210> 98

<211> 2280

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: NM_005610.1

<400> 98

cgcgcgacaca gagegagctc ttgcagcctc cccgccccctc ccgcaacgct cgaccccagg 60
 attcccccg ctcgcctgcc cgccatggcc gacaaggaag cagccttcga cgacgcagtg 120
 gaagaacgag tgatcaacga ggaatacaaa atatggaaaa agaacacccc ttttctttat 180
 gatttgggtga tgacctatgc tctggagtgg ccagccttaa ctgcccagtg gcttccagat 240
 gtaaccagac cagaagggaag agattcagc attcatcgac ttgtcctggg gacacacaca 300
 tcggatgaac aaaacatct tgttatagcc agtgtgcagc tccctaatga tgatgctcag 360
 ttgatgcgt cacactacga cagtgagaaa ggagaatttg gaggttttgg ttcagttagt 420
 ggaaaaattg aaatagaaat caagatcaac catgaaggag aagtaaacag ggcccgttat 480
 atgccccaga acccttgat catcgcaaca aagactcctt ccagtgatgt tcttgtcttt 540
 gactatacaa aacatccttc taaaccagat ccttctggag agtgcaaccc agacttgcgt 600
 ctccgtggac atcagaagga aggetatggg ctctcttga acccaaatct cagtgggcac 660
 ttacttagtg ctacagatga ccataccatc tgctgtggg acatcagtgc cgttccaaag 720

gagggaaaag tggtagatgc gaagaccatc ttacagggc atacggcagt agtagaagat 780
gtttcctggc atctactcca tgagtctctg ttgggtcag ttgctgatga tcagaaactt 840
atgatttggg atactcgtc aaacaatact tccaaaccaa gccactcagt tgatgctcac 900
actgctgaag tgaactgcct ttcttcaat ccttatagt agttcattct tgccacagga 960
tcagctgaca agactgttc ctgtgggat ctgagaaatc tgaactta gttgcattcc 1020
tttagtcac ataaggatga aatattccag gttcagtggc cacctcaca tgagactatt 1080
ttagctcca gtggtactga tcgcagactg aatgtctggg attaaagtaa aattggagag 1140
gaacaatccc cagaagatgc agaagacggg ccaccagagt tgtgtttat tcatggtgg 1200
catactgcca agatatctga ttctcctgg aatccaatg aacctgggt gatttgtct 1260
gtatcagaag acaatatcat gcaagtgtg caaatggcag agaacttta taatgatga 1320
gacctgaag gaagcgtgga tccagaagga caagggtcct agatatgtct ttactgttg 1380
tgattttaga cccccctt ttcttcaa cctgagagt gatttaacac tggtttgag 1440
acagacttta ttacgtatc ccttatata ataggtacca ccgataatgc tattagccca 1500
aaccgtgggt ttcttaaat attaataggg gggcttgatt caacaagcc acagactta 1560
cgttgaaatt ttctcagga atttctagt aaccaggtc taaagtagct acagaaagg 1620
gaatattatg tgtgattatt ttcttcta tgctatatcc ccaagtttt cagactcatt 1680
taagtaaagg ctgagttag taaggaatag agccaaatga gtaggtgtc tgagccatga 1740
agtataata ctgaaagatg tcactttat tcaggaaata gggggagttc aagtcgtata 1800
gattcctact cgaatactt gacacctgac ttccaggat gcacatttc atacgtagac 1860
cagttcctc ttggttctt cagttaagc aaaacaacac gttccttt cccatata 1920
tcatatatt ttctcgtta gtgtattct tgagctgtt tcatgtgtt tatttctgt 1980
ctgtgaaatg gtgttttt ttgtgtgt ggtttttt tttttttt aactgggac 2040
caccaagtg taaagatga tgttttacc tgacgttat accacagga gactgcaag 2100
ttgagaagag tgaatcaata actgtattt gtttaaaaa ttaataat cctgataag 2160
agttgtttt ttttttagg agttagtct tgaccactag ttgatgcca tctcattt 2220

gggtgacctg ttaccaccagg aggcctgtta ctctccatga ctaactgtgt aagtgcctaa 2280

<210> 99

<211> 1144

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<301> Bauer and Burgers

<302> Molecular cloning, structure and expression of the yeast proliferating cell nuclear antigen gene

<303> Nucleic Acids Research

<304> 18

<305> 2

<306> 261-265

<307> 1990

<308> x16676

<309> 1993-09-30

<400> 99

acgcgtaact tttttttt ggatttcaac tgatagttt cgtactttgc ttctctggt 60

acataaaatt atatataaga aacacttttg ctttagcctt ccttctttc cacttgcacc 120

tttactttc gccgtccttt ttactcaca gcaacaagca gcaagcacta agtacgcagt 180

caaaagagag aaaaaatgtt agaagcaaaa ttgaagaag catcccttt caagagaata 240

attgatggtt tcaaagattg tgcacgttg gtcaatttc aatgtaaaga agatggatc 300

attgcacaag ctgtcgatga ctcaagagt ctattggtct ccttggaat aggtgtcgaa 360

gccttccaag aatatagatg tgaccatcct gttacgttag gtatggatct aacctacta 420

agtaaatcc tacgttgttg taacaacacc gatacattaa cactaattgc tgacaacaca 480

ccggattcca tcactttatt attgaggat accaagaaag accgtatagc cgaatactct 540

ctgaaattga tggatatcga tgcgtatttc ttaaagattg agaattaca gtacgactcc 600

accctgtcat tgccatcttc cgaattctct aaaattgttc gtgactgtc ccaattgagt 660

gattctatta atatcatgat caccaagaa acaataaagt tttagctga cggatgatc 720

ggatcaggtt cagtcataat aaaaccattc gtggatatgg aacatcctga aacaagcatc 780

aaacttgaat tggatcaacc tgcgacttg acgttcggag cttaatatt attggacatc 840

attaagggt cctcccttc tgatagagtt ggtatcaggc tctccagcga agctcctgct 900
 ttattccaat ttgattgaa gagggtgtc ctacagttt tctggctcc taaattaat 960
 gacgaagaat aaatgtaaat tatctatata gtgtatact aaaaataata aacaaaaaa 1020
 aaacagtaaa gttgtttta aatgaaaata aataacaag aaaataaaga ctaagtagtc 1080
 agttaatac agcattttg tgtgacttat acagtattta tgacatact tacattaac 1140
 taga 1144

<210> 100

<211> 1245

<212> DNA

<213> Candida albicans

<400> 100

atgtcacacc aacaagaaga cgtcgtagac gatactcaag aagaatatat caatgttaat 60
 gaagtggctg aggaagtgc agatgatgat caagcgccac ccgatgaaga agatgaggag 120
 atggaattag atgatgagca tgagacttta gaaatgaca tgtccaacaa ttcattgact 180
 tatattgata aacataccga tagtatatt actattttt cacatcctaa attgccaatg 240
 gtattgactg aggggtgtga caacacggca tacttatgga ccacacacac ccaaccacca 300
 agatttgtg gcgaaatcac tggacataaa gattcgtta tatctggagg gttactgca 360
 gacggcaagt ttgtgttac tgcagacatg aatggattaa ttcaagttt caaagccaca 420
 aaaggagggt aacagtgggt gaaatttgt gaattggacg aagtgaaga agtgtgtti 480
 gttactgtgc atccaacatt accattctt gcctttggtg ctaccgatgg atctatatgg 540
 gtctacaaa tagacgaatc cagtaaactg ctagtcaaa ttatgtctgg gtttcacac 600
 acattaaaal gtaatgtgc tgtattata caaggaaaag atgaaaatga ttgacattg 660
 gtctctataa gtgaagatgg tactgtgtg aactggaact gttttacagg acaagtgaat 720
 tataaattgc aacctcatga tgactttaa ggagttgaga gtccgtgggt caggtcaaa 780
 gtacatggtg atctgtggc cattgtggc agagatggcc agctatcaat tgtgaacaat 840
 gacactggtg aaatcgtca tactctaaa acattggata atgtcgacga cattgcagaa 900

ctctcaattg aggcattgag ttggtgtgaa agcaaaaata ttaacctctt ggcagtgggt 960
 ttggtttctg gtgacgttta ttatttgata ctgagcaatg gagattgaga aagaactga 1020
 aagttgacga tgccatcacc aaattacaat ttgttggcga aacccccatt ttggtgggaa 1080
 atagtatgga tggtaaaatt acaaatggga acctagaact ggtgaaaaat gtttgcctgt 1140
 gtgggaacaa acatgggagt attggacttt gctattttag atggaggtaa aaagtgggt 1200
 actgctgggtg atgaagggtg tgcattggtc ttgtacatg aatag 1245

<210> 101

<211> 1231

<212> DNA

<213> Homo sapiens

<300>

<301> Almendral, Huebsch, Blundell, MacDonald-Bravo and Bravo

<302> Cloning and sequence of the human nuclear protein cyclin: Homology with DNA-binding protein

<303> Proc. Natl. Acad. Sci. U.S.A.

<304> 84

<305> 6

<306> 1575-1579

<307> 1987

<308> M15796

<309> 1993-04-27

<400> 101

aggtctcagc cgtctctgcg gacgttcgcc cgctcgtct gaggtcctg aagccgaaac 60

tagctagact ttctccttc ccgcctgcct gtagcggcgt tgttgccact ccgccaccat 120

gttcgaggcg cgcttggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180

cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240

ctcgtccac gtctcttgg tgcagctcac cctgcggctt gagggcttcg acacctaccg 300

ctgcgaccgc aacctggcca tgggcgtgaa cctcaccagt atgtccaaa tactaaaatg 360

cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420

agtatttgaa gcaccaaacc aggagaaagt ttgagactat gaaatgaagt tgatggattt 480

agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540

tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa ctgggaaatg gaaacattaa 660
attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagticaa ctaacttttg cactgaggta cctgaacttc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc ctgtgttag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaatca agaaaataaa actaagctct ttgagaactg ctcttaagat 960
gccagcatat actgaagtct tttctgtcac caaatttga cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctatttttt tctctattct ctccaattg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta ttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagtttaag aagtgtttt 1200
gaatttaaat aaagttactt gaatttcaaa c 1231

<210> 102

<211> 840

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: BAA77792.1

<400> 102

atgtctgctc ccactatgag atccaccica atattgacag agcatttggg atatccgccc 60
atctcgcttg ttgatgatat cattaatgct gtaaatgaaa ttatgtacaa gtgcactgct 120
gccatggaaa aatatctgct atccaagagc aaaatcggcg aggaagatta tggagaagag 180
atcaaaagtg gagttgctaa gttggaatca ctttggaaa actccgtgga taagaatttt 240
gacaaactag aactatatgt tttaggaac gtccttcgaa tccctgaaga gtatttgac 300
gccaatgttt ttagattgga gaaccaaag gatctggta tttagatga gaatgagttg 360
aagaaaagtg aggagaaact tcgagagaaa gtgaacgacg tggagttagc gttcaaaaag 420

aatgaaatgc tattgaaaag agttacaaaa gtgaaaagac tgtgtttac gataagagga 480
 ttcaacaaaa agctaaacga gttactgaaa tgcaaagacg atgtacaatt gcagaaaatt 540
 ttggagtcgt taaaacctat agatgacaca atgactctac tgactgattc attacgtaaa 600
 ctatatgttg atagtgaag taccagtta acagaggagg tagaggcact actgcagaga 660
 ttgaagacca acgggaagca aaataataag gatticagaa cacgatatat cgaataaagg 720
 acgaataatg tcctacgaaa atgggggcta ctagggtgata aagaggacga aaaacagtct 780
 gccaaagccgg atgcgaggac gcaagcaggg gatatagtta gtatagatat tgaagagcct 840

<210> 103

<211> 945

<212> DNA

<213> Candida albicans

<400> 103

atgtcagata aaactttaga cgaacgtact acagcaattc ttactgaaca tttagaattt 60
 gctcccttga cacttattga tgacgtgac aatgcggtga atgaaatcat gtacaaggga 120
 acaacagcta ttgaaacata tttaaagaa caaaaacaat taatgaaaaa tgggatattt 180
 accaaagtta ctgaagatga aatagaaatt ggtatgggga aattagaatc attattagaa 240
 tcgactatag ataagaattt tgataaattt gaattatatt gttaagaaa tattttcaat 300
 atacctaaag atctaatacc atatatacag ttaagccatc aacaaggaat tgaatttaa 360
 agtgataatg ttgaacaaaa acgtgaattt gatcaacaaa ttaaaaattt acaattgaaa 420
 atcatgcaag aattacaact tcgaaaaatc ttaaattac aacttgtaa agtccaaaaa 480
 ttaattaaag tattaatagc cattgataat gatticaaga aaatagattt tgctagtgg 540
 ggtgggtgga atgaagaatc aataagaatt ttgaaaaatc ttcaacctat tgatgaaca 600
 ttatatttt taattagta aattaaaaat ctaataaatc aaattgaaca attatcaaat 660
 aaagttaata ccaatttgaa aactcaaaaa ttataccca atttgcgtga taaattcatt 720
 gatggtagaa catttagagt ttacaacaa acgggggatt ggaaagattt ggaaaaaat 780
 gatatcaaga ttctggtgca gggaaatgac aataataata ataataataa taataataat 840

aataccttaa cagattfaca aaatcaagac gacattgafa tgataatacc agaacaagac 900

gatatagatg tggatgcaat aaagaatata aatgctcaaa tttaa 945

<210> 104

<211> 5718

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: AAB64747.1

<400> 104

atgtcacatt ccggagctgc catthttgag aaagtttctg ggataattgc cataaatgag 60

gatgtttcac ccgcagaatt gacatggagg tctacggacg gtgacaaggt tcacacagtt 120

gtcttatcca ctattgacaa gttacaagct acccctgctt ccagtgaaaa aatgatgttg 180

aggctaatcg ggaaagtga tgagtcaaaa aagagaaaag acaacgaagg aaatgagggt 240

gtgcccacac cgcaacgtca tatgttttcg ttaacaata gaacagttat ggataataac 300

aagatgaccc ttcaacaaat catctcacgg tataaagatg cagatatcta cgaagaaaag 360

agaagaagag aggagtctgc gcaacacaca gaaacaccaa tgagctcttc ttctgttact 420

gcagggactc ccacaccaca tctcgatata ccacaattga ataatggggc tccgttgatt 480

aatacagcca aactagatga ttctctctct aaagaaaaat tgtgaccaa tttaaagcta 540

cagcaatctt tactgaaagg aaacaaagtt ctaatgaagg ttctcagga aacagtcatt 600

aacgccgggt tgcctccalc tgaattttgg tcaactagaa ttccgttatt gagggctttt 660

gccttatcta ctctcaaaa agttgggcct tacaacgttt tgtcaactat caagccgggtg 720

gcttcacggtg aaaacaaagt caatgttaat ttgtcaagag aaaaaatttt gaatattttt 780

gagaactatc caattgtaaa gaaagcttac actgataatg tgcccaaaaa ttcaaagaa 840

ccagagttct gggcaaggtt ctctctctcg aagttattca gaaaallaag ggggtgaaaag 900

atcatgcaaa atgatagagg tgacgtaac attgacaggt acttgacatt ggatcaagag 960

ttcgacagaa aagatgatga catgctattg calcctgtga aaaaaattat agatttagat 1020

ggtaacatac aggacgaccc agttgtacga ggcaacaggc ccgacttcac tatgcagcca 1080
gggtgtggata ttaatggtaa tagcgaagggt accgtggaca tcttaaagggt tatgaataga 1140
ttgagtgaaa aaatgattat ggctttgaag aatgagtatt caaggacaaa tctacagaac 1200
aaatctaata ttacaaacga tgaggaagat gaagataatg atgaaagaaa tgaactgaaa 1260
atcgatgact taaacgaaag ctacaagaca aactatgcaa tcatacatct gaaaaggaaac 1320
gcacatgaaa agacaaccga caacgatgcg aaaagctcgg cagactcgat aaagaatgca 1380
gatttgaagg ttictaatca acaaatgtta caacagttgt cattgggtcat ggataattta 1440
attaataagc tagacttgaa ccaagtagtt cctaacaacg aagtcagcaa caagatcaat 1500
aaaagagtca taactgcaat caagaltaac gccaaacagg ctaagcataa caatgttaat 1560
tcagcactcg gctcttttgt cgacaacact tctcaagcaa atgaattaga ggtgaaaagt 1620
accctaccaa tagacctatt agaaagttgt agaattgtac acacaacgtg ctgtgaattt 1680
ctaaagcact ttatattca ttctcagagc ggtgaacaaa agcaagccag taccgtcaaa 1740
aaactttata atcatttgaa ggactgtatt gaaaagctga atgagctatt tcaagacgtc 1800
cttaatgggt atgggtgaatc tatgtcaaac acatgtaccg cctatttgaa gccagttttg 1860
aactccatta ctttggttac tcataagtac gatgagtact tcaacgaata taacaacaat 1920
tcgaactagg atgtttcacc cgcagaattg acatggaggt ctacggacgg tgacaaggtt 1980
cacacagttg tttatccac tattgacaag ttacaagcta cccctgcttc cagtgaaaaa 2040
atgatgttga ggctaatacgg gaaagtggat gagtcaaaaa agagaaaaga caacgaagga 2100
aatgaggttg tgcccaaacc gcaacgtcat atgttttctt ttaacaatag aacagttatg 2160
gataatatca agatgaccct tcaacaaatc atctcacggt ataaagatgc agatatctac 2220
gaagaaaaga gaagaagaga ggagtctgcg caacacacag aaacaccaat gagctcttct 2280
tctgttactg cagggactcc cacaccacat ctcgatacac cacaattgaa taatggggct 2340
ccgttgatta atacagccaa actagatgat tctctctcta aagaaaaatt gttgaccaat 2400
ttaagcttac agcaatcttt actgaaagga aacaaagttc taatgaaggt ttctcaggaa 2460
acagtcatta acgccgggtt gcctccatct gaattttgtt caactagaat tccgttattg 2520

agggcctttg ccttatctac ttctcaaaaa gttgggcctt acaacgtttt gtcaactatc 2580
aagccgggtgg cttcatcgga aaacaaagtc aatgttaatt tgcaagaga aaaaattttg 2640
aatatttttg agaactatcc aattgtaaag aaagcttaca ctgataatgt gcccaaaaat 2700
ttcaaagaac cagagttctg ggcaagggtc ttctcttcga agttatlcag aaaattaagg 2760
ggfgaaaaga tcatgcaaaa tgatagaggt gacgtaatca ttgacaggtc ctgacattg 2820
gatcaagagt tcgacagaaa agatgatgac atgctattgc atcctgtgaa aaaaattata 2880
gatttagatg gtaacataca ggacgacca gttgtacgag gcaacaggcc cgacttcact 2940
atgcagccag gtgtggatat taatggtaat agcgtatgga ccgtggacat cttaaagggt 3000
atgaatagat tgagtcaaaa aatgattatg gcttgaaga atgagtattc aaggacaaat 3060
ctacagaaca aatctaatac tacaacgat gaggaagatg aagataatga tgaagaaat 3120
gaactgaaaa tcgatgactt aaacgaaagc tacaagacaa actatgcaat catacatctg 3180
aaaaggaacg cacatgaaaa gacaaccgac aacgatgcga aaagctcggc agactcgata 3240
aagaatgcag atttgaagggt ttctaataca caaatgttac aacagttgtc attggtcatg 3300
gataatttaa ttaataagct agacttgaac caagtagttc ctaacaacga agtcagcaac 3360
aagatcaata aaagagtcac aactgcaatc aagattaacg ccaaacaggc taagcataac 3420
aatgttaatt cagcactcgg ctcttttgc gacaacactt ctcaagcaaa tgaattagag 3480
gtgaaaagta ccctaccaat agacctatta gaaagttgta gaatgctaca cacaacgtgc 3540
tgtgaatttc taaagcactt ttatattcat ttccagagcg gtgaacaaaa gcaagccagt 3600
accgtcaaaa aactttataa tcatttgaag gactgtattg aaaagctgaa tgagctattt 3660
caagacgtcc ttaatggga tggatgaatc atgtcaaca catgtaccgc ctatttgaag 3720
ccagtttga actccattac ttgggtact cataagtacg atgagtactt caacgaatat 3780
aacaacaatt cgaactagat ggaactagag cccactcttt ttgtataat agaggcattg 3840
gctcctcaat tattgtcgca gactcattg cagacattg tatctgatgt agtcaattta 3900
ctgcgatcat ccaccaaatc ggcaactcaa ttaggccctt taattgattt ttacaaatta 3960
caatcactag attgcctga aacaacaatt atgtggcata aaattgagaa atttctcgat 4020

gctttatttg gaatccagaa caccgatgat atggtaaagt acctctctgt ctttcaatct 4080
ttgcttccat caaattacag agcaaaaatt gtccaaaaat catctgggct caatatggag 4140
aaccttgcta accatgaaca ttacttagc ccagtgcggg ctccaagtat atalacagaa 4200
gcttcatttg aaaacatgga cggatttct gaaagaaggt ccatggatc ttcgcctaata 4260
cgttacgttc cctctcaac ctacagtct gttactttga gacagttgc aaatccttat 4320
tatgtgaaca ctataccga ggaagatc ctaaaatag tatcatatac attattagct 4380
acgacatcgg cactattcc gttgatcat gagcaaatc aaatccgtc taagataccc 4440
aatttgaga gtggactttt acatttaata ttgaagcgg gttattata tcaaagttg 4500
gggtataaag tggagaagtt taggatgttg aatatatctc caatgaaaa agcattgatt 4560
atagaaattt cagaagaatt acaaaactac acagcatttg tgaacaatct ggtctctca 4620
gggacagtag tgcattgaa atcggtatat cgtgaaatat atgaaatat aataaggctt 4680
cgaatatact glaggttac agaacacctt gaagaattga gcggagatac attcttgatt 4740
gaattaaata tttcaaact ccacggagat ctactataa gaaaaatagc aacgaatttg 4800
tttaattcaa tgatttctct ttattatgag tatttaatga attggtgac taaaggctca 4860
ctccgagcta cttatggaga attcttcatt gctgaaaaca ctgatacaaa tggtagagac 4920
gatgatttta ttaccacat tcctatagag ttcaaccaag aaagagttcc ggccttcata 4980
ccgaaagagt tggcatataa aatattcatg atcggcaaat cgtatctct cctagaaaag 5040
tactgtaaag aggttcaatg gacaaacgaa ttttctaaaa agtatcatgt cctgtaccag 5100
agcaattctt atcgggggaat atcaacgaac tttttgaaa ttataaatga tcaatattct 5160
gaaattgtta atcactacta tcaaattcta aatcagaagt ttcatcacag agacgtgta 5220
tttgcgttaa agaatttct tctcatgggt aaatctgatt ttatggatgc tottatagaa 5280
aaggccaatg atattctgc gacaccatcg gattcattgc caaattataa gtaacaagg 5340
gtttacagg aagccgtgca gctttctcc ttaagacatt taatgaatag tccccgtaat 5400
agttctgtca ttaatggatt ggatgcgagg gtactcgatc ttggacatgg atccgtgggt 5460
tgggatgttt ttactttaga ttacatccic tacccccctt tgagtttatt attaaacgta 5520

aatcgctctt ttggcaggaa agagtatcta cgaattttca attttttatg gagatttaa 5580
 aagaacaatt atttctatca aaaggaaatg ttgaagagta atgatataat cagatcattc 5640
 aagaaaatca gaggttacaa cccgctcatc cgtgatatta tcaataaact ttctagaatc 5700
 agtatactta gaactcaa 5718

<210> 105
 <211> 2082
 <212> DNA
 <213> Candida albicans

<400> 105
 atggatataa ttgaggtgc atgttcagtt gataaaattg gggggatggt gtatattaga 60
 gaagatttag caccgctgat gtiggaatgg aaaccaattg atgaacaaga agaagataga 120
 gcaatttcaa tccattgaa ttctttaact acattacaaa gtaccaaaga aacctaccg 180
 aaaatgatac taaaaattgt atacaaacta acatctgggc cacctaatac aaatgcagat 240
 ggaactgaca atgggtgggtg tgggtgggtg gaacaaaaat catttaaatt gacatttact 300
 aatagaccaa ccatgaacac tattaaagat tctctacaaa caattgttgc tagatcaaga 360
 actaagggtt tgaaggtagc agtactcaa ctccagctcc agcaccagct tcaacattg 420
 gggtcagcac cacaagctga ttctaccaga gattcgacat catcatcaac accaatacca 480
 cctacaacat ctggaacttc tactagtcca tcattattat cattagcagc atcacaatca 540
 ttatctgatg caaatttatt gaaaaattc gaactacagc aaaaactttt attagaagat 600
 cgtcaattac gtgatgtttt cactaaatca gtcattgcaat ttaaattatc tctcaagta 660
 ttttggtcat caagattaaa tcaattacga acatttgctt tgacaatatc tcaacataaa 720
 ggtccatata atgtattgag tacaattaaa ccggtggcca ctctgataa tcaagtgaat 780
 gttaatgltt cgcgtgatac cattaatgaa atatttacta ttaccccat cataaangaaa 840
 gcatttgatg atttggttcc taacaagttt aatgaaggag aattttgggc gagattttc 900
 aattctaaat tgtttagacg cttaagaggt gataaaatca gtattagtaa tagtcgagga 960
 gatgttgtat tggacaaata ttgtatata gatcaaaact atcaagaaaa attacaaaaa 1020

tcattctactt tggaaaacaa cggttctggt ggtggtggtg gtggcgctgg tgggtgtagt 1080
ggtaattcag aacaaggaat acaaacattg gaattctccac atgttaaaaa atttcttgat 1140
ttgatgggaa atcaacaaga taattcacia aaattgggga atagaccaga ttftactatg 1200
agatatgatg aagacaccaa ttagatgatg gataataaaa aacctacttt aggaaatgaa 1260
aatgaaatga ttatattgat gaaaaatag aatcgattat cgtcgaaaat gatgagtatg 1320
agttctacta atggaccaga gaaaccttca gaaactacia ttgatggatt atctgctgct 1380
gaattgaatg aatatgaaga agaattagat ttgatgatt taaatgattc agaaaattta 1440
caatatataa aattaaacat taatactgat attgccaagg gaacaaaact tgattcatat 1500
gaaggatcaa atactaataa caagatttct caagatgaat tacataaata ttacaatct 1560
caaaacttcc aaggacaaat agaattaaca gaaacttata ctgtgaaaag tgaagaaatt 1620
gaaaaaacct ccatggaaat agccatgctt attaaacaaa atttccgaac atttaaatta 1680
attaataaag aaaatgatat tgcggggaca aacattgttc ctaattcatt aatacaagaa 1740
atcattactt ataataattac gatagttgaa tttttatctc atttttgga gattttttta 1800
catgggaata atcctggtca attaaagaaa atttcacca gtttgaaaaa ttgtcaatct 1860
ggtttaatag aattagaaaa taaagcgatt gatcaattca aatctatgga tatattacaa 1920
aaaaatcaaa aattacaaga taaagtttta aaagattttg catcatgtct tcaacccatg 1980
aaaatagcat tagataaagc atgtaatgaa tatgttgaag cagtaaagaa agctaaacct 2040
gaattaaatg aaaatggtaa acgtcctcta ccagaggagt ga 2082

<210> 106

<211> 466

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: W19128

<220>

<221> misc_feature

<222> (1)..(466)

<223> n is unknown

<400> 106

ngncacattc tgcnnagaga tccttgacc ctgnatncag ccgatccctg tgaaaataat 60

ggganiggaa aaaacgtgtc cagnattcct tctctgtcat gtngtgggna acattttctg 120

catatttcat tttnactgct ggataggctc tnaatatgga ctcaatgata ncagaagtta 180

aattatatct tagaccgtta nagccatcag ttgggggccg gacatcagcn agaaatgcag 240

caganatgcc aanatcctgc ttatgattgg atntggaaga actatctgtt gcattcacat 300

ttaaaccgat tggncagaa ttctcagca ctgacactt gactcacgaa caaggtcttt 360

ataaagctga aacaaaacca ggatcttctt gcagcattct gticattccc tccagtcct 420

gnatttgct tccncttgaa ttgggcagc anctgctgan gaaggt 466

<210> 107

<211> 2460

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> misc_feature

<223> GENBANK Accession Number:CAA96007.1

<400> 107

atggaaactag agcccactct ttttggtata atagaggcat tggctcctca attattgtcg 60

cagagtcatt tgcagacatt tgtatctgat gtagtcaatt tactgcgac atccaccaa 120

tcggcaactc aattaggccc ttaattgat tttacaaat tacaatcact agattcgct 180

gaaacaacaa ttatgtggca taaatigag aaatttctcg atgctttatt tggaatccag 240

aacaccgatg atatggtaaa gtacctctct gtcttcaat ctttgctcc atcaaatlac 300

agagcaaaaa ttgtccaaaa atcatctggg ctcaatatgg agaacctgc taacctgaa 360

catttactta gccagtgcg ggctccaagt atatatacag aagcttcatt tgaaaacatg 420

gaccgatttt ctgaaagaag gtccatggta tcttcgcta atogtlacgt tccctctca 480

acctacagtt ctgttacttt gagacagttg tcaaatcctt attatgtgaa cactataccc 540
 gaggaagata tcctaaaata cgtatcatat acattattag ctacgacatc ggcactattt 600
 ccgtttgac atgagcaaat acaaattccg tctaagatac ccaattttga gaggggactt 660
 ttacatttaa tatttgaagc gggtttatta tatcaaagft tgggttataa agtgagagaag 720
 tttaggatgt tgaatatatc tccaatgaaa aaagcattga ttatagaaat ttcagaagaa 780
 ttacaaaact acacagcatt tgtgaacaat ctggctctct caggacagc agtgcattg 840
 aaatcggtat atcgtgaaat atatgaaaat ataataaggc ttcgaatata ctgtagggtt 900
 acagaacacc ttgaagaatt gagcggagat acattcttga ttgaattaaa tattttcaaa 960
 tcccacggag atcttactat aagaaaaata gcaacgaatt tgtttaattc aatgatttct 1020
 ctttattatg agtatttaat gaattgggtg actaaaggc tactccgagc tacttatgga 1080
 gaattcttca ttgctgaaaa cactgataca aatggtacag acgatgattt tatttaccac 1140
 attcctatag agttcaacca agaaagagtt ccggccctca taccgaaaga gttggcatat 1200
 aaaatattca tgatcggcaa atcgtatatc ttcctagaaa agtactgtaa agaggltcaa 1260
 tggacaaacg aattttctaa aaagtatcat gtctgtacc agagcaattc ttatcgggga 1320
 atatcaacga acttttttga aattataaat gatcaatatt ctgaaattgt taatcatact 1380
 aatcaaattc taaatcagaa glttcattac agagacgtgg tatttgcgtt aaagaatatt 1440
 ctctcatgg gtaaacttga tttatggat gctcttatag aaaaggccaa tgatattctc 1500
 gcgacaccat cggattcatt gccaaattat aagttaacaa gggltttaca ggaagccgtg 1560
 cagcttctt ccttaagaca ttaaatgaat agtccccgta atagttctgt cattaatgga 1620
 ttggatgca gggctactga tcttgacat ggatccgtgg gtgggatgt tttacttta 1680
 gattacatcc tctaccccc tttgagtta gtattaaacg taaatcgtcc tttggcagg 1740
 aaagagtac tacgaatttt caatttttga tggagattta aaaagaacaa ttatttctat 1800
 caaaaggaaa tgttgaagag taatgatata atcagatcat tcaagaaaat cagaggttac 1860
 aacccgtca tccgtgatat tatcaataaa ctttctagaa tcagtatact tagaactcaa 1920
 ttccagcaat tcaactcgaa gatggaaatct tattatttga actgcattat agaggaaaat 1980

tttaaagaaa tgacccggaa actgcaacgc acagagaata aaagccaaaa ccaattcgac 2040
 ttaattagat taaataatgg caccatagaa ttaaatggga tttaacccc aaaagctgaa 2100
 gtactaacia agtcttcaag cagtaaacc caaaaacacg caatcgaaaa gacgctgaat 2160
 attgatgaat tagaaagtgt acataacacg ttcttgacga atattcttc tcataagctt 2220
 ttgcaacta acacaagtga aataagcgtt ggtgattatt ctgggcaacc ataccaact 2280
 tcattggtt tacttttaa ttgggttac gagttcgca aagttattg taattigaac 2340
 gacattgat acgaaatctt cattaaatg aatcacaatg atcacgaagc atctaacgga 2400
 ttattgggaa aatttaatac gaatttaaag gaaattgta gccagtataa aaattttaaa 2460

<210> 108

<211> 1921

<212> DNA

<213> Candida albicans

<400> 108

atggcgtaa acaaggtaca actaataaaa ttatattcca atcgattagt gaaatcattg 60
 gttcctgtgg aattcgggtg ggcattcatc caaagtataa tcaatgactt gcaaaccact 120
 ttactaaata ctcttctga agaacaaaat ttgtcaataa ttataacaa gcttaaaatg 180
 caatttttaa gtaacaattt aaaaaatgaa tgggtcgaat ttcaaacat tgtaattica 240
 ttaagcaaat tcaagtcgtt ggatcagatt tgaattatc tcgatttct tgatgettta 300
 agagatgaga aaccagaaga tatattatca acatcaacag cgagcttgc tcccggtaag 360
 caaaatgtaa tgatcaatac ggtaaacaca gcattgacgt tatcacagtt aatcgagcct 420
 tactatgata ctttatcgga acaaaccatt ttaacctact taccctacac gatgttaggt 480
 ctggattcca aaataatcac cttcagcaat aattalacac gattggagat accgaaagat 540
 ataaacaaca gtttcagctc attgctacgc gaagttttg agtttgcaat actatataaa 600
 caattggcaa ttgttggtga taggtataaa ggaacttag tactggccat aaagacagct 660
 tacatagcaa tactagagc tcaattgaac aaatatgtga atgatattaa caatatcttc 720
 aataataaac cgaattccat attagttgtt tacaattcca tttccctg gatatttata 780

ctacgatttt tatalcgagt ctcaaacaga cttaacagat tagatggta tgaatttctc 840
 acatttattt atagtttcac caaccatgga gatcccaaaa tacggggcat tgctgtgact 900
 gcattcaccg aggttgctca accgtattat aatattgtgg aacattggat agtgaagg 960
 gagtgattg ataataataa cgagttttc attatcttg atcaagagca gaatgaattc 1020
 aatagtataa ttaattatt gcccaaaaa ataccagcct ttattaaac gagtgataaa 1080
 atatttcaga ttgggaaaac attaatTTTT cttaataaat attgtcgtga actaaatgg 1140
 gtaaatcagt ataactgaa atattctgt atattgtca ataaccatca aggcttggca 1200
 tccatgacaa caaatgaaat gatcaaatg attgatctgc aatataatga gatattaacg 1260
 ttctcaccc aaataatcca aggaacaat aaattgttta ctcatgttta taatttcaag 1320
 aggtttatt ttatggagac caatgattt attgatgca ttatggtgaa agggaaggac 1380
 gttttaatg agtctctgt taatatttca tcaacctatc ttaggaaagt cttacaagac 1440
 gctatacaaa ttctgcggt gaaaaattt gagtatgtg acagactcga ttcgagagtg 1500
 ttgaatcccc aacacgggaa ttgggctgg gaatcgttca ccattgaata caaatgat 1560
 gatcttccca tgagttattt atttgaaggc caccaacatt tacaatttt aaaaatgtt 1620
 callttctat ggaaattaag acaattgaat aatttattaa attggcattt tgagatgtt 1680
 aatgagtga atcataatgt ggtgacgaag ttgtcaagca gaaatagaag accttggcg 1740
 aaatcattga gcataatcac cagtataaga ttccatttta cccagtttct taacgaacta 1800
 atagcttatt tgtcttatga tgttattgaa gaaaatttc gacagactgt atatttttag 1860
 ggcagattta aagaacgatg gcgatgaaga gcttttctta ttgagcaaat cgctccgta 1920

a

1921

<210> 109

<211> 3829

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: AF042378.1

<400> 109

caggaagggc gcgggccgcg gtccctgcgc gtgcggcggc agtggcggct ctgcccgac 60
 caccgtgcac ggctccgggc gaggatggcg accccggacc agaagtcgcc gaacgttctg 120
 ctgcagaacc tgtctgcag gatcctgggc aggagcgaag ctgatgtagc ccagcagttc 180
 cagtatgtcg tgcgggtgat tggcagcaac ttcgccccaa ctgttgaaag agatgaattt 240
 ttagtagctg aaaaaatcaa gaaagagctt attcgacaac gaagagaagc agatgtctga 300
 ttatttcag aactccacag aaaacttcac tcacagggag ttttgaaaaa taaatggta 360
 atactctacc tottctgag cctcagttag gaccacgca ggcagccaag caaggtttct 420
 agctatgcta cgttatttc tcaggcctta ccaagagatg cccactcaac cccttactac 480
 tatgccaggc ctgagacct tcccctgagc taccaagatc ggagtgccca gtcagcccag 540
 agtccggca gcgtgggcag cagtggcatc agcagcattg gcctgtgtgc cctcagtggc 600
 cccgcgcctg cgccacaatc tctctccca ggacagtcta atcaagctcc aggagtagga 660
 gattgccttc gacagcagtt ggggtcacga ctgcgatgga cttaactgc aaatcagcct 720
 tcttcacaag cactaccctc aaaagggtgc ccagtgctg tgtctcgaa catgacaagg 780
 tccaggagag aaggggatac ggggtgtact atggaaatta cagaagcagc tctggttaagg 840
 gacattttgt acgtcttca gggcatagat ggcaaaaaca tcaaatgaa caacactgaa 900
 aatgttaca aagtagaagg aaaggcaaat ctaagtaggt cttgagaga cacagcagtc 960
 aggctttctg agttgggatg gttgcataat aaatcagaa gatacacgga ccagaggagc 1020
 ctggaccgct cattcggact cgtcgggcag agcttttgig ctgccttgca ccaggaactc 1080
 agagaatact atcgattgct ctctgttta cattctcagc tacaactaga ggatgaccag 1140
 ggtgtgaatt tgggacttga gagtagtta acactcggc gcctcctggt ttggacctat 1200
 gatcccaaaa tacgactgaa gaccttgcg gcctagtgg accactgcca aggaaggaaa 1260
 ggaggtgagc tggcctcagc tgtccacgcc tacacaaaaa caggagaccc gtacatcgcg 1320
 tctctggtgc agcacatcct cagcctcgtg tctatcctg tttgagctt cctgtaccgc 1380
 tggatatatg atggggagct tgaggacact taccacgaat ttttgtagc atcagatcca 1440

acagttaaaa cagatcgact gtggcacgac aagtatatt tgaggaaatc gatgattcct 1500
 tcgtttatga cgatggatca gtctaggaag gtccttttga taggaaaatc aataaattc 1560
 ttgaccaag ttgtcatga tcagactccc actacaaaga tgatagctgt gaccaagtct 1620
 gcagagtcac cccaggacgc tgcagacctt ttcacagact tggaaaatgc atttcagggg 1680
 aagattgatg ctgcttattt tgagaccagc aaataacctgt tggatgttct caataaaaag 1740
 tacagcttgc tggaccacat gcaggcaatg aggcgggtacc tgcttcttgg tcaaggagac 1800
 ttataaggc acttaattga ctgtctaaaa ccagaacttg tccgtccagc tacgactttg 1860
 tatcagcata acttgactgg aattctagaa accgctgtca gagccaccaa cgacagttt 1920
 gacagtcctg agatcctgcg aaggctggac gtgcggctgc tggaggtctc tccaggtgac 1980
 actggatggg atgtctcag cctcgattat catgttgacg gaccaattgc aactgtgtt 2040
 actcgagaat gtatgagcca ctacctaaga gtatttaact tctctggag ggcgaagcgg 2100
 atggaatata tcttactga catacggaag ggacacatgt gcaatgcaa gctcctgaga 2160
 aacatgccag agtctccgg ggtgctgcac cagtgtcaca ttitggcctc tgagatggtc 2220
 catttcatic atcagatgca gtattacatc acatttgagg tgcttgaat ttcttgggat 2280
 gagctttgga acaaagtcca gcaggcccag gatttggatc acatcattgc tgcacacgag 2340
 gtgttcttag acaccatcat ctcccgtgc ctgctggaca gtgactccag ggcactttta 2400
 aatcaactta gagctgtgtt tgatcaaatt attgaacttc agaattgtca agatgcaata 2460
 tacagagctg ctctggaaga attgcagaga cgattacagt ttgaagagaa aaagaaacag 2520
 cgtgaaattg agggccagtg gggagtgacg gcagcagagg aagaggagga aaataagagg 2580
 attggagaat ttaagaatc tatacaaaaa atgtgctcac agttgcgaat attgacccat 2640
 ttctaccagg gtatcgtgca gcagttttg gtgtactga cgaccagctc tgacgagagt 2700
 cttcggtttc ttgcttcag gctggacttc aacgagcatt acaaagccag ggagcccagg 2760
 ctccgtgtgt ctctgggtac cagggggcgg cgcagctccc acacgtgaag ctgcggtcc 2820
 tccaggggag ctgcgggiga tgtcgttgc actgctagac acgaaattcc cattgacgtc 2880
 ctgcaggaac tgcattgctg aggtgtcctg cccttccgcc cagagtgcg ccatgtttca 2940

gcggagcggc gtgtgggaga agccacgtcg tgttcacat gtcggagtcg aatgcatttg 3000
taaatcccta agtcaagtag gctggctgca ctgtcacat ttgtctctaa aagtcttcat 3060
cgctaaaaga taccataatt tgcagaggct tcttaagctt tctatgtat aatttatatt 3120
tgtcacttta aaaaatccat tctttttaga aaaaattagg gtgataggat attcattagt 3180
taagatggta acgtcattgc tatttttta acatcctctt tagaggtaat tttgttaac 3240
ataacaaaa attaaattga aacaaaatgt cccaactaag aaaatatata gagcatttta 3300
tttttttta gtgttgtaaa atattaacct ctgtgagatc cttgtatct taatgcatta 3360
cctttacaca tatttattct tattttctct ccttcagag ttacattti tatatttaat 3420
ttactatttc agatttttaa aatagtatag aaaaaagtag gagtgataga gaacaaaaat 3480
actcttatac agtgcaaccc aaataccgag aatgcacag ctaaagcagc gtgtaaatag 3540
gagtgatgag aaagttaatg gagtatttta tttcaaagt tctgataag caltggaag 3600
aaatgcacat ggataatgaa gatttccttt ttcttgcct atttttcat tgtaaatatt 3660
tatatactac tgaccaagat gtgggggtgg gggggattgt ttttgtaaa aatgtcatta 3720
tcaggtcaca taaatctgcc ttatgttgc ataagtgaag atttagaaa taaaagcaa 3780
ttatcttca aaaaaatgg aataaattgc tttctacat aaaaaaaaaa 3829

<210> 110

<211> 1560

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number:AAB64735.1

<400> 110

atggaaaaat cactagcgga tcaaatctc gatacgcca ttaaccggt caataaagac 60

ttcgatattg aagatgagga aaatgcatct tatttcaac acaatgaaaa aaatggagaa 120

agtgatttaa gcgactatgg aaatagcaac acagaagaaa ccaagaaggc gcactatttg 180

gagggtgaaa agtctaagtt aagagcagaa aaaggtttag aactaaacga tccaaaatat 240

acaggtgtta aaggttcaag acaagcatta tatgaagaag ttccgagaa tgaggacgaa 300
 gaagaagaag aagaagagga agaagaaaa gaggaagatg ctcttcatt caggacagat 360
 tctgaagatg aagaagtaga gattgatgaa gaagaatcag acgcggacgg cgggtgaaacg 420
 gaggaggctc aacagaaaag gcatgcacta tcgaaactaa ttcaacaaga gactaaacaa 480
 gctattaaca aactgtctca atcagttcaa agagatgctt cgaagggtta ttccatttta 540
 caacagacaa aattatttga caacatcatt gatitgagaa taaaactaca aaaagctgta 600
 attgcagcaa ataagctccc attaactaca ggtcctggg aagaggctaa aatggatgat 660
 tcagaggaaa caaagcgttt gctgaaggaa aacgaaaaac tgttcaataa ttattcaat 720
 cgggtgataa attcagaat aaaattccaa ctggcgatc atactactca aatgaagag 780
 gtggcgaagc ataaattgtc caaaaaaaga tcttcaaag agctttacca agaaactaat 840
 agcttagact cagaactaaa agaglacagg actgccgtat taaacaagtg gtctacaaa 900
 gtttctctg catcaggtaa cgctgcttta tcatctaaca aattcaaagc tatcaactta 960
 cctgcagatg tacaagtcga aaaccaatta tccgatatgt cccgtttgat gaaaagaaca 1020
 aagltgaaca ggagaaacat aacgcctttg tatttccaaa aagactgtgc taatggcagg 1080
 ctaccagaat tgatttctcc cgttgtaaaa gatagtgtg atgacaatga gaattcggat 1140
 gatgggcttg atatcccgaa aaactatgac ccaagaagaa aggataacaa tgccattgac 1200
 attaccgaaa acccatatgt tttgatgac gaagatttt accgtgttt actaaacgat 1260
 ttaattgaca aaaagatttc caacgtcac aattctgaaa gtgcagcaat tacaatcacc 1320
 tcaactaatg ctggttcgaa caacaagcta aagaagaata tcgatactaa ggcttccaag 1380
 ggtaggaaat tgaactactic agttcaagat ccaattgcga attatgaagc ccccatcaca 1440
 tccggataca aatggtcaga cgaccaaac gatgaattct ttgcgggatt gttaggtaaa 1500
 cgagtgaact ttaatgaaaa tgaggatgag gaacaacatg ccagaataga aatgacgaa 1560

<210> 111

<211> 1596

<212> DNA

<213> Candida albicans

<400> 111

atgagcttct tcggcttaca ctttcaactt aattcattga cattgaacat ttcaaatatg 60
 gcaaaaaagt ctttatcaga gcaaatttct agtttatata caccaaagac tgattatgat 120
 attgaggatc atgatttaga tgtatctaaa gacaatggca ttttcagca tcatgacggt 180
 ggttctgaaa acgaatctga agacgaggat actggcttaa gaaatgagca ttatgttgaa 240
 tcttcaaat caaagttgag acaacagaat gaaggtgtga acttggggga aaaatcgtg 300
 ggcaatgtca caagcagaag caaattgtat gacgatgagg atgacaaca accaacagaa 360
 gctagctccg gagaggagtt agatgctgaa tcagcggag aagaagagga tgaagaatct 420
 gaagatgtag cagatgatga tgaagatgac caagagtcag atcgcagtag ctcaagtgat 480
 gcagagaatg acgaggacga gaacatttca cacaaaaggg aattattaaa acaattaatg 540
 agcaaagaga gaagtcacat cgtaacaga ttatccaat cagcaacaaa tgatgcatta 600
 aaaggttatt caatacaaca gcaaaacaaa acttttgaaa aaatcattga tgtgagggtg 660
 aaatttcaga aatcggtaac ttcaagtaat atgttaccta taaatacaag tacatattca 720
 gaaaccaaat ctgaagatag cgatgaatta gtgactaaag ccaagaaaca attgtatagt 780
 ttgttgatc atttattcac acttagaac gaactagacg aaagtacctc agtcaagacc 840
 cccaaaaaac gatcatttgc taaatttcg gaggttcat ctgctgcaga tgcacaattg 900
 aattcccgtc gtaaccaaatt attaaccaag tggtcagcta aagtgccaa ttcacccgtt 960
 agaaatgcc aagaatgctaa taaattcaaa actataaacc aatcttttga acaacaggtt 1020
 aacaacaact tgtctgacat ggatagatta atcaaaagaa caaaattgaa ccgaagaaac 1080
 gtaactccca ttggttatac caccaaagag gaggatgatc atgaaaatgg caataaaaac 1140
 aaatctatcg acgaggacga cgacgataat cccgaagata cttctgttcg taagaaaacc 1200
 caaggcttgg aaaatgatta tatatttgat gacgaagatt tctatagagt attgttgaat 1260
 gatttagtgc acaagaaagt gcaacaagt gatccaacat caggtataac tatcagttta 1320
 agagctgctc aaaagtccaa taaattgaaa aataatgttg atacaaaagc atctaaaggt 1380
 aggaaattga gatatcacgt gcaagaacca attgctaatt ttgaaacttc aagaggcagc 1440

tggagatgga atgatgaica aattgacgag ttttcgcat ctttattggg ccaaaaggtc 1500
 aatatgaatg agatagatga tgaacaagaa gaagaacaag agaatgatga taatgatatt 1560
 attccagagg ataacggaat ccagttgttt ggttaa 1596

<210> 112
 <211> 2444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Human GENBANK Accession Number: NM_000055

<400> 112
 agtaacagtt gattgttaca ttcagtaaca ctgaatgtca gtgcagtcca atttacaggc 60
 tggagcagca gctgcatcct gcatttcccc gaagtattac atgattttca ctcttgcaa 120
 actttaccat ctttgttgca gagaatcgga aatcaatatg catagcaaag tcacaatcat 180
 atgcatcaga ttctcttttt ggtttctttt gctctgcatg ctatttgga agtcacatac 240
 tgaagatgac atcataattg caacaaagaa tggaaaagtc agagggatga actlgacagt 300
 ttttgggtggc acggtaacag cctttcttgg aattccctat gcacagccac ctcttggtag 360
 acttcgattc aaaaagccac agtctctgac caagtgtgtc gatatttga atgccacaaa 420
 atatgcaa atcttctgtc agaacataga tcaaagtttt ccaggcttcc atggatcaga 480
 gatgtggaac ccaaacactg acctcagtga agactgttta tatctaaatg tatggattcc 540
 agcacctaaa ccaaaaaatg ccaactgtatt gatatggatt tatggtggtg gttttcaaac 600
 tggaaacatca tctttacatg ttatgatgg caagtttctg gctcgggttg aaagagttat 660
 ttagtgatca atgaactata ggggtgggtgc cctaggattc ttagctttgc caggaaatcc 720
 tgaggctcca gggaacatgg gttatttga tcaacagttg gctcttcagt gggttcaaaa 780
 aaatatagca gccttgggtg gaaatcctaa aagtgtlaact ctcttggag aaagtgcagg 840
 agcagcttca gtagccctgc atttgcttgc tcttgggaagc cattcattgt tcaccagagc 900
 cattctgcaa agtggatcct ttaatgctcc ttgggcggta acatctcttt atgaagctag 960

gaacagaacg ttgaacttag ctaaattgac tggltgctct agagagaatg agactgaaat 1020
 aatcaagtgt cttagaata aagatcccca agaaattctt ctgaatgaag catttgttgt 1080
 cccctatggg atccttttgt cagtaaaactt tgggccgacc gtggatgggt attttctcac 1140
 tgacatgccca gacataattac ttgaacttgg acaalltaaa aaaaccacaga ttttgggtggg 1200
 tgttaataaa gatgaaggga cagctttttt agtctatggt gctcctggct tcagcaaaga 1260
 taacaatagt atcataacta gaaaagaatt tcaggaaggt ttaaaaatat ttttccagg 1320
 agtgagttag ttggaaagg aatccatcct tttcattac acagactggg tagatgatca 1380
 gagacctgaa aactaccgtg aggccttggg tgatgttgtt ggggattata atttcatatg 1440
 ccctgccttg gagttcacca agaagtctc agaattggga aataatgcct ttttacta 1500
 tttgaacac cgatcctcca aactccgtg gccagaatgg atgggagtga tgcattggcta 1560
 tgaaattgaa ttgtctttg gtttacctt ggaaagaaga gataattaca caaaagccga 1620
 ggaaatttg agtagatcca tagtgaaacg gtgggcaaat ttgcaaaat atgggaatcc 1680
 aatgagact cagaacaata gcacaagctg gcctgtcttc aaaagcactg aacaaaaata 1740
 tctaaccttg aatacagagt caacaagaat aatgacgaaa ctactgtctc aacaatgtcg 1800
 attctggaca tcatittttc caaaagctt ggaaatgaca ggaaatattg atgaagcaga 1860
 atgggagtgg aaagcaggat tccatcgctg gaacaattac atgatggact ggaaaaatca 1920
 atttaacgat tactactaga agaaagaag ttgtgtgggt ctctaattaa tagatttacc 1980
 ctttatagaa catattttcc tttagatcaa ggcaaaaata tcaggagctt tttacacac 2040
 ctactaaaaa agttattatg tagctgaaac aaaaatgccca gaaggataat attgattcct 2100
 cacatcttta acttagtatt ttacctaga tticaaaacc caaatggcta gaacatgttt 2160
 aaltaaatt cacaatataa agttctacag ttaattatgt gcataataa acaatggcct 2220
 ggttcaattt ctttcttcc ttaataaatt taagttttt cccccaaaa ttatcagtgc 2280
 tctgctttta gtcacgtgta tttcattac cactcgtaaa aaggatatct ttttaaatga 2340
 attaaatatt gaaacactgt acaccatagt ttacaatatt atgttcccta attaaaataa 2400
 gaattgaatg tcaatatgag atattaaaat aagcacagaa aatc 2444

<210> 113
<211> 1200
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> GENBANK Accession Number: CAA90206.1

<400> 113
atggctacct tgcacttcgt tcctcagcac gaggaagaac aagtttactc catctctggg 60
aaggcactca agttaacaac cagtgcacgat atcaaaccat acctggaaga attggcagct 120
ttgaaaacct gtaccaaaatt agacctttca gggaatacaa tcggtactga agcttcggaa 180
gcattagcta aatgcacgc tgaaaataca caggtcaggg aatctttggt tgaagtaaat 240
tttgcctgact tatacacttc gaggttggtt gacgaagtcg ttgattcgtt gaagttttta 300
ttgcctgttc tgttgaaatg tcctcacttg gagattgtga acctttctga taatgcgttt 360
gggctaagaa caatcgagtt actagaagat tacattgcac atgccgtgaa tatcaaacat 420
ttgatcttaa gtaacaatgg tatgggccct ttgctggtg aaaggattgg taaggcccta 480
tttcatctcg ctcaaaaataa gaaagctgct tccaaaccat ttttgaaac ttttatctgt 540
ggtagaaata gattagagaa tggatccgca gtctacttag ctctgggttt gaaaagccac 600
tccgaagggt tgaagtcgt aaagctgtac caaatggta ttaggcctaa aggtgtcgcc 660
acgctaaltc attacggttt acagtacttg aaaaacttgg aaatcttga tctcaagac 720
aatactttca cgaaacatgc ttctttgalc ctgtctaagg ccttgcctac atggaaggat 780
agtttatttg aattgaattt gaacgactgt ctttgaaaa ctgctgggtc agatgaagtc 840
tttaaagtat tcaccgaagt taaattcccc aatttgcatt tcttgaaatt cgaatataat 900
gaaatggctc aagaaaccat tgaagtatcc ttctaccgg ctatggaaaa gggaaattta 960
cctgaattgg aaaagctaga aataaatggt aacagattag atgaagattc tgatgcttta 1020
gatttgctcc aaagcaaatt tgatgattta gaggttgacg atttgaaga ggtcgatagt 1080
gaagatgagg aaggcgagga cgaggaagac gaggacgagg atgaaaaact cgaagaaatt 1140

gaaacggaaa ggcttgaaaa ggaactgcta gaagtacaag tagatgatct tgctgaacgt 1200

<210> 114

<211> 1245

<212> DNA

<213> *Candida albicans*

<400> 114

atggcatcag tagaagtga attaggagt actccagaaa ccacttattc aatttcagga 60

aaacaactaa aatttgattc tgaatcggaat attgctccat atatcaagga attgacggaa 120

aaagaaaatg tcaaaaaagt tgattttca ggaaatacta ttggtattga agcatcaaaa 180

gcattaagtg aagcattatt aaaacataaa gacactatcg ttgaaatcaa cttttctgat 240

ttatacactg gtagattgaa tactgaaatt cctcaatctt tagagtattt gttaccagca 300

ttgtcgaaat tgccaaattt gaaattgac aacttgagtg acaatgcitt tggattgcaa 360

actattgac caattgaagc ttacttggcc aaagctgttt ccatcgagca ttgtatttg 420

tcaacaatg gtatgggtcc atttgcgtgg tcaagaattg gaggatcttt gttaagtta 480

gctaaggcta agaaagcaga aggaaaggag tcttgaaaa catttatttg tggtagaac 540

agattggaaa atggttctgt taactatita tctgttgggt taagaaatca caaggattg 600

gaagtggta gattgtatca aaatggtatt agacctgctg gtatttctaa attggttgag 660

caaggtttat ctaacaacaa aaaattaaaa gtgcttgatt tgcaagacaa taccatcaact 720

accagaggag ctattcacat tgcagaatca ttatctaact ggccactttt ggttgagttg 780

aatcctaacg attccttatt gaagaacaaa ggttctttga aattagtcga agccttccat 840

gctggagatg aaaaaccgca attaatacc ttgaaattac aatataatga gttagaacaa 900

gatagtttaa gagttttggc tgatgcaatt gccagtaaatt taccacaatt gaagttcttg 960

gaattgaacg gtaatatgatt tgaagaggat tccgaacata tcgataaaat caatggaatc 1020

ttcgaagaaa gaggctatgg cgaaatagat gaattggatg aattagaaga gcttgatagt 1080

gaagaagaag aagatgacga ggatgacgaa ggagaagacg acacattaga ggaagacctt 1140

gatttgacac aattagaaga agaattggct ggagtttctt tggaagacaa agatggtaac 1200

gtggatgaaa ttgccgaaga attatccaaa actcatatta aatag 1245

<210> 115

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: X82260.1

<400> 115

atggcctcgg aagacattgc caagctggca gagacacttg ccaagactca ggtggccggg 60

ggacagctga gtttcaaagg caagagcctc aaactcaaca ctgcagaaga tgctaaagat 120

gtgattaaag agattgaaga ctttgacagc ttggaggctc tgcgtctgga aggcaacaca 180

gtgggcgtgg aagcagccag ggtcatgcc aaggccttag agaagaagtc ggagttgaag 240

cgctgccact ggagtgacat gttcacggga aggctgcgga ccgagatccc accagccctg 300

atctcactag gggaaggact catcacagct ggggctcagc tggaggagct ggacttaagc 360

gacaacgcat tcgggcccga cgggtgtgca ggcttcgagg ccctgctcaa gagctcagcc 420

tgcttcccc tgcaggaact caagctcaac aactgtggca tgggcattgg cggcggcaag 480

atcctggctg cagctctgac cgaatgtcac cggaaatcca gtgccaagg caagcctctg 540

gccctgaagg tclttgtggc tggcagaaac cgtctggaga atgatggcgc cactgccttg 600

gcagaagctt ttaggtcat cgggaccctg gaggaggtcc acatgccaca gaatgggatc 660

aaccaccctg gcatcactgc cctggcccag gcttcgctg tcaacccct gctgcgggtc 720

atcaacctga atgacaacac cttcactgag aagggcgccc tggccatggc cgagaccttg 780

aagacctgac ggcaggtgga ggtgattaat ttggggact gcctggtgcg ctccaagggt 840

gcagttgcca ttgcagatgc catccgccc ggctgccc agctaaagga gctgaacttg 900

tcattctgig aaatcaagag ggatgtgcc ctggctgtg ctgaggccat ggagacaaa 960

gctgagctgg agaagctgga cctgaatggc aacaccctgg gagaagaagg ctgtgaacag 1020

cttcaggagg tgctggaggg cttaacatg gccaaagtgc tggcgtccct cagtgtgac 1080

gaggacgagg aggaggagga ggaaggagaa gaggaagaag aggaagcaga agaagaggag 1140
gaggaagatg aggaagagga ggaagaagag gaggaggagg aggaagaaga gcctcagcag 1200
cgagggcagg gagagaagtc agccacgccc tcacggaaga ttctggaccc taacactggg 1260
gagccagctc ccgtgctgtc ctccccacct cctgcagacg totccacctt cctggctttt 1320
ccctctccag agaagctcct gcgcctaggg cccaagagct ccgtgctgat agcccagcag 1380
actgacacgt ctgaccccgga gaagggtgtc tctgccttcc taaaggtgtc atctgtgttc 1440
ltagctgaaa ctgaaatcaa atagaaggac gaagctactg tgaggaiggc agtgcaggat 1500
gcagtagatg ccctgatgca gaaggcttc aactcctcgt ccttcaactc caacaccttc 1560
ctcaccaggc tctcgtgca catgggtctg ctcaagagtg aagacaaggt caaggccatt 1620
gccaacctgt acggccccct gatggcgctg aaccacatgg tgcagcagga ctatttcccc 1680
aaggcccttg caccctgtct gctggcgctc gtgaccaagc ccaacagcgc cctggaatcc 1740
tgctccttg cccgccacag tctgctgcag acgctgtaca aggtctag 1788

<210> 116

<211> 1140

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: AAB67337.1

<400> 116

atgtccttc aagcattcac ttcagtacat ccgaatcgg caacatctga tgtgaatgtt 60
accattgaca ctttcgttgc taagttaaaa agaagacaag tgcaagggtc atacgccatc 120
gccttgaaa ctttacaact gttaatgcga lltatctcig cagcicgltg gaaccatgtt 180
aatgacctta ttgaacaaat cagagattta ggtaatagtc tagaaaaagc tcacctact 240
gctttcagtt gcggtaacgt aattagaaga atactggctg ttttgaggga tgaagtagaa 300
gaagacacta tgagcacaac tgtcacatcc acatccgttg ctgaaccttt gatttcctct 360
atgtttaatt tattacagaa accggagcaa cctcatcaga atagaaaaaa tagttcaggg 420

agctctagta tgaaaaccaa gactgattac cgtcaagtag ccattcaggg tatcaaggat 480
 cttatagatg agataaaaa cattgatgaa ggtattcagc aaattgctat tgatttgatt 540
 cacgatcatg agattttatt aactcccaca cctgattcaa aaaccgtatt aaaatttctg 600
 attactgctc gcgaacgtag taatagaaca ttacgggtt tagttacaga ggggttcct 660
 aataacacca agaatgcaca tgagttgcc aaaaattag cacagcaca catagaaacc 720
 ctagtagtcc cagactcagc tgttttgc ttaatgtccc gtgtgggtaa ggttattatc 780
 ggcactaaag ccgttttgc caatgggggg actatctcgt caaattcagg tgtatcatcc 840
 gtttggaat gcgcccaga attagaacc cctgtattg ctgttcagg ttgtataag 900
 ctttctctc tatatccgtt cgacgtagag aagttgtcg aatttggtg gtccaacgt 960
 atattacctt gaatgatcc aagaaaaaga ttagatacag ttaatcaat taccgattat 1020
 gtccgcctg aaaatattga tatctacatt acaaacgtc gtgggttcaa tccaagtatt 1080
 atatacgtt ttgcgtggga taattacaag caaattgatg tgcatttga taaaataag 1140

<210> 117

<211> 1098

<212> DNA

<213> Candida albicans

<400> 117

atgtcgaaat tgctactcc tgaaattcta gcgctcatag acccagtgg gtctagtgtg 60
 aaacgtcatc agcttggtga tgataaggag atagcattaa caattgccca gttgtgatg 120
 aaagtcatat cagcagcaag atggtctaata acatattgatt taattgaatt gataagacaa 180
 gttggtgtta tattaccga agcatatcct agaaaagtca ttccaggaaa tattgtgaga 240
 agagtgttag cttaatacgt tgatgaaacc gaaactgaaa ctgagacaga gactgaacaa 300
 acagataaca tccaatgat gagcttatg ttagtttat tggcaacaca taacaaaat 360
 gaaactataa aggaacaaac acaattacaa ctgaagaaac aaacaagcga tatgagagcc 420
 ataattatac aagggttag agatttagtt gatgaaatt ccaatgttaa tgatgggatt 480
 gaaactatgg cggttgattt gattcatgac gatgaaatat tattaactcc aaccctaatt 540

tcggaaacag tgcaacattt tttaatcaaa gcaagattga aaagaaaatt cacagtagtt 600
gttactgaaa actatccaaa cgacatcaag gcagcccaca agtttgtaaa gacactagct 660
gaacacaaca tcgaaacaat tttaattcca gacacaacaa ttatgcagt gatgtcaaga 720
gttgggaaag ttataatagg tactaatgct gtatttgcca atgggtggctg ttgtcagat 780
tcaggtgttg ccaatgtagt tgaatgtgcc aaagaacaca gaacacctgt gttgtctgtg 840
gcagggttat tcaaatatc tccattgtat ccatttaca gaaacgattt gattgaagta 900
ggaaactccg ggaagggttt gaactacgac gatttgaat tggtaaaaa tgttgatgtt 960
gtgactaatc ctttgaaga ttatatacct cctcaacata tcgacatttt tatgaccaat 1020
attggagggt ttctccttc atttatttat agaattgttt tggataatta taaagctgaa 1080
gacaacaaac ttgaataa 1098

<210> 118
<211> 1450
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GENBANK Accession Number: L40395.1

<220>
<221> misc_feature
<222> (1367)..(1367)
<223> n is unknown

<400> 118
aaaaagggtt cggagtgtc agagaggatc gagagcttcg tggagaccct gacgcggggt 60
ggtgggccgc gcagggtccga ggaaatggtc gggagaccct aggggtgctg cgccagatca 120
tcacggacca ccgatggaga aacgcggggg agctgatgga gctgatccgc agagagggca 180
ggaggatgac ggccgctcag cctccgaga ccaccgtggg caacatggtg cggagagtgc 240
tcaagaltat cggggaggag tatggagact ccatggacgc agcgacggag agtgcacgc 300
aggagtccct ggacaaactg ttgacayccg gaggcctaaa cgaggatttc agcttcatt 360

atgsccaact ccagccaac atcattgagg cgattaatga gctgctagt gagctggaag 420
ggacaatgga gaacattgca gccaggctc tggagcacat tcactccaat gaggtgatca 480
tgaccattgg ctctcccgga acagtagagg ccttctcaa agaggctgcc cgaagagga 540
aattccatgt cattgtagca gagtgtgctc cttctgccca gggcatgaa atggctgtga 600
attgtccaa agcaggatt gagacaactg tcagtactga tgctgccatt ttgccgta 660
tgtcaagagt caacaagggtg atcattggca ccgaagacca tcctggccaa tggggccctg 720
agagctgtga caggaactca cactctggca ctggcagcaa aacaccattc caccctc 780
atcgtctgt gcacctatgt tcaaacttc tcacagttc cccaatgaag rrgmcycatw 840
wmataagttt ggtggctcct gaagaagtc tgccattcac agaaggggam atyctggaga 900
aggtcagcgt gcattgycct gtgttgact acgytcccc agagtcawt accctcttta 960
gcgtgatctc caacattggt gggaatgcac ctcttacct ctaccgctg atgagtgaac 1020
tctaccatcc tgatgawcat gtttatgac cgaccacagc tgcctaagc agattgctta 1080
ggcagataca gawtgaagag gagacttgag tgttgctgct gaagcacatc cttgcaatgt 1140
gggagtgac aggagtcac cwaaaaaaaaa aatccttgat actgttgctt gccttttag 1200
tcaccccgta acaagggcac acatmcagca ytgtgtctg ccttcagat ctaacagag 1260
cagcagggtc taactgttg attkggags ctctagtga cctggtgcg tctgtgtcag 1320
gaacttaaac ttctggctc agtagtgtgk taaacataac rctgwanacc ttactggat 1380
acagatttt gtcagaaat ggctatgaca cttttctag gctctacaa taaaarccac 1440
ttgaaggctc 1450

<210> 119

<211> 720

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA97221.1

<400> 119

atgtcaagac tagaaatata ctgccagaa gggctacgtc tcgalggacg tcgalggaat 60
gaactccgcc gtttgaaag ttccatcaac acacatccgc acgtgcaga cggttcatcc 120
tacatggaac aaggaataca caaaattatc actcttgta aaggtccaaa agagccaaga 180
ttgaaatctc aaatggatac ctcaaaggct ttattgaacg tatcggtaaa cattacaaaa 240
ttctccaat tcgaaagaag taaalcaagc cacaagaatg aaaggcgtgt tcttgagata 300
caaacctccc tggtaggat gttgagaag aatgtcatgc tgaatatcta cccagaaca 360
gttatcgata tcgagatcca tgccttgag caagatggcg gtattatggg atctttaatc 420
aacggtatta cctcgcctt aatagatgcc ggtatatcaa tgtcgatta cataagtgt 480
atatccgtcg ggctgtacga tactaccca ttattagata ccaattcatt agaagaaaat 540
gctatgagta cagtgcact aggtgtgta gggaagtcag aaaaacttc tctttatg 600
gtggaagaca aaatccgtt agataggta gagaacgttc ttgccatcgg catgcaggt 660
gctcataggg taagagattt gatggatgaa gaactgagga aacatgctca gaaaagagtc 720

<210> 120

<211> 723

<212> DNA

<213> Candida albicans

<400> 120

atggaattat attcacctga gggacttaga atagacggaa gaagatggaa cgaattgcgt 60
agattgaaat gccgtatcaa caticatcca aatcatcgg atggtcctc atatgtcgaa 120
caaggttaata ccaaagtgat gtgcacagta caaggacaa tagaaccagc attaagatct 180
caacaacatt cagaacgagc aaatatagaa gtgaattga atattgctag ttttcaact 240
tttgaaagga aaaaacgaag tagaaatgaa agaagattag ttgaacttaa aactacttta 300
gaaaaaacat ttgaagaaag tgttatgata aatttatatc caagaacaaa tattgttata 360
aatgttcaag tattatgcca ggtatgtggg atgttagctg cagttatcaa ctctattaca 420
ttagcacica ttgacgtcgg tatalcaatg tatgattatg tgagtgggtg atcttgtgga 480
ttatatgatc aaacaccatt attagatgta aataacttag aagaacacga tatgattgt 540

ttaacagltg gtgtlattgg taaaagttag aaattggcat taatgttgtt agaagataaa 600
 atgccattgg atagattgga atcagtattg tcaattggta ttgctggaag tcataaaata 660
 agagaattaa tggatcaaga agtgaggang catggaatta ttagggcttc taaaatgcaa 720
 taa 723

<210> 121
 <211> 840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Human GENBANK Accession Number: AK000598.1

<400> 121
 agagagcgga cctggcggcc gggcagcatg gcggggctgg agctcttgc ggaccagggc 60
 taccgggtgg acgggcggcg cgccggggag ctgcgcaaga tccaggcgcg gatgggcgtg 120
 ttgcgcagg ctgacggctc ggcttacatt gagcaggga acaccaaggc actggctgtg 180
 gtctacggcc cgcacgagat ccggggctcc cgggctcgag ccctgccgga cagggcccta 240
 gtgaactgtc aatatagttc agcgacctc agcacagggt agcgcaagcg acggccacat 300
 ggggaccgtg agtctgtga gatgggcctg cagctccgcc agactttcga agcagccatc 360
 ctcacacagc tgcaccacg ctcccagatt gatatctatg tgcagggtgct acaggcagat 420
 ggtgggacct atgcagcttg tgtgaatgca gccacgctgg cagtgtgga tgccgggata 480
 cccatgagag actttgtgtg tgcgtgtca gctggcttcg tggacggcac agccctggcg 540
 gacctcagcc atgtggagga agcagctggt ggccccagc tggccctggc cctgctgcca 600
 gccacaggac agattgcgct gcttgagatg gatccccggc tgcacgagga ccacctggag 660
 cgggtgttgg aggctgtgtc ccaggctgcc cgagatgtgc acaccctctt agatcgagtg 720
 gtccggcagc atgtgcgtga ggctctatc ttgtggggg actgaccacc cagccacca 780
 tgtccagaat aaaacccccc tctgccaca caaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840

<210> 122
 <211> 2340
 <212> DNA
 <213> *Saccharomyces cerevisiae*
 <220>
 <221> misc_feature
 <223> GENBANK Accession Number: A46417

<400> 122
 atgtccggtt tctttcgtc taattacgaa tacgatgtag ccagttcttc atccgaagaa 60
 gactctttat ctctgtctga agaagatttg ttaagctctt cctcctciga gtctgaattg 120
 gaccaagaat ctgacgactc cttttcaat gaaagtgaag gtgaaagtga agctgatgta 180
 gactctgatg attctgatgc aaagccttat ggtcctgact ggttcaagaa atctgagttc 240
 agaaaacaag gtggagggtc aaataaatt ttgaaaagct ctaactatga ttccagtgat 300
 gaagaatccg atgaagaaga tggcaagaag gtagtcaagt ctgccaaga aaaactattg 360
 gatgaaatgc aagacgttta taataagatc tctcaagctg agaactctga tgactggttg 420
 actatttcta atgagtttga ttgatctcg cgtctcttag ttagggctca acaacaaaac 480
 tgggggactc caaatatttt catcaagggtt gttgcccaag tggaggacgc tgtgaataat 540
 acacaacaag ctgatttgaa gaataaagct gttgcaagag ctataacac tacaagcaa 600
 agagtcaaga aagtttctag agaaaatgaa gactcaatgg ctaaattcag aaatgatcct 660
 gaatcatttg ataaggaacc aaccgcagat ttggataatt ctgctaattg attcacaatt 720
 tcttctctc aaggcaatga ccaagcggta caagaagatt tcttactag attacaaaca 780
 ataattgact caagaggtaa gaagactgtc aatcaacaat ccttgatttc tactttggag 840
 gagliattaa ctgtagctga aaaaccatat gaattcalaa tggcttattt gactttgatt 900
 ccatcaagat tcatgcctc agctaacctt tcttaccac caattgatca atggaaatct 960
 tcatcaacg atattagtaa attattgtct atttagacc agacaattga cacctaccaa 1020
 gttaatgaat ttgtgatcc aatcgatttc attgaagatg aacctaaaga agattctgat 1080
 ggtgtcaaga ggattctggg ttccatttct tcatttggtg aaagattaga tgacgaattc 1140

atgaaatccc tgttaaacaat cgaicctcat tccagtgatt attgatccg ttaagggat 1200
 gaacaatcaa tctataattt gatcctaaga actcaattgt acttgaagc gactttgaaa 1260
 gatgaacacg acctagaaaag agcattgaca cgtccattcg tcaagagatt ggalcatac 1320
 tactataaat ccgaaaattt gataaaaatt atggaaactg ctgcttgaa tatcatacct 1380
 gctcaattca aatctaaatt tactcaaaa gaccagctcg attctgctga ttatgtcgac 1440
 aatttaatag acggattatc gacaatctta tccaagcaaa acaacattgc tgttcaaaa 1500
 cgtgctatit talacaacat ttactacact gcattaaaca aagatticca aactgctaaa 1560
 gatatgttac taactcecca agttcaaaca aatatcaacc aattcgattc atccctaaa 1620
 attttattca acagggttgt tgttcaattg ggtctatccg cctttaaatt atgtttgatt 1680
 gaagaatgic atcaaatttt gaatgatctt ctgtcaagtt ctcacttaag agaaattttg 1740
 ggccaacaat cctacacag aatatctctc aattctagta acaatgcttc agctgatgag 1800
 cgtgctagac aatgtttgcc atatcaccaa cacatcaatc tcgatttaac cgatgtcgtc 1860
 ticttaacat gttccttatt gatcgaaatt ccaagaatga ctgccttcta ttccgggtatt 1920
 aagggtcaaga gaattcctta ctctccaaaa tccattcgtc gttccttaga acattacgac 1980
 aagttaagtt tccaagggtc accagaaaact ttaagagatt atgtcttgtt tgetgcaaaa 2040
 tcaatgcaaa aaggttaactg gagagactct gttaaatact taagagaaat aaaatcttgg 2100
 gctttattac caaacatgga aacgggtgtg aatagttaa cggaaagagt acaagttgaa 2160
 tcttgaaga ctatttctt ttcttcaag aggttctatt caagttttc tgttgctaaa 2220
 ctagccgaat tatttgatct tccagaaaat aagggtggtg aagttttgca atctgttatc 2280
 gcagaattgg aaatcccagc caaattaac gacgagaaga ccatctttgt tgtcgaag 2340

<210> 123

<211> 2099

<212> DNA

<213> Candida albicans

<400> 123

atgtctcggt tttttgttc aggatacact tctgactctt ctctgaaga ggaggattta 60

ttgagtactt cigaagaaga gttattatct tcttctgatg aaggagaaga caacgaafca 120
 gatagttcat tttttggtga agatgatgat gaacagaag aatctagttc tgatgatgaa 180
 gatggctgac catctggtcc agcatatctt ttaaagaaat catttttaa aggagctgga 240
 ggagatgatt ctgacagtga tagtgatgat gaaggctgta aagttgttaa atcagctaaa 300
 gataaattat tagatgatat gaaatcttca attgaaatta taaattccaa caaatataat 360
 aacaattgga gtatagtctt aggtgaattt gataagttg gtagattttt gattagatgt 420
 aatcaaacca atttgggtac accaaaattt tatattaaat tgttgactag tttagataac 480
 tccataactg aaactagtaa taatgaaaga gatgataaaa cattaaaagc tgatgaagcc 540
 agagctttca atactttgag acaagaattt aaaaaacaaa taagagaatt ccaagtttat 600
 tatgatttgt ataaggaaaa tccagaagaa ttgatgaaa atgaagatga accattagaa 660
 tctgttcaag ctggtcttaa cgataatgtt aaaaatgaag ctgataatc taatgttggt 720
 gctcttgct caaacagagt attgagtcct atttccata ctttgaaaac tatttccgaa 780
 agtcgttgga aaaagaatg tgataaattg gaacaaattg ctactttgga aaaattatta 840
 gaagcaaag ttctaaaag ttaccattt gaattgattt ctatttatca gatgttatta 900
 tcagttgat ttgatgctc atctaataa gcctttatgc ctttgaaca atggcaaaag 960
 aatgaacacg atttaggtaa attattggat ttgttgaag ctaattgtga tacttatcaa 1020
 gtttctgaat tgggttcaac tactgatgat attgatattg aaccagttgc taatgcccaa 1080
 ggtgttaaag ttatttctcg atcaatcact tcttctattg atagattgga cgaatgaattg 1140
 accaaatctt tacaacatac tgaccacat tctattgaat atgttgaag attgaaggat 1200
 gaaagtacta ttacaattt gattgttaga ggtcaagcat atgttgaatc cataactcca 1260
 gaagatgca agtataatc tgaacaattg gcaagaattg ttttgagaag attggaacac 1320
 atttattata aaccaaaca attgattaaa gctaataag aagaagcttg gcgtaatat 1380
 gaatacaatt catctattgt cagtaaaggt tcttcagttg atgaagttat tgatcaattg 1440
 acggaatttt taaaaagca acaaaaaaac aaaacttatg ggaacatgc tatactattc 1500
 tccatttatt attatgctgt caatagtcaa tatgaaaagg ctaaagaatt atttttgaga 1560

tctcaatttt atagtaacat caattctgct gaattcttct tacaagtcca atataatcgt 1620
 gctttagttc aattagggtt aagtgccttt agagcaggta gtattgaaga atctcataaa 1680
 attttgaatg aaattgtcaa ttctcaaaga tctaaagaat tattgggtca aggtttcaat 1740
 tctaaattcc ccaatcaagc tactgttttg gaaagacaaa aattattacc attccatcaa 1800
 catattaatt tggaattait ggaatgtgta ttatgactt gtctttait aattgaaatt 1860
 ccaactttgg ctgctattgc taataatcat aaggattcaa aacgtaaaaa tgcttcattg 1920
 aaatctttca aaagtaaatt ggatttccat gatagacaat tttcactgg tccaccagaa 1980
 agtattaaag atcatattgt ggtgatgaaa ttactaaatt ggaagaagca atggtaaaa 2040
 tgaacaaaga atataaaatc gctaaagaac gtcttaaccc accatcaaat cgtcgttga 2099

<210> 124

<211> 2898

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: U46025.1

<400> 124

tgactcgagg gctcagctgg tccggccgta gcacctccgc gccgtcgcca tgcgcgggtt 60
 ttaccacc ggttcggaca gcgagtcga gtcgtccttg tccggggagg agctcgtcac 120
 caaacctgtc ggaggcaact atggcaaaca gccattgttg ctgagcgagg atgaagaaga 180
 taccaagaga gttgtccgca gtgccaagga caagaggttt gaggagctga ccaaccttat 240
 ccggaccatc cgtaatgcca tgaagattcg tgatgtcacc aagtgcctgg aagagtttga 300
 gtccttgga aaagcatatg ggaaggccaa aagcattgtg gacaagaag gtgtccccg 360
 gttctatc cgcaccttg ctgacctaga ggactatctt aatgagcttt gggaagataa 420
 ggaagggaag aagaagatga acaagaacaa tgccaaggct ctgagcacct tgcgtcagaa 480
 gatccgaaaa tacaaccgtg atttcagtc ccatacaca agctacaagc agaaccocga 540
 gcagtcgag gatgaagatg ctgagaaaaa tgaaggaggat tcagaaggct cttcagatga 600

ggatgaggat gaggacggag tcagtgtgc aactttctg aagaagaaat cagaagctcc 660
ttctggggag agtcgcaagt tcctcaaaaa gatggatgat gaagatgagg actcagaaga 720
ttccgaagat gatgaagact gggacacagg ttccacatct tccgattccg actcagagga 780
ggaagaaggg aaacaaaccg cgctggcctc aagatttctt aaaaaggcac ccaccacaga 840
tgaggacaag aaggcagccg agaagaaacg ggaggacaaa gctaagaaga agcaccgacag 900
gaaatccaag cgcttgatg agggaggagga ggacaatgaa ggcggggagt gggaagggt 960
ccggggcgga gtgccgttg ttaaggagaa gccaaaaatg ttgccaagg gaactgagat 1020
cacccatgct gttgttatca agaaactgaa tgagatccta caggcacgag gcaagaagg 1080
aactgatcgt gctgccaga ttgagctgct gcaactgctg gttcagattg cagcggaaaa 1140
caacctggga gagggcgta ttgtcaagat caagttaac atcatgcct ctctctatga 1200
ctacaacccc aacctggcaa cctacatgaa gccagagatg tgggggaagt gcctggactg 1260
calcaatgag ctgatggata tcctgttgc aaatccaac attttgtg gagagaatat 1320
tctggaagag agtgagaacc tgcacaacgc tgaccagcca ctgcgtgtcc gtggtgcat 1380
cctaactctg gtggaacgaa tggatgaaga attaccaa ataatgcaa atactgaccc 1440
tcactccaa gactacgtgg agcactgaa ggatgaggcc caggtgtgtg ccatcatga 1500
gcgtgtcag cgctacctg aggagaagg cactaccgag gaggtctgcc gcactacct 1560
gctgcgcatc ctgcacacct actacaagt ttattacaag gccatcagc gacagctgac 1620
ccgcctgag ggctcctcaa agtctgagca agaccaggca gaaaatgagg gcgaggactc 1680
ggctgtgtg atggagagac tgtgcaagta catctacgcc aaggaccgca cagaccgat 1740
ccgcacatgt gccatcctt gccacatcta ccacatgct ctgcactgc gctggtacca 1800
ggcccgac ctcatgctca tgagccacti gcaggacaac attcagatg cagaccgcc 1860
agtgcagatc ctttacaacc gcacatggt gcagctgggc atctgtgcct tccgcaagg 1920
cctgaccaag gacgcacaca acgcctgct ggacatccag tcgagtggcc gagccaagga 1980
gccttgggc cagggcctgc tgctgcgag cctgcaggag cgcaaccagg agcaggagaa 2040
ggtggagcgg cgccgtcagg tcccttcca cctgcacatc aacctggagc tgctggagt 2100

tgtctacctg tgtctgccca tgctcctgga gatccccctac atggccgccc atgagagcga 2160
 tgcgcccgga cgcatgatca gcaagcagtt ccaccaccag ctgcgcgtgg gcgagcgaca 2220
 gcccctgctg ggtccccctg agtccatgcg ggaacatgtg gtcgctgcct ccaaggccat 2280
 gaagatgggt gactggaaga cctgtcacag tttatcatc aatgagaaga tgaatgggaa 2340
 agtgtgggac ctttccccg aggctgacaa agtccgcacc atgctggtta ggaagatcca 2400
 ggaagagtca ctgaggacct acctcttcac ctacagcagt gtctatgact ccatcagcat 2460
 ggagacgctg tcagacatgt ttgagctgga tctgcccact gtgcactcca tcatcagcaa 2520
 aatgatcatt aatgaggagc tgatggcctc cctggaccag ccaacacaga cagtggatgat 2580
 gcaccgcact gagccccactg cccagcagaa cctggctctg cagctggccg agaagctggg 2640
 cagcctggtg gagaacaacg aacgggtgtt tgaccacaag cagggcacct acgggggcta 2700
 ctccgagac cagaaggacg gctaccgcaa aaacgagggc tacatgcgcc gcggtggcta 2760
 ccgccagcag cagtcctcaga cggcctactg agctctccac tctgtttccc gcctgggcca 2820
 tccaaccttg aagtctaaa ccacacctca gtcactaaag gtctglttaa agttgttctg 2880
 gttgattgct tgttgcca 2898

<210> 125

<211> 1020

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: AAC03225.1

<400> 125

atgtctgaac ttaatgcatt attaaaagat atcaacggct cgctcactgc gacatcagaa 60
 tccttgaga ggttgtctgg gatttatagt aattctgcga ccgatgagat tcctgaaagt 120
 aaccaactac atgagcatct attttacgac gctaagaagc ctgctgagaa agtatcgtg 180
 ctatccttaa aaaatgggag catgctaggg tacataaatt ctctaltgat gcltataggc 240
 aataggctag acgacgagtg caaagatcct tctgctatgg atgcacgtga acgctctatt 300

caacaccgtg tggattaga gcgtgggtt aaaccactag aaaaaagti ggcttaccaa 360
 ttggacaagc tgactagagc atatgtgaaa atggaaaagg aatataaaga cgctgagaag 420
 cgtgcactgg aaaaatctac cttagtgaat catagcggca acgacgatag cgaagatgat 480
 gagtctagtg aggatgaaat agcatacagg ccaaatacct ctggaattat caacacaaat 540
 aaaaaatcat cagcatacag ggtggaggaa acggctaagc aagaaaacgg ggaagaaaac 600
 gatgacaatg agactggcgt gtataacca ccaaagatta cggtgttct accaccgcaa 660
 caaacgcatt ttgaagatag attcgatgcc agagaacaca aagatcgtag taacaaatcg 720
 cgtatgcaag ccatggaaga atataataga gagtcatcgg accaaccgga ctggagtgca 780
 tctattggtg ctgacattgt gaaccatgga agaggcggta tcaaatttt gagagacaca 840
 gagaaggaa gtagagtcac ttcatcgaa gaagataatt ttaccagatt gaatattaca 900
 aataaagctg aaaaaggaa gcaaaagcaa cgagaaagaa atgcaaggat gaacgttacc 960
 ggtgggaag atttggat attcagctca aagaggaagc tggaagatag cacttcgaga 1020

<210> 126

<211> 1086

<212> DNA

<213> Candida albicans

<400> 126

atgtcaaagg tagacactgt attaaaggaa atcatctcgt ctaccaagtc aactgaagct 60
 tcagtgaag agttgatagc tttgtcaag gactcgtctt cccaacalcc agaattggtg 120
 cggaactlgt tagcaaaatc aaacctgctg ttgaagggg tatcgttgtt ggggttgaaa 180
 aacgaatcgt tgggtccta tatcaacaat atagtgttg ttgtttgtc tcatctagag 240
 cgtctagaaa gcgatctgga gacgggatcc agcgtgtcg aacgatcgt aattcaaagg 300
 gtgacattgg aaaaggcgt taaacctcta gaaaagaaac tcagttatca gttggataaa 360
 atgatcaggg catatggacg gatggaacaa gacgaaatca aagctgaaca gaagttaaac 420
 gatagaggaa gtggggagaa cgatgagaac gatgagaacg attctgagga agattcigaa 480
 gaagattctg aagacgactc tgaggacgac gaattggctt atagaccaga tgcacatcg 540

ttgctaaat tgacatggc caaaacaaa ctgaaacaa catcatcagc agtctctaca 600
 tcgaatgaaa aglatagacc accaaagata tcagcaatgg caccitcaac tgcagtaaag 660
 agccacgacc ttgatgcaa caccacgtcg tcaaagaacc gtaaattaca gagcatggaa 720
 gagtacttgc aagagcaaag tgatatgcca atgggtggagg catcgggtggg gtctacaatt 780
 gtggagcaig gaagagggtg tgtaaaaca cagcacgac gtaagaaaga acgagagata 840
 caaacgtatg aagaggataa tttgtcaga ctaccaacca gtcaacaaa gaaaagtgc 900
 aaggaaaaac aacgtgatat ccgtaataca ttgctgggtg aagactggc gatgttaat 960
 aataacaagg atgtgacccg tcaaggcaca tcgcgaaaga gaaaggcaac caccgttgg 1020
 gacaaagtca agaaaagaa gaatacttag atgtaagta gacgctgaca tttgctgca 1080
 gtatag 1086

<210> 127

<211> 1134

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: AL050003

<400> 127

gggggcttgg cgaagatggc ggcgctgggg gtgctggagt ccgacctgcc aagtccctg 60
 acacttctga aaaatctcca ggagcaagt atggctgtaa ctgcacaagt gaaatcactg 120
 acacaaaaag ttcaagctgg tgcctatcct acagaaaagg gtctcagctt cttggaagtg 180
 aaagaccagc tgctgctcat gtaccttatg gatttgacct acctcattct ggacaaagcc 240
 tcaggaggat ctcttcaggg acatgatgca gtttgagac tgggtggagt tcgcacggtt 300
 ttggaaaagc ttctgccctt ggacaaaag ctgaagtatc aaattgacaa gctgatcaag 360
 actgcagtga caggcagcct tagtgagaat gaccacttc gtttaagcc tcatcccagc 420
 aatatgatga gcaagttgag ctctgaggat gaggaggaag atgaagcaga agatgaccag 480
 tctgaggctt cagggaagaa atctgtgaag ggagtgtcta agaatatgt tctccacgc 540

ttggtccag tacattatga tgaacagaa gctgagcggg agaagaagcg tctagaacga 600
gccaagagac gggcattgag cagctctgtc attcgtgaac ttaaggagca gtactcagat 660
gctccagagg aaatccgtga tgctcggcat ccccatgtta cccgccagag tcaggaggac 720
caacacagga ttaactatga ggagagcatg atgggtcgtt tgagcgtcag taagcgagag 780
aaaggacggc gaaaacgagc aaatgtcatg agctcacaac ttcattccct tacacacttc 840
agtgacatca gtgctttgac agggggaact gttcatcttg atgaggatca gaatcctatt 900
aagaagcgga agaagatacc tcagaaaggt cggaagaaaa aaggccagtg aactgctggg 960
acttaggtga tcagggtgcaa ggtggggagt acaaattgag tctctttgga ttigccattc 1020
tgggtctcac caagccctgt agtatctctt ccatactggg caataatctc cttaggtggg 1080
cgtggggcca agaagactcg ttctgcctgg gatagagctc aaaggagact gtag 1134

<210> 128

<211> 666

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA95901.1

<400> 128

atgagcgcta ccgaatcttc atctatattc acattgagtc acaactcaaa cctacaagat 60
atcttgccg ccaatgccaa atgggcctcc cagatgaaca acatacagcc aactttgttc 120
ccagatcaca atgcgaaggg ccagtcacct cacactcttt tcatcggttg ctccgattcg 180
cgttacaacg aaaactgttt aggtgtcttg cccggcgaag tgtcacttg gaaaaatgtt 240
gtaacatat gtcactcaga ggatttaact tgaaggcca ctttagagtt tgccattatt 300
tgtctaaaag ttaacaaagt tattatttgt ggccacactg attgtgtgg tataaagaca 360
tgtttaacta accaaaggga agccttacaa aaagttaact gttctcatct gtacaagtac 420
ttagacgata ttgacacat gtaccatgaa gagtcacaaa attgatcca ttgaaaacg 480
caacgtgaaa aatctcatta cctgtcgcac tgtaacgtca aaaggcagtt taataggatt 540

attgaaaacc ctactgtgca aactgctgta caaaatggag aattacaggt atacggtctg 600
 ctttacaacg tagaggacgg tctactgcaa acagttagca cttacacaaa agttacccca 660
 aaatag 666

<210> 129
 <211> 846
 <212> DNA
 <213> *Candida albicans*

<400> 129
 atgggttagag aaaatatattt gaaatatcaa ttggaacatg atcalgaatc tgactctgtt 60
 actgaaaaag atcaatcatt attacttgat aataataaca acctaacgg gatgaataat 120
 accattaaaa ctcatccggg acgtgttagt tcaggaaatc ataataattt tccttcact 180
 ttatcttcag aatctacatt acaagatttt ttaaataata ataaattttt tgttgattcc 240
 ataaaacata atcatggttaa tcaaatattt galltgaatg gicaaggta atctccat 300
 acattatgga taggggtgtag tgattcaaga gcagggtgac aatgtttagc tacattacca 360
 ggagaaatat ttgttcatag aaacattgct aatatagtca atgccaatga tataagtagt 420
 caaggggtta tacaatttgc tattgatgta taaaagtga aaaaaatcat tgtttgtggt 480
 cactactgatt gtgggtggtat ttgggcatca ttatcaaaga aaaaaattgg tgggtgttta 540
 gatttatggt taaatccagt tagacatatt cgtgctgcta atttaaaatt attagaagaa 600
 tataatcaag atcctaaatt aaaggccaaa aaattggctg aattaaatgt cattctctct 660
 gtaacagcat tgaaaagaca tcttagtgct agtgttgcat taaagaagaa tgaaattgaa 720
 gtttggggga tgttatatga tgtggcaact ggttatattt ctcaagtaga gattcctcaa 780
 gatgaatttg aggatttatt ccatgttcat gatgaacatg atgaagaaga atataaccct 840
 cattga 846

<210> 130
 <211> 840
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: BAA09266.1

<400> 130

atgaaagcta ggaatcgca gagaaaagcg ggcagtaaac caaatcttat ccagtctaaa 60

ttgcaagtta ataattggtc gaaatcgaat aaaatagtc agtgtgataa atgtgagatg 120

tcatactct cgacatcaat agaagatcg gccatccacg agaaatacca cactttacag 180

ctgcatggac gtaaatggc gccgaattgg ggttctatag tatacacaga gcgaaccat 240

lcaaggacgg tgcattatc aagatcgaca gggacaataa cgccattgaa ctctcacct 300

ttgaaaaaa gtagtcgctc tattacccat caggaggaga agattgtata tgtgagacca 360

gataagtcga atggtgaagt ccgagccatg acggagataa tgacactagt gaataacgag 420

ctgaatgcgc cacacgatga gaatgtcatt tggaacagta ccacagaaga aaaaggcaaa 480

gcgtttgtat acataagaaa tgacagggcg gtcggaataa taattataga gaacctttat 540

gggggcaatg gtaaacatc tagtcgtgga cgttgatgg ttatgattc tagaagattg 600

gtacagaatg tgtacccga tttaagatt ggcatatcga gaatttgggt gtgcaggaca 660

gcaaggaagt tgggtatcgc aaccaaatg attgacgtg caagagaaaa tattgtttac 720

ggtgaagtta ttctaggtta ccaggtagca tggtcgcaac ccacagacag cgggtgaaaa 780

ctggctagca aatacaacgg cattatgcat aaatcaggca agttactatt gccggtatac 840

<210> 131

<211> 843

<212> DNA

<213> Candida albicans

<400> 131

atgggtcca ttaatttca aaaacctcaa aaaatccaat caattcttgc attaccatct 60

aatttcaaaa aaattacttg ttcaaatgt gatatgacat ataatcccca tatatctcaa 120

gataaattac tacataacaa ataccacaca aatttcatca atggaatacc ctggaattat 180

aaaactgata atgatgtttt aataattgag aattttacat tagttgaaac cccgaaattg 240

aattccacgg ggaaatcatt aaagctgaca aaaacgcgic agacatttaa aggttctata 300
atttgataa ataatccaa caaacgacat atacaaaaag tggaactact attaacatg 360
gtgaatcaag agttgaatgc tagtcaagat tcaggacaat ggaagaaacc tgaatttgat 420
agaagtaaag catttgat aataatagac agtaaggcca ttggattatg cacaacagat 480
acaattcaac ctgalcaagg aaggtggatg atacataaaa cacaatctat agtacctaata 540
cagattaata aaaatgttgt cattggaatt tcaagaatat ggataagtcg gaaatggaga 600
caatatggat taggtaaaaa acttttaaat gttgtttga aaaattctat ttacagtgtg 660
caattattga agaatcaagt tgcctttagt caaccaagtt ttagtggtgg aatgttgca 720
aaatcattca atggggtgaa acataaaagt ggtgaaatgt tgttaccgt atatattgaa 780
tgatccttic aggtttcgg aggcggcggg gattatgggt gtacatattt gtatatttt 840
tgt 843

<210> 132

<211> 1800

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA85003.1

<400> 132

atgctaaatg gggaagactt ttagagcat aatgatalcc tatcgtctcc ggcaaaaagc 60
aggaatgtaa ccccaaaaag ggttgacca catggagaaa gaaactgag aagaattcat 120
tcatcaaaga agaatttgtt ggaaagaatc tcgctttag gcaacgaaag gaaaaataca 180
tctccagatc cggcactcaa acctaaaacg ccaagtaaag ctccccgtaa acgtggaaga 240
ccaagaaaga tacaggaaga attaactgat aggatcaaga aggatgagaa agatacaatt 300
tcctctaaga aaaagaggaa attggacaaa gatacatcag gtaatgtcaa tgaggaaagc 360
aagacttcta acaacaagca ggtgatggaa aagacgggga taaaagagaa aagagaacgc 420
gaaaaatac aggtagcgac cacaacatat gaagataatg tgactccaca aactgatgat 480

aattttgtat caaatccacc cgagccacca gaacctgcaa caccatctaa gaagtcttta 540
accactaatc atgattttac ttcgccccta aagcaaatta taatgaataa tttaaagaa 600
tataaagact caacctcccc aggtanatta accttgagta gaaattttac tccaaccct 660
gtaccgaaaa ataaaaagct ctaccaaact tcggaacca agtcagcaag ctctttttg 720
gatacttttg aaggatatit cgaccaaaga aaaattgtca gaactaatgc gaagtcaagg 780
cacaccatgt caatggcacc tgacgttacc agagaagagt ttccctagt atcaaacitt 840
ttcaacgaaa atttcaaaa acgtcccagg caaaagtat ttgaaattca gaaaaaatg 900
ttccccagt attggttga attgactcaa ggattctcct tattatttta tgggttaggt 960
tcgaaacgtia atttttgga agagtttgcc attgactact tgtctccgaa aatcgcgta 1020
tcgcaactgg cttatgagaa tgaattacaa caaaacaac ctgtaaattc catcccatgc 1080
cttattttaa atggttacaa ccctagctgt aactatcgtg acglttcaa agagattacc 1140
gactttttg tccccgtga gtigacaaga agcgaaacta agtactgggg caatcatgtg 1200
attttgcaga tccaaaagat gattgatttc taaaaaatc aacctttaga tatcaaat 1260
atactttag tgataatct ggatggctc agcataagga aaacactti tcagacgatg 1320
ctaagcttcc tctccgtcat cagacaaatc gccatagtcg cctctacaga ccacattac 1380
gctccgtccc tctgggacaa catgaaggcc caaaactaca actttgtctt tcatgatatt 1440
tcgaattttg aaccgtcgac agtcagatct acgttccaag atgtgatgaa gatgggtaaa 1500
agcgatacca gcagtgtgc tgaagggtgc aaatacgtct tacaatcact tactgtgaac 1560
tccaagaaga tgtataagtt gcttattgaa acacaaatgc agaataaggg gaatctatcc 1620
gctaacacag gtctaagcg tggactcaa agaactggag tagaacttaa actttcaac 1680
catctctgtg ccgtgatit tattgcttci aatgagatag ctctaaggic gatgcttaga 1740
gaattcatag aacataaaat ggccaacata actaagaaca attctggaat ggaaattatt 1800

<210> 133

<211> 2130

<212> DNA

<213> Candida albicans

<400> 133

atgtcacact caaatgctct accaaatagt ccattccggt cacctaaaa acaacgtatg 60
 gaggtcatag gaccactcaa tgcgtctcgt ttctctttt cgccggtaaa gacacctcct 120
 catgggagag ctggtctatc atctccagag aaaagattag tcaaagacct tgacaagtcg 180
 gcgagaaaa gagccaacaa tagcttatat aaccgaltaa tggatgagta tctggacaca 240
 gatgattatt tggatgaaca agataggata ttggccgaca gaattatcaa acagtcgagg 300
 ggagaacccg acgaagtcaa ttatggcagc gacgtggaat tggaaattga tctaactcag 360
 cagagacgaa cccgaagaag agaaaagaaa gttgtttact cgagcgatag tagcaacgaa 420
 tatgaggata caggaatgcc agaagaatct tcaagcgagg aagaagaggc agatgatgat 480
 gatggcaatg tggagtttgt ttatggacca ccaaagaaa gaaaacgtc gttatcaagc 540
 tcaccacca cagtcaagcc tactgtgcgc cgaaccaagc gaggtagacc aagcaagagt 600
 gacgtgttc tgggtcaaat caaaaglata ttccatcaag atgacgtgtt gttcagtaca 660
 gatagaaaa cgttcacacc gactaaacca accgcagcga aaaaaccagt cagcaattat 720
 ttgacatcta ttttgatca aaattcgaat agaagcaagg tgccaagtct aagtgggaatt 780
 cccaaatcaa ccaacacgca tgaagagaag aaaacgttg tccgcttcc tattccacc 840
 ctcatgctg acggaaatat cactgacaag gactacatct ccaatactt tgatggagtt 900
 gaccctgcaa agttcaaaga aggcaggttt gtggacgaaa aagtatttta cttagaaggg 960
 ccagaaggat actttgaaca gcaactacc agagttaaac aaagtggcaa ctctttaaca 1020
 gcattggcac ccagattga glacaaagat ttgccaggt tagtaaagtt gggcgacaac 1080
 ctcatgttc aacgcaaacg ccacctttc gaattgcaca agtatatcta tcaccagtgg 1140
 tgtttgaaa tgtcacaagg gttaatttg aatttctac ggtcggatc caaatcgat 1200
 ctactccgag attttgccac aaactattti ggcatctggt gggaaaatgt ggtacacgcc 1260
 gatttgcaa aggttttggg ggtaacggt ttaacccta gcatcaatat caaaaaacta 1320
 attctgaaa tcgcttccat ccttttgcca aacgaactgt acccaaaaca tatagctgga 1380
 acggttcct tttgtgttga ttatctaaac aaccatagac tgcctgttg aagtatcggt 1440

ttccataaac ccaaaatcctt gttgattatt cacaatcttg atggggaagt ttttagagta 1500
 gacaagacac agacgctttt gtcgcaatta atgacactac cagaagtatg ggccatgtca 1560
 tctaccgacc acatcaatgc atcattgtta tgggacctgt ccaaagttaa aaactgaaat 1620
 ttcatctggc ataattcac aacatatgcc acttaccac gagaaacatc ttccgagac 1680
 gtgataaglt taggcaaatc caaaaaatit gtgggtggcc ttggtgcaa gtagtcttg 1740
 cgctcgctta ccgacaatca ccgaaacctc taccgcgagc tattgattgc acaattggat 1800
 aaaatggaga aagctgtccc atctgcttct ggaagagtgg gtttgaagg taatccaag 1860
 gttgctgttg acctaaaaag cctatacaat acatgtttgg acgagttcat tactccaac 1920
 gagatgaact ttagaacatt cttaaaagag tatgttgagc ataaatgtg tcagctagta 1980
 aaagatcctt caggagtga gaaggtattc altccgtca cacaagaaga gatacaaac 2040
 atatatagc aagaattga tgtatagtgg gtaccctaca cgtatcgga acttgaaaaa 2100
 ctctgaaaa ccglttaaa tactctataa 2130

<210> 134

<211> 2640

<212> DNA

<213> *Homo sapiens*

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: GI:4433811

<400> 134

ggcggaatt actgaaatt ggcctttccc gttggggccg aaggtacctt cctgcggcg 60
 gcgactcagc ggggtgtcgt tcggccggcg tgacgcagcc ggatcggcg cagacggaaa 120
 cctagcggtg actgtatctg aattttgcag ctgcagaatg ttagtacct taaaagggtg 180
 gcaacaatga glaaaccaga attaaaggaa gacaagatgc tggagggtca ctttgtggga 240
 gatgatgatg ttctaatca cattctagat agagaaggag gagctaaatt gaagaaggag 300
 cgagcgcagc ttttggtcaa ccccaaaaaa ataataaaga agccagaata tgattggag 360
 gaagatgacc aggaggtctt aaaagatcag aactatgttg aaattatggg aagagatgtt 420

caagaatcat tgaaaaatgg ctctgctaca ggtgggtggaa ataaagttaa ttcttttcag 480
aatagaaaac actctgaaaa gatggctaaa ttagcttcag aactagcaaa aacaccacaa 540
aaaagtgttt cattcagtti gaagaatgat cctgagatta cgataaacgt tcctcaaagt 600
agcaagggcc attctgcttc agacaagggt caaccgaaga acaatgacaa aagtgaattt 660
ctgtcaacag caccctgtag tctaagaaaa agattaatag ttccaaggtc tcattctgac 720
agtgaagcg aatattctgc ttccaactca gaggatgatg aaggggttgc acaggaacat 780
gaagaggaca ctaatgcagt cataatcagc caaaagattc aagctcagaa tagagtagti 840
tcagctcctg ttggcaaaga aacaccttct aagagaatga aaagagataa aacaagtgc 900
ttagtagaag aatatttga agctcacagc agttcaaaag tttaacctc tgatagaaca 960
ctgcagaagc taaagagagc taaactggat cagcaaactt tgcgtaactt attgagcaag 1020
gtttccctt cctttctgc cgaacttaaa caactaaac aacagtatga aaaattattt 1080
cataaatgga tctgcaatt acaccttggg ttcaacattg tgcattatgg ttgggttct 1140
aagagagatt tactagaaag gtttgaacc actatgctgc aagattccat tcacgttgc 1200
atcaatggct tcttctctgg aatcagtggt aaatcagtc tgaattctat aacagaagaa 1260
gtctcgtac atatgggtac ttccgcagt atactggatc agctagactg gatagtaaac 1320
aaatttaaag aagattcttc tttagaactc ttcttctca tcacaattt ggatagccag 1380
atgttgagag gagagaagag ccagcaaac attggtcagt tgcattctt gcataacatt 1440
taccttatag catccattga ccacctcaat gctccttca tgtgggatca tgcaaagcag 1500
agtcttita actggctctg gtatgaaact actacataca gtcccttatac tgaagaaacc 1560
tcctatgaga actctcttct ggtaaagcag tctggatccc tgccacttag ctcccttact 1620
catgtcttac gaagccttac ccctaatgca aggggaattt tcaggctact aataaaatac 1680
cagctggaca accaggataa ccttcttac attggccttt ctttcaaga ttttaccag 1740
cagtgtcggg aggcattcct cgtcaatagt gatctgacac tccgggcccc gttaactgaa 1800
tttagggacc acangcttat aagaacaaag aagggaactg atggagtaga gtatttatta 1860
attcctgttg ataatggaac attgactgat ttcttgaaa aggaagaaga ggaggcttga 1920

agcttctctt tattcttgaa tcctccatgg aagggttgta ccccagctgc cactcctcta 1980
 gttgaaagtg ttgtgtttac atctgacatt aaattattt tccagcatac aagatttaaa 2040
 ttgggaagg gggggatgct ctcaattaga actttttgat cagcctggct ggtaccgtct 2100
 agtactatgc agcggctctc aagttggaga aaatgtgcct ttcattcatt acctctctgg 2160
 agactcttg ctggaatgaa cagtgtgctc agggactatt tggaactgga tgttttgaa 2220
 ttattttata cttagagata ttctgaattt ttgagggcc tttaacact ccccagctg 2280
 attgtttgca agtgtgtttg ttccagagtg tggaagtata aagacatggg catcacgtaa 2340
 attggtttg ttgtctatc tgtgtgtcag aaccaacgag tgtaatggag agggcaggtc 2400
 atctcttatt gtttctaaaa caacttaaaa ggtgtagatt gggaagaggt gagtgatcca 2460
 gctttctcct ttggattga ggctatgtac ttggtggggg caggggaggg aatatattat 2520
 aatactatc agttgggata atgggaaaaa cagagtatat agggatctta cccagcctag 2580
 aaagcacagg aacaatcgt catatattg gaacagttat tgtctgtgcc atgacctca 2640

<210> 135

<211> 617

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA85114.1

<400> 135

ccaatcaag gatgacca gagaacaaat caatttgaa tatgttatca gtgattgata 60
 gaaaagaaca agaattgaaa gcaaaagaag aaaaacagca aagagaagct caggaacgtg 120
 aaaaacagaa aattatgta gagagcgcaa tgacgctgag aaacalaact aacatcaaaa 180
 ctactctcc agtagagta cttaatgagg gtaaaataag gctagaagac ccaatggatt 240
 ttgaatctca attgatctat cccgcattaa ttatgtacc cagcaagat gaatttgatt 300
 tttaggtga agtaagtga ttaactactg tgcaagaact tgttgaccta gttttggaag 360
 ggccgcaaga acgcttcaaa aaagaaggta aggaaaact cacaccaag aaagtgttg 420

tgttcatgga aacaaaggca ggtggttga ttaaagctgg taagaaactg acatttcacg 480
 atatcttgaa gaaagagtcg ccagatgtac cattgttcga taacgcttg aaaatatata 540
 ttgtgccaaa ggtagaaagt gaagggtgga ttccaagtg ggataagcaa aaagccttag 600
 aaagaagatc tgtgtga 617

<210> 136
 <211> 1173
 <212> DNA
 <213> Candida albicans

<400> 136
 atgtccaaaa tagagccagt cactgaaaa gaagaagaat acgtttccga atgggataga 60
 agaagatatg ttcccaaacg aggtgaacct gaattacctc cccaattatc agaattctct 120
 aacaagacca cagacgaggt tattgaggaa ttgaatagat tgccattttt tatgacaaag 180
 ttatagtaaa ctgatggaga tggcggagaa aatgtaaact tggagcact taaaagtttg 240
 gcataagaag gtgatcctga cgaaattgcc tcaaatttca aaaatcaggg gaataattgt 300
 tacaatttta aaaaatacaa agalgcaatt atattitata cgaaagggtct tgaagtaaac 360
 tgtgacgtgg acgcaatcaa ttacgcatfa tacttgaatc gtgctgcttg taacttgag 420
 ttgaaaaatt accgtcgggt cattgaagat tgtaagaaag tattaatgct tgatgagaag 480
 aatattaagg ctgtttccg ttacaggaaag gcattctttg caattgaaaa atacgatgaa 540
 gcaatcaaag tgcttgaata cggcttaaat atagaaccag aaaacaaaga ttacagaaa 600
 ttattacagc aagtcaaaa gaggcaagaa actttagctc aaataaaagc taaaaggca 660
 caagaagagg aacaagagcg gttgaaaaat atcgtgttg agaattctat aaaattaaga 720
 cacattgaaa tagtgaagtc clcatctcct ccagaagtct tgaagactgc caagatacga 780
 ttggaagacc ccaaagatta tcagtcacaa ttaatatcc ctgctatgat actatacccc 840
 accaccgatg aatttgactt tattgcagaa ataagcgaat taactactcc ttggaattg 900
 ctagagalgg tattaaatag acctagggaa tggttgatg atccaaaaca caaggatttc 960
 aatgtcaaaa aattggaatg ctttatggaa actgaatcig gtgggttgat taaagtgggc 1020

aagaaaattg aagttaacaa tgctttgatg aatgaaaaac ctaaggcacc attgtttgat 1080

aacgccttaa gactttatgt cgttccaaaa ttagacgtcg ccaaattggac atctgaatgg 1140

aataaagaaa ccgccttggc agctcgtaaa tag 1173

<210> 137

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: NM_004623.1

<400> 137

ctgggacccg ggctggaagg cagggcatca gctatggaac aacctgggca ggatcccacc 60

tcagacgacg tcatggactc gttcctggaa aagttccaga gccagcctta ccgtggcggc 120

tttcatgagg accagtggga gaaggaattt gaaaaggccc ccctatttat gtcgagagcg 180

ccatcagaaa ttgatccag ggagaatcct gacttggcct gtctccagtc aattattttt 240

gatgaggagc gtttccaga agaacaggcc aagacctata aagatgaggg caatgattac 300

tttaaagaaa aagactacaa gaaagctgta atttcalaca ctgaaggctt aaagaagaaa 360

tgtgcagatc ctgattgaa tgctgtcctt tataccaacc gggcagcagc acagtactat 420

ctgggcaatt ttggttctgc tctcaatgat gtgacagctg ccagaaagct aaaaccctgc 480

cacctcaaag caataataag aggtgcctta tgccatctgg aactgalaca ctttgccgag 540

gccgtgaact ggtgtgatga gggactgcaa atagatgcca aagagaagaa gcttctggaa 600

atgaggggcta aagcagacaa gctgaagcga attgaacaga gggatgtgag gaaagccaac 660

ttgaaagaaa agaaggagag gaatcagaat gaggctttac tccaggccat caaggctagg 720

aatatcaggc tctcagaagc tgcctgtgag gatgaagatt cagcctcaga aggtctagg 780

gagcttttcc tggatggact cagcactgag aacccccatg gagccaggct gactctagat 840

ggccaggggca ggctgagctg gcctgtgctc ttctgtacc cagagtatgc ccagtcggac 900

ttcatctctg cttttcatga ggactccagg ttattgatc atctaattgt gatgtttggt 960

gaaacacctt cttgggacct agagcaaaaa tattgcctga taatttggag gtctactttg 1020
 aggatgagga cagggcagaa ctataccggg tgcctgccaa gagcaccttg ctacaggttc 1080
 tacagcacca gaggtacttt gtaaaagccc tgacaccagc atttttggc tgtgtaggat 1140
 cctctccttt ttgaagaat ttctccggg ggagaaaggt gtaccagata cgatgactaa 1200
 gccagggccc ctggatctcc tcccttacc tctctgtctg ggaacctagc acacctgaat 1260
 cagctggaca tactgtctga gtccagtct tctttccgt caccctgggg atagtccttc 1320
 ctggcatcgt ggtgggggag gagcctctgg ctccctaaa ctgcagctct ctggctggtc 1380
 ttactttcc tcagttgata taaaactctg gtcttgcca tgatgtcctt ggattccatc 1440
 gctaaaggga ccatctctg cagttaccac agcaactgac ttgagcggca cctggtctgt 1500
 ggagatggac tcaggatcca gtgacatgat tctgaacttt tgtggagttt gacaccttag 1560
 agaagctacc cctcaactg cacatctaca cacaacaaa caatgcatag gattccaagg 1620
 ctttaaagct gagagaccct ggcccaagt tatttcatgc gcacagaggg aagccatgtg 1680
 ggggtgtcga agatgccttg aggtgaaatg ggggcaggaa agccacatct tgctctgcat 1740
 ttataagac cgtacaaact cagatccttg gtaccctaa aaagattgcc aattttcttc 1800
 atctttgcca tatggaggac tgtgacagac ttggacagt ggccctctga gttcctctgc 1860
 agttttgaca tttaggattt tgtgtctttt aaactggaaa atctctagc atgttgggtt 1920
 gttacagagt atattttgt ctgcagctgt ttgtgcccc attcctaaga ggagtttata 1980
 catcctgaaa aaaaaaaaaa aaaaa 2005

<210> 138

<211> 504

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> misc_feature

<223> GENBANK Accession Number: CAA98815.1

<400> 138

atgtctacta ttccctcaga aatcatcaat tggacatct taaatgaaat tatatctatg 60

galgacgatg attccgattt ttctaaaggt ctaattatc aatttatcga ccaggcaca 120
 acaacttttg ctcaaatgca acgacagctg gacggtgaaa aaaatcttac cgaattagac 180
 aatctgggcc attttttaa gggttcttct gctgcattag gcttacaag aatgcctgg 240
 gtttgtaaa gaattcaaaa ctgggaaga aaaatggaac atttctccc caacaagacc 300
 gaattggtca acactctgag cgataaatcg attattaatg gaatcaatat tgatgaagat 360
 gacgaggaaa taaagataca agtggacgat aaagacgaaa attccatata tctcatcttg 420
 atagcaaaag ctttgaacca gtctaggttg gagttcaaac tggcgagaat tgagttatct 480
 aaatattaca acacaaacct ataa 504

<210> 139
 <211> 555
 <212> DNA
 <213> Candida albicans

<400> 139
 atgtcagaag ataaattaca aaaattaca gactcaggac ttgtcactg ggcagtgtt 60
 agtgaatatg tgaccatgga cgaggatgaa gaagggttt ccaatcact agtagaagtc 120
 ttgttagcc aagtgaaga aacattgaa gaaatlgata aatatttaa ggaaaagaat 180
 ttggagaaat tgatcatgctc gggtcattt ttgaaaggat ctgctgctgc ttgggggttg 240
 accaaaattt caaatcaatg cgaacgaatt caaaactatg gccataagat caactttgac 300
 aattttcaat tggaagatat aaaaactaaa ggcgattcgg ccgtaagtgc ggaaaatgtg 360
 gccgttaatg atggtgaaac taatccagaa aatggatcca atggcaacga aacaagtaat 420
 aacaaaacaa atactagcaa tataccgat gaatcaagcg atgacttttg gatagcatta 480
 attgaggatg cattagccaa ggcgagagat ggattcgacc aatctagaag agcattggac 540
 gaatattacg aatag 555

<210> 140
 <211> 7992
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: Z15005.1

<400> 140

atggcggagg aaggagccgt ggccgtctgc gtgcgagtc gcccgctgaa cagcagagaa 60
 gaatcacttg gagaaactgc ccaagtttac tggaaaactg acaataatgt cattatcaa 120
 gttgatggaa gtaaatccct caattttgat cgtgtcttc atggtaatga aactaccaa 180
 aatgtgtatg aagaaatagc agcaccaatc atcgattctg ccatacaagg ctacaatggt 240
 actatatctt cctatggaca gactgcttca ggaaaaacat ataccatgat gggttcagaa 300
 gatcatttgg gagttatacc cagggaatt catgacattt tccaaaaat taagaagttt 360
 cctgataggg aatttctctt acgtgtatct tacatggaaa tatacaatga aaccattaca 420
 gatttactct gtggcactca aaaaatgaaa ccittaatta ttcgagaaga tgcaatagg 480
 aatgtgtatg ttgtgtatct cacagaagaa gttgtatata catcagaaat ggctttgaaa 540
 tggattacaa agggagaaaa gagcaggcat tatggagaaa caaaaatgaa tcaagaagc 600
 agtcgttctc ataccatctt taggatgatt ttggaaagca gagagaaggg tgaaccttct 660
 aattgtgaag gatctgttaa ggtatcccat ttgaatttgg ttgatcttgc aggcagtga 720
 agagctgctc aaacaggcgc tgcaggtgtg cggctcaagg aaggctgtaa tataaatcga 780
 agcttattta ttttgggaca agtgatcaag aaacttagtg atggacaagt tgggtgttct 840
 ataaattatc gagatagcaa gtaaacacga attcttcaga attccttggg aggaaatcca 900
 aagacacgta ttatctgcac aattactcca gtatcttttg atgaaactct tactgtctc 960
 cagtttgcca gtactgctaa atatatgaag aatactcctt atgttaatga ggtatcaact 1020
 gatgaagctc tctgaaaag gtatagaaaa gaaataatgg atcttaaaaa acaattagag 1080
 gaggttctt tagagacgcg ggctcaggca atggaaaaag accaattggc ccaacttttg 1140
 gaagaaaaag atttgcctca gaaagtacag aatgagaaaa ttgaaaactt aacacggatg 1200
 ctggtgacct ctcttcctc cacgttgcaa caggaattaa aggctaaaag aaaacgaaga 1260
 gttacttggg gccttggcaa aattaacaaa atgaagaact caaatatgc agatcaattt 1320

aatalaccaaa caaatalaac aacaaaaaca cataagcttt ctataaattt attacgagaa 1380
attgatgaat ctgtctgttc agagtctgat gtttcagta acactcttga tacattaagt 1440
gagatagaat ggaatccagc aacaaagcta ctaaatcagg agaatataga aagtgagttg 1500
aactcacttc gtgctgacta tgataatctg gtattagact atgaacaact acgaacagaa 1560
aaagaagaaa tggaaattgaa attaaaagaa aagaatgatt tggatgaatt tgaggctcta 1620
gaaagaaaaa ctaaaaaaga tcaagagatg caactaattc atgaaatttc gaacttaag 1680
aatttagtta agcatcgaga agtatataat caagatcttg agaatgaact cagttcaaaa 1740
gtagagctgc tttagaaaaa ggaagaccag attaagaagc tacaggaata catagactct 1800
caaaagctag aaaatataaa aatggacttg tcatactcat tggaaagcat tgaagaccca 1860
aaacaaatga agcagactct gtttgatgct gaaactgtag cccttgatgc caagagagaa 1920
tcagcctttc ttagaagtga aaatctggag ttgaaggaga aaatgaaaga acttgcaact 1980
acatacaagc aaatggaaaa tgatattcag ttatatcaaa gccaatgga ggcaaaaaag 2040
aaaatgcaag ttgatctgga gaaagaatta caatctgctt ttaatgagat aacaaaactc 2100
acctccctta tagatggcaa agttccaaaa gatttgcctt gtaatttga attggaagga 2160
aagattactg atcttcagaa agaactaaat aaagaagttg aagaaaatga agctttgcgg 2220
gaagaagtca ttttctttc agaattgaaa totttacctt ctgaagtaga aaggctgagg 2280
aaagagatac aagacaaatc tgaagagctc catataataa catcagaaaa agataaattg 2340
ttttctgaag tagttcataa ggagagtaga gttcaagggt tacttgaaga aattgggaaa 2400
acaaaagatg acctagcaac tacacagtcg aattataaaa gcactgatca agaattccaa 2460
aatttcaaaa cccctcatat ggactttgag caaaagtata agatggctct tgaggagaat 2520
gagagaatga atcaggaaat agttaatctc tctaaagaag cccaaaaatt tgattcgagt 2580
ttgggtgctt tgaagaccga gctttcttac aagaccaag aacttcagga gaaaacacgt 2640
gaggttcaag aaagactaaa tgagatggaa cagctgaagg aacaattaga aaatagagat 2700
tctccgctgc aaactgtaga aaggagagaa acactgattt ctgagaaact gcagcaaact 2760
ttagangaag taaaaacttt aactcaagaa aaagatgatc taaaacaact ccaagaaagc 2820

ttgcaaattg agagggacca actcaaaagt gatattcacg atactgttaa catgaatata 2880
 gatactcaag aacaattacg aaatgctctt gagtctctga aacaacatca agaaacaatt 2940
 aatacactaa aatcgaaaat ttctgaggaa gttccagga attgcatat ggaggaaaat 3000
 acaggagaaa ctaaagatga atttcagcaa aagatggttg gcatagataa aaaacaggat 3060
 ttggaagcta aaaatacca aacactaact gcagatgtta aggataatga gataattgag 3120
 caacaaagga agatatcttc ttaatacag gagaaaaatg aactccaaca aatgtagag 3180
 agtgttatag cagaaaagga acaattgaag actgacctaa aggaaaatat tgaatgacc 3240
 attgaaaacc aggaagaatt aagacttctt ggggatgaac taaaaagca acaagagata 3300
 gtgcacaag aaaagaacca tgccataaag aaagaaggag agctttctag gacctgtgac 3360
 agactggcag aagtgaaga aaaactaaag gaaaagagcc agcaactcca agaaaaacag 3420
 caacaacttc ttaatgtaca agaagagatg agtgagatgc agaaaaagat taatgaaata 3480
 gagaatttaa agaattgaatt aaagaacaaa gaattgacat tggaacatat ggaaacagag 3540
 aggcttgagt tggtcagaa acttaatgaa aattatgagg aagtgaatc tataaccaa 3600
 gaaagaaaag ttctaaagga attacagaag tcatitgaaa cagagagaga ccaccttaga 3660
 ggatatataa gagaaattga agctacaggc ctacaaacca aagaagaact aaaaattgct 3720
 catattcacc taaaagaaca ccaagaaact attgatgaac taagaagaag cgtatctgag 3780
 aagacagctc aaataataaa tactcaggac ttagaaaaat cccataccaa attacaagaa 3840
 gagatcccag tgcttcatga ggaacaagag ttactgccta atgtgaaaaa agtcagttag 3900
 actcaggaaa caatgaatga actggagtta ttaacagaac agtcacacac caaggactca 3960
 acaacactgg caagaataga aatggaaagg ctgaggtiga atgaaaaatt tcaagaaagi 4020
 caggaagaga taaatctct aaccaaggaa agagacaacc ttaaacgat aaaagaagcc 4080
 cttgaagtta aacatgacca gctgaaagaa catattagag aaactttggc taaatccag 4140
 gagtctcaaa gcaacaaga acagtcctta aatatgaaag aaaaagacaa tgaactacc 4200
 aaaaactgta gtgagatgga gcaattcaaa cccaagatt cagcactact aaggatagaa 4260
 atagaatgc tcggattgtc caaaagactt caagaaagtc atgatgaaat gaaatctgta 4320

gctaaggaga aagatgacct acagaggctg caagaagttc ttcaatctga aagtgaccag 4380
ctcaaagaaa acataaaaga aattgtagct aaacacctgg aaactgaaga ggaacttaaa 4440
gttgctcatt gttgcctgaa agaacaagag gaaactatta atgagttaag agtgaatctt 4500
tcagagaagg aaactgaaat atcaaccatt caaaagcagt tagaagcaat caatgataaa 4560
ttacagaaca agatccaaga gatttatgag aaagaggaaac aacttaatat aaaacaaatt 4620
agtggaggtc aggaaaacgt gaatgaactg aaacaattca aggagcatcg caaagccaag 4680
gattcagcac taaaaagtat agaaagtaag atgctcgagt tgaccaacag acttcaagaa 4740
agtcaagaag aaatacaaat tatgattaag gaaaaagagg aaatgaaaag agtacaggag 4800
gcccttcaga tagagagaga ccaactgaaa gaaaacacta aagaaattgt agctaaaatg 4860
aaagaatctc aagaaaaaga atatcagttt cttagatga cagctgtcaa tgagactcag 4920
gagaaaatgt gtgaaataga aacttgaag gagcaattg agaccagaa gttaaactg 4980
gaaaacatag aaacggagaa tataagggtg actcagatc tacatgaaaa ccttgaagaa 5040
atgagatctg taacaaaaga aagagatgac cttaggagtg tggaggagac tctcaaagta 5100
gagagagacc agtcaagga aaacctaga gaaactataa ctagagacct agaaaaacaa 5160
gaggagctaa aaattgttca catgcatctg aaggagcacc aagaaactat tgataaacta 5220
agagggattg tticagagaa aacaaatgaa atatcaata tgcaaaagga cttagaacac 5280
tcaaatgatg ccttaaaagc acaggatctg aaaatacaag aggaactaag aattgctcac 5340
atgcatctga aagagcagca ggaactatt gacaaactca gaggaattgt ttctgagaag 5400
acagataaac tatcaaatat gcaaaaagat ttagaaaatt caaatgctaa attacaagaa 5460
aagattcaag aacttaaggc aaatgaacat caacttatta cgttaaaaaa agatgtcaat 5520
gagacacaga aaaaagtgtc tgaatggag caactaaaga aacaaataaa agaccaaagc 5580
ttaactctga gtaaattaga aatagagaat ttaaattgg ctcaagaact tcatgaaaac 5640
cttgaagaaa tgaaatctgt aatgaaagaa agagataatc taagaagagt agaggagaca 5700
ctcaaactgg agagagacca actcaaggaa agcctgcaag aaaccaaagc tagagatctg 5760
gaaataaac aggaactaaa aactgctcgt atgctatcaa aagaacacaa agaaactgtt 5820

galaaactta gagaanaaat ttcagaaaag acaattcaaa ttccagacat tcaaaaggat 5880
 ttgataaat caaaagatga attacagaaa aagatccaag aacttcagaa aaaagaactt 5940
 caactgctta gaggtaaaga agatgtcaat atgagtcata aaaaaattaa tgaaatggaa 6000
 cagttgaaga agcaattga gccaaactat ctatgcaagt gtgagatgga taacttcag 6060
 ttgactaaga aacttcatga aagccttgaa gaaataagaa ttgtagctaa agaaagagat 6120
 gagctaagga ggataaaga atctctcaaa atggaaaagg accaattcat agcaacctta 6180
 agggaaatga tagctagaga ccgacagAAC caccaagtaa aacctgaaaa aaggttacta 6240
 agtgaaggac aacagcacct tatggaaagc ctgagagaaa agtgctctag aataaaagag 6300
 ctttgaaga gatactcaga gatggatgat cattatgagt gcttgaatag atgtctctt 6360
 gacttggaga aggaattga attccacaga atcatgaaga aactgaagta tgtgttaagc 6420
 tatgttaca aaataaaga agaacaacat gaatgcacata ataaattga aatggattt 6480
 attgaagaag tggaaaagca aaaggaattg ctaattaaaa tacagcacct tcaacaagat 6540
 tgtgatgtac catccagaga attaaggat ctcaaattga accagaatat ggatctacat 6600
 attgaggaaa ttctcaaga ttctcagaa agtgagtcc ctgcataaa gactgaattt 6660
 caacaagtac taagtaatag gaaagaaatg acacagtttt tggaagagtg gttaataact 6720
 cgttttgata tagaaaagct taaaatggc atccagaaag aaatgatag gatttgtcaa 6780
 gtgaataact tctttaataa cagaataatt gccataatga atgaatcaac agagtgtgag 6840
 gaaagaagtg ctaccatata caaagagtgg gaacaggacc tgaaatcact gaaagagaaa 6900
 aatgaaaaac tatttaaaaa ctaccaaca ttgaagactt ccttggtatc tgggtcccag 6960
 gttatccta ccacacaaga caataagaat cctcatgta catcaagagc tacacagtta 7020
 accacagaga aaattcgaga gctggaaaat tcaatgcatg aagctaaaga aagtgtatg 7080
 cataaggaaa gcaagattat aaagatgcag aaagaacttg aggtgactaa tgacataata 7140
 gcaaaacttc aagccaaagt tcatgaatca aataaatgcc ttgaaaaaac aaaagagaca 7200
 attcaagtac ttcaggacaa agttgcttta ggagctaagc calataaaga agaaattgaa 7260
 gatctcaaaa tgaagcittg gaaaatagac ctagagaaaa tgaaaaatgc caaagaattt 7320

gaaaaggaaa tcagtgtac aaaagccact gtagaatafc aaaaggaagt tataaggcta 7380
 ttgagagaaa atctcagaag aagtcaacag gcccaagata cctcagtgat atcagaacat 7440
 actgatcctc agccttcaaa taaaccctta acttgtggag gtggcagcgg cattgtacaa 7500
 aacacaaaag ctcttatitt gaaaagtga catataaggc tagaaaaaga aatttctaag 7560
 ttaaagcagc aaaatgaaca gctaataaaa caaaagaatg aattgttaag caataatcag 7620
 calctttcca atgagggtcaa aacttgaag gaaagaacct ttaaagaga ggctcacaaa 7680
 caagtaactt gtgagaattc tcaaagtct cctaaagtga ctggaacagc ttctaaaaag 7740
 aaacaaatta caccctctca atgcaaggaa cggaatttac aagatcctgt gccaaaggaa 7800
 tcacaaaat ctgtttttt tgatagccga tcaaagtctt taccatcacc tcatccagtt 7860
 cgctattttg ataactcaag tttaggcctt tgtccagagg tgcaaatgc aggagcagag 7920
 agtgtggatt ctgagccagg tccttggcac gcctcctcag gcaaggatgt gcctgagtgc 7980
 aaaactcagt ag 7992

<210> 141

<211> 282

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> misc_feature

<223> GENBANK Accession Number:AAB68435.1

<400> 141

atgtctttct taggtttcgg tgggtgtcag cctcaattat catctcaaca aaagattcaa 60

gctgcggaag ctgaactaga ttgtgtcaca gacatgttca ataaattggt taataactgt 120

tataaaaaat gtatcaatac ttcttatcc gaggtgagc tgaataagaa tgaatcttcg 180

tgcclagaca gatgtgtggc caaatatttt gagaccaatg ttcaagtcgg tgaaaacatg 240

cagaaaatgg gccaatcatt taacgcagcc ggtaagtttt ag 282

<210> 142

<211> 278

<212> DNA

<213> Candida albicans

<400> 142

atgtttggct taggtgggtac tactcctcaa atttcatttc aacaaaaact tcaagctgct 60

gaagctgaat tagatatggt tactggcatg ttcaatgctt tagttccca atgtcacacc 120

aaatgtatca acaaatcata taatgaagct gatatttcaa agcaagaatc tttatgtctt 180

gatagatgtg ttgccaataa ttttgaaacc aatgttcaag ttggtgaaaa tatgcaaaaa 240

ttaggtcaat ctgggtcaatt tatgggtaga agataaat 278

<210> 143

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human GENBANK Accession Number: NM_012456.1

<400> 143

ggagcctcac grgagcgkkg taacgttata gtaattgtca gaagtgggg tctccgtggg 60

cattgtgatc cgtcccaggc agtggattag gaggccagaa ggagatccct tccacgggtc 120

taggtgaga tggatcctct cagggcccaa cagctggctg cggagctgga ggtggagatg 180

atggccgata tgtacaacag aatgaccagt gcctgccacc ggaagtgtgt gcctcctcac 240

tacaaggaag cagagctctc caagggcgag tctgtgtgcc tggaccgatg tgtctctaag 300

tacctggaca tccatgagcg gatgggcaaa aagttgacag agttgtctat gcaggatgaa 360

gagctgatga agagggtgca gcagagctct gggcctgcat gaggtccctg tcagtataca 420

ccctgggggtg tacccacccc cttcccactt taataaacgt gctccctgtt ggggtgcatc 480

tgtgaagact gccaggccta ggctctctgt agagagcttt caagatcccg gagtggtagc 540

gctgtctcct ggtgaaggag tatttgtcac actggaatgt gactgtgtgt gtatgtatgt 600

gtatatatat atatatatat atatataaac aagttgttg acacctacaa aaaaaaaaa 658

<210> 144
<211> 1980
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> misc_feature
<223> GENBANK Accession Number: AAB64555.1

<400> 144
atgacaacgg aagatccaga ttcaaatcac ttaagttccg aaactggcat taaattggca 60
ttggacccga acttaattac attggcacta agttctaate caaactctag ccttcattca 120
ccaacgtctg atgaacccgt acctgaatct gcaggaaaag cagatactag tattcgacta 180
gaaggtagtg agttagagaa taaaactaag aaagacaatg ataagaactt aaaatttttg 240
aagaataaag attctctagt cagtaatcca cacgaaattt atggctccat gccgttggag 300
caattgatcc caatcatctt aagacagcgt ggtccaggct ttaaattcgt tgatttaaat 360
gaaaaagaat tgcaaatga gattaagcag cttggtagt atagtagtga cggtcataac 420
agcgagaaga aggacactga tggcgctgat gagaatgtac aaattggaga agatttcattg 480
gaagtggatt atgaagataa agataatcca gtggattcac gaaatgaaac agaccacaaa 540
acgaatgaaa atggcgagac ccatgataat attgaaacgg taatgacaca ggaacagttt 600
gttaaaagaa ggagggatat gctagagcat ataaatctgg ccatgaacga atcgtctttg 660
gctttggaat tcgtttcttt gctactgtcg agtggttaaag agtctacagg tatgtcatca 720
atgtcaccat ttcttaggaa agttgttaaa ccttctagtt taaacagtga taaaattcca 780
tatgttcac ctacaaaaaa agaataatc gagttggata tattgaataa gggatggaag 840
ttacaaagtt taaacgaatc taaagatctc ctacgcgcaa gtttaataa actgagttcc 900
atattacaga acgaacatga ctattggaat aagataatgc agagtattag caacaaggat 960
gttattttta agattaggga caggactagt ggtcaaaagc tgttggaat taagtatggt 1020
tacgaagact ctggatctac ctataagcat gacagaggta ttgctaataa aaggaataat 1080
atagaatcac aaaatttga ttgatcccc cacagtagtt cagtgttcaa aggactgat 1140

ttctacatt cagtaaagaa attcttaagg gttcgtatct tcacaaaaat cgaatcagaa 1200
 gatgattaca tattgagtgg cgaaagtgtg atggataggg atagtgaag tgaagaagct 1260
 gaaacgaaag atatcagaaa gcaaatccaa ctttgaaaa agatcatttt tgaanaagaa 1320
 ctgatgtacc aaataaagaa agaatgcgtt ttgttgattt cctatggtgt cagtattgaa 1380
 aacgaaaaca aggtataat tgaactacct aacgaaaaat ttgaaatcga gttgtgtcc 1440
 cttgacgatg actccattgt caatcatgaa caagacttac caaaaatcaa cgacaagaga 1500
 gcaaatttaa tgcttgtat gttgagacta ttattagtcg ttatatcaa gaaaacatta 1560
 cgtcgcagaa taagctcacc ccacggactg atcaattga atgttgacga tgatatctta 1620
 ataatacgtc ccattcttgg taaagttcgg ttgctaatt acaactgtt actaaaaaaa 1680
 atcataaagg attacgtgct cgatatagtt cctggctcaa gtataacaga aacggaagtt 1740
 gagagagaac aacctcaaga aaataaaaac attgatgatg aaaatataac taaattaaat 1800
 aaagagatcc gtgccttcga taaactattg aatataccta gacgtgaact caaaataaat 1860
 ctaccattaa ctgagcacia aagccctaatt ctaagtttaa tgctcgaaag tctaactat 1920
 tgtaacgcac tcattcacat caagttttca gctggtacgg aagccaacgc agtgccttt 1980

<210> 145

<211> 1849

<212> DNA

<213> Candida albicans

<400> 145

atgggtgaaa aacagtttaa catagaccta gagttaaag atactggtca tatagatcca 60
 ttcttacaag atgagtatgt ttgctticta actttattgg tattttgggt tctgttttt 120
 agtttactaa ccttgaccac gagataaatt gaaacttgag gaactaatc cacgaatttt 180
 attgaacgt aaatcatttt tgaatgtgac ggaggattct ttgagaaaag aaatagacaa 240
 ttcatgaag atttccgaag aggatgcttt agacactgaa gaaagtagag aggacacagt 300
 tgaagcagat caacaagaag tgttcaataa acacaagttt gaattatcga aaaatataaa 360
 caatgcactt aatgaaaccc aactttcctt agattttgta tccttattaa tatcttcagt 420

gaaaccaagt ttggcaaaat ctaccatttc accacacttg tcaaaatttg tcaaaccgac 480
 atctttaaat tcggatagat tgggtcaaga tagtaatgat aatcaagaga gtaaggctac 540
 tgattctttt ggacaaggat ggaaattgga gtcacttgga aagataaccg atcttttcag 600
 agaagctagt actaatttaa acgatcaagt tatcaagaa agacgatatt ggaatatgat 660
 aaatttggcg ctgccaacg acgaggttct atttcgaatg agggaccccc aaaataatgc 720
 tagagcaata ggagtgaat atgggtatgg agattcagga tcaaatttc acgaccaagg 780
 gttggcattg ttacgcaagg acaaccaaac aggagaaatc tcatttcacc ccatatcgtc 840
 aatcaacaat gctaaaattg tagaaaaagt ttcgagattt attagagtga aaattttgag 900
 ccaaatagat ggggactata tgcttacagg acagtcaatt tttaatttg attttgaaaa 960
 aagcaagcaa agcataatta atgacatga aaaggctaga ttctttttat ttgaggagga 1020
 ctgttttcat caattgatac gcgaggccaa attgttggta aactacaatg tgtcaatcat 1080
 atcgaataaa ataataattg aaatcaacaa cattattat gaaatagagt ctatcgtgta 1140
 tgalgagttg aatgaggagg aactagaaaa ctattaccag aatgtaaatg aatatccac 1200
 cttacacaat aaaaagtgtc agcttatttt aaactacttg aaacttatgc ttgttgta 1260
 ttacaatac aatctcaat tgaacagaa ggtccaaca gcattgacta aatggaagca 1320
 gagtaactcc catccttga ttttgcgtcc gttagtgggt aatatgaggc atgagttaa 1380
 ttgctaaat atgaagagtg ttttagatcg attaatgcac gctcatgaga gtgaacttc 1440
 ttattccaaa ctgatgtgg agaagtttat taacttagcc acaagaagca aaaagcaaaa 1500
 cccattccaa aagtcaattg aaaagccaat ttcaaagtc catttagttt tatgaacaa 1560
 aacctctaat atgttggacg tcaacataca attgacaact aatgagctgt ttgtcaatct 1620
 aatcatcaat atgacaatta ttgatttga aacagaagac gattttaaga acaatgcaa 1680
 tggtattaac gtctacagc ttgggttcag tgattcaat gaaatcgaag aatgcttgga 1740
 ttggtcgatc caaaatttg tataggacac aacattttct gattttaag aagtagagga 1800
 cttcctacat ttattgtcg ctgagtacat ccagcaaaag aagggtgaa 1849

<210> 146
 <211> 2760
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Human GENBANK Accession Number: AB015617.1

<400> 146
 atgtatggaa gtgcccgtc tgttgggaag gtggagccga gcagccagag ccctgggcgt 60
 tcaccaggc ttccacgtc ccctcgttg ggtcacgtc gaaccaacag tacgggaggg 120
 agttcggga gcagtgttg aggtggcagt gggaaaacc ttcaatga aaatataca 180
 tctttaatg ctgcctatg cacctctgc cctatgtatc taagtacca tgaatatgt 240
 ggttcagaa cacctaaaag caccatgaca ctggccgtt ctgggggacg tctgcctac 300
 ggtgttcgga tgactgctat gggtagtagc cccaatatag ctacagtggt ggttgctagt 360
 gacacatag catttggaga gcatcacct cctcctgtga gtatggcatc cactgtacct 420
 cactccctc gtcaggcgag agataacaca atcatggatc tgcagacaca gctgaaggaa 480
 gtattaagag aaaatgatc ctgcggaag gatgtggaag taaaggagag caaattgagt 540
 tctcaatga atagcatca gacctcttg agcccagagc tgaagaagga acgagccctg 600
 agaaaagatg aagcttcaa aatcaccatt tggaaagaa agtacagagt tgtacaggag 660
 gaaaaccagc acatgcagat gacaatccag gctctccagg atgaattgcg gatccagagg 720
 gacctgaatc agctgttca gcaggatagt agcagcagga ctggcgaacc ttgtgtagca 780
 gagctgacag aggagaactt tcaggagctt catgctgagc atgagcggca ggccaaagag 840
 ctgtttctc ttgaaagac attggaggaa atggagctgc gtattgagac tcaaaagcag 900
 accctaaatg ctgggatga atccattaag aagcttcttg aaatgttca gagcaaagga 960
 ctttctcca aggctaccga ggaagacat gagagaacaa gacgactggc agaggcagag 1020
 atgcacgtc atcacctaga aagcctttg gagcagaagg aaaaagagaa cagtatgtt 1080
 agagaggaga tgcacgaag gtttgagaat gctcctgatt ctgcaaac aaaagctctg 1140

caaactgtta ttgagatgaa ggalicaaaa alttcctcta tggagcgtgg gcltcgagac 1200
 ctggaagagg aaattcagat gctgaaatcg aatgggtgctt tgagtactga ggaaagggaa 1260
 gaagaaatga agcaaatgga agtgtatcgg agccattcta aatttatgaa aaataagatt 1320
 ggccagggtga aacaggagct gtccagaaag gacacagaac tactcgcctt gcagacaaag 1380
 ctagaacac tcacaaacca gtttcagat agtaaacagc acattgaagt gttgaaggag 1440
 tccttgactg ctaaggagca gagggctgcc atcctgcaga ctgagggtga tgctctccga 1500
 ttgcgtttgg aagagaagga aaccatgttg aataaaaaga caaaacaaat tcaggatatg 1560
 gctgaagaga aggggacaca agctggagag atacatgacc tcaaggacat gttggatgtg 1620
 aaggagcgga aggttaatgt tcttcagaag aagattgaaa atctcaaga gcagcttaga 1680
 gacaaggaaa agcagatgag cagcttgaaa gaacgggtca aatccttgca ggctgacacc 1740
 accaacactg acactgcctt gacaacttg gaggaggccc ttgcagagaa agagcggaca 1800
 attgaacgct taaaggagca gagggacaga gatgagcgag agaagcaaga ggaaattgat 1860
 aactacaaaa aagatcttaa agacttgaag gaaaaagtca gcctgttgca aggcgacctt 1920
 tcagagaaag aggcttact tttggaatcg aaagagcatg cttcttctt ggcatcctca 1980
 ggactgaaaa aggactcacg gcttaagaca ctagagattg ctttgagca gaagaaggag 2040
 gagtgtctga aaatggaatc acaattgaaa aaggcacatg aggcagcatt ggaagccaga 2100
 gccagtccag agatgagtga ccgaatacag cacttgaga gagagatcac caggtacaaa 2160
 gatgaatcta gcaaggccca ggcaagaatg gatcgactct tagaaatctt gaaggagggtg 2220
 gaaaatgaga agaattgaca agataagaag atagctgagt tggaaagtct cacctcaagg 2280
 caagtgaag accagaataa gaaggtagca aatctgaagc acaaggaaca ggtggaaaaa 2340
 aagaagagtg cacaaatgtt agaggaggcg cgacgacggg aggacaatct caacgacagc 2400
 tctcagcagc tacagggtga ggagtactg atggccatgg agaaggtaaa gcaggaacta 2460
 gaatccatga aagcaaagct gtctccacc cagcagcttc tggcagaaaa ggaaactcac 2520
 ttgactaatc ttggggcaga gagaaggaaa cacttagagg aagtcttga gatgaagcaa 2580
 gaagctcttc tggctgccat tagtgaaaaa gacgccaata tagctctctt ggagctttcg 2640

tcctctaaga agaagacca agaggaagtg gctgccctga agcgggagaa ggaicgtctg 2700

gtacagcagc ttaagcagca gacgcaaat cgaatgaagc taalggccga caactacgag 2760